

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problems Mailbox.**



SEQUENCE LISTING

- <110> Pompejus, Markus
Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor
Lee, Heung-Shick
Kim, Hyung-Joon
- <120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
RESISTANCE AND TOLERANCE PROTEINS
- <130> BGI-124CP
- <140> 09/603,208
<141> 2000-06-23
- <150> 60/141031
<151> June 25, 1999
- <150> 60/142692
<151> July 1, 1999
- <150> 60/151214
<151> August 27, 1999
- <150> DE 19930429.7
<151> July 1, 1999
- <150> DE 19931413.6
<151> July 8, 1999
- <150> DE 19931457.8
<151> July 8, 1999
- <150> DE 19931541.8
<151> July 8, 1999
- <150> DE 19932209.0
<151> July 9, 1999
- <150> DE 19932230.9
<151> July 9, 1999
- <150> DE 19932914.1
<151> July 14, 1999
- <150> DE 19940764.9
<151> August 27, 1999
- <150> DE 19941382.7
<151> August 31, 1999
- <160> 306
- <210> 1
<211> 1566
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)...(1543)

<223> RXA01524

<400> 1

```

ttgtggcact ctttagtagt tttttctcat agctcagttt cgcaacttta gagaactcta 60

gaaactgagc ttcattgctgt gaaaggcctt ttctccattc atg gat tcc caa att 115
                                         Met Asp Ser Gln Ile
                                         1           5

aat act cag acc tct ccg gca gct gcg aag ctg cct agg gag gtc gtt 163
Asn Thr Gln Thr Ser Pro Ala Ala Ala Lys Leu Pro Arg Glu Val Val
                        10                        15                        20

gtt gtt ctt tcg atc ctc gtg gtt tcc gcg atg atc atg att ctt aat 211
Val Val Leu Ser Ile Leu Val Val Ser Ala Met Ile Met Ile Leu Asn
                        25                        30                        35

gaa acc att ctg tcg gtt gcg ttg cct tcc atc atg gaa gat ttc tcc 259
Glu Thr Ile Leu Ser Val Ala Leu Pro Ser Ile Met Glu Asp Phe Ser
                        40                        45                        50

gtg cct gaa act act gca cag tgg ttg acc act ggc ttt atg ttg acg 307
Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr Gly Phe Met Leu Thr
                        55                        60                        65

atg gca gtg gtg att cca act act ggt tat ctg ctt gat cgt ttt tcc 355
Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu Leu Asp Arg Phe Ser
                        70                        75                        80                        85

act aag acg atc ttt gtt act gcg ttg ttg ttc ttt acg gtt ggt acg 403
Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe Phe Thr Val Gly Thr
                        90                        95                        100

ttg act gcg gcg ttg gct cca acg ttt gcg gtg ctg ctt ggt gct cgt 451
Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val Leu Leu Gly Ala Arg
                        105                        110                        115

atc gtt cag gcg gtt ggt act gcg ctg gtg atg cct ttg ctg atg acg 499
Ile Val Gln Ala Val Gly Thr Ala Leu Val Met Pro Leu Leu Met Thr
                        120                        125                        130

gtt acg ttg acg gtg gtt cct gcg gag cgt cgt ggt tcg atg atg ggc 547
Val Thr Leu Thr Val Val Pro Ala Glu Arg Arg Gly Ser Met Met Gly
                        135                        140                        145

att att tcc atc gtg att tct gtt gcg ccg gcg ctt ggt cct acg ttg 595
Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala Leu Gly Pro Thr Leu
                        150                        155                        160                        165

tct ggt gtc att ctt aac tct ttg acc tgg cac tgg ttg ttt tgg atg 643
Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His Trp Leu Phe Trp Met
                        170                        175                        180

atg ctt ccg atc gtt gtt atc gct ttg gta att ggt ttc ttc ttg atc 691
Met Leu Pro Ile Val Val Ile Ala Leu Val Ile Gly Phe Phe Leu Ile
                        185                        190                        195

aaa aat atc ggc gaa acc aag atc acc cca ctg gat gtt ctg tct gtc 739

```

Lys	Asn	Ile	Gly	Glu	Thr	Lys	Ile	Thr	Pro	Leu	Asp	Val	Leu	Ser	Val	
		200					205					210				
atc	ctt	tcg	gtg	ttt	gcc	ttc	ggg	ggg	ttg	gtg	tac	ggc	ttc	agt	tcc	787
Ile	Leu	Ser	Val	Phe	Ala	Phe	Gly	Gly	Leu	Val	Tyr	Gly	Phe	Ser	Ser	
	215					220					225					
ttc	gga	gca	atc	ctg	gag	ggc	gaa	ggc	acc	gta	ggg	atc	ttc	gcg	atc	835
Phe	Gly	Ala	Ile	Leu	Glu	Gly	Glu	Gly	Thr	Val	Gly	Ile	Phe	Ala	Ile	
230					235					240					245	
gtc	gtt	ggc	gcc	atc	gca	ctc	ctc	atc	ttt	gct	ttg	cga	cag	cac	caa	883
Val	Val	Gly	Ala	Ile	Ala	Leu	Leu	Ile	Phe	Ala	Leu	Arg	Gln	His	Gln	
				250					255					260		
ctc	ggc	aag	caa	gac	aaa	gca	ctg	atg	gat	ctc	cga	gcc	ttc	aag	gtg	931
Leu	Gly	Lys	Gln	Asp	Lys	Ala	Leu	Met	Asp	Leu	Arg	Ala	Phe	Lys	Val	
			265					270					275			
agg	aac	ttc	agc	ttc	tcc	ttg	acc	acc	atc	ctt	ttg	gcg	ttc	ggc	gcg	979
Arg	Asn	Phe	Ser	Phe	Ser	Leu	Thr	Thr	Ile	Leu	Leu	Ala	Phe	Gly	Ala	
	280						285					290				
atg	ctc	gga	acc	gtc	atg	gtt	ttg	cca	atc	tac	ctg	cag	act	tcc	ctc	1027
Met	Leu	Gly	Thr	Val	Met	Val	Leu	Pro	Ile	Tyr	Leu	Gln	Thr	Ser	Leu	
	295					300					305					
gga	gtt	act	gct	ttg	gtg	acc	ggg	ttg	gtt	gtt	atg	ccc	ggc	ggc	ctc	1075
Gly	Val	Thr	Ala	Leu	Val	Thr	Gly	Leu	Val	Val	Met	Pro	Gly	Gly	Leu	
310					315					320					325	
ctc	cag	ggg	ctg	atc	agc	cca	ttc	atc	gga	cgt	ttc	tac	gac	aag	gtc	1123
Leu	Gln	Gly	Leu	Ile	Ser	Pro	Phe	Ile	Gly	Arg	Phe	Tyr	Asp	Lys	Val	
			330						335					340		
ggg	cca	cgt	ccg	ctg	ctg	att	ccc	gga	gca	att	gcg	ctg	gct	atc	gcg	1171
Gly	Pro	Arg	Pro	Leu	Leu	Ile	Pro	Gly	Ala	Ile	Ala	Leu	Ala	Ile	Ala	
			345					350					355			
gca	tcc	tcg	atg	act	ttt	ctc	aat	gag	aat	tca	ccc	gtg	tgg	atg	gtc	1219
Ala	Ser	Ser	Met	Thr	Phe	Leu	Asn	Glu	Asn	Ser	Pro	Val	Trp	Met	Val	
			360				365					370				
gtg	gtc	atg	cac	gtt	gtg	ttc	agc	atc	ggc	atg	tgt	ttg	atg	atg	acc	1267
Val	Val	Met	His	Val	Val	Phe	Ser	Ile	Gly	Met	Cys	Leu	Met	Met	Thr	
	375					380					385					
cct	ctc	atg	acc	acc	gct	ctc	ggc	gcc	ctt	ccg	aag	cac	ctc	tat	ggg	1315
Pro	Leu	Met	Thr	Thr	Ala	Leu	Gly	Ala	Leu	Pro	Lys	His	Leu	Tyr	Gly	
390					395					400					405	
cac	ggc	tcc	gca	att	ttg	aac	acg	ttc	caa	cag	ctc	gca	ggc	gca	gcc	1363
His	Gly	Ser	Ala	Ile	Leu	Asn	Thr	Phe	Gln	Gln	Leu	Ala	Gly	Ala	Ala	
				410					415					420		
gga	aca	gcg	atc	atg	att	gca	gca	ctt	tcc	ttc	ggc	act	tcc	att	gca	1411
Gly	Thr	Ala	Ile	Met	Ile	Ala	Ala	Leu	Ser	Phe	Gly	Thr	Ser	Ile	Ala	
			425					430					435			
gcg	tct	tcg	gga	tct	gcg	cat	gct	gaa	gct	gtt	gcc	gct	ggg	acc	aag	1459
Ala	Ser	Ser	Gly	Ser	Ala	His	Ala	Glu	Ala	Val	Ala	Ala	Gly	Thr	Lys	


```

          440                      445                      450
gtt gcg ttc atc gca ggc gca atc atc gcg gtg atc gct ttg gtt gtt 1507
Val Ala Phe Ile Ala Gly Ala Ile Ile Ala Val Ile Ala Leu Val Val
    455                      460                      465

tcc ctc ttc gtc act cgc gtc gag gaa gaa gct cac taaataccaa 1553
Ser Leu Phe Val Thr Arg Val Glu Glu Glu Ala His
    470                      475                      480

aaaatggggc aga 1566

<210> 2
<211> 481
<212> PRT
<213> Corynebacterium glutamicum

<400> 2
Met Asp Ser Gln Ile Asn Thr Gln Thr Ser Pro Ala Ala Ala Lys Leu
  1              5              10              15

Pro Arg Glu Val Val Val Val Leu Ser Ile Leu Val Val Ser Ala Met
      20              25              30

Ile Met Ile Leu Asn Glu Thr Ile Leu Ser Val Ala Leu Pro Ser Ile
    35              40              45

Met Glu Asp Phe Ser Val Pro Glu Thr Thr Ala Gln Trp Leu Thr Thr
    50              55              60

Gly Phe Met Leu Thr Met Ala Val Val Ile Pro Thr Thr Gly Tyr Leu
    65              70              75              80

Leu Asp Arg Phe Ser Thr Lys Thr Ile Phe Val Thr Ala Leu Leu Phe
      85              90              95

Phe Thr Val Gly Thr Leu Thr Ala Ala Leu Ala Pro Thr Phe Ala Val
    100              105              110

Leu Leu Gly Ala Arg Ile Val Gln Ala Val Gly Thr Ala Leu Val Met
    115              120              125

Pro Leu Leu Met Thr Val Thr Leu Thr Val Val Pro Ala Glu Arg Arg
    130              135              140

Gly Ser Met Met Gly Ile Ile Ser Ile Val Ile Ser Val Ala Pro Ala
    145              150              155              160

Leu Gly Pro Thr Leu Ser Gly Val Ile Leu Asn Ser Leu Thr Trp His
    165              170              175

Trp Leu Phe Trp Met Met Leu Pro Ile Val Val Ile Ala Leu Val Ile
    180              185              190

Gly Phe Phe Leu Ile Lys Asn Ile Gly Glu Thr Lys Ile Thr Pro Leu
    195              200              205

Asp Val Leu Ser Val Ile Leu Ser Val Phe Ala Phe Gly Gly Leu Val
    210              215              220

```

Tyr Gly Phe Ser Ser Phe Gly Ala Ile Leu Glu Gly Glu Gly Thr Val
 225 230 235 240
 Gly Ile Phe Ala Ile Val Val Gly Ala Ile Ala Leu Leu Ile Phe Ala
 245 250 255
 Leu Arg Gln His Gln Leu Gly Lys Gln Asp Lys Ala Leu Met Asp Leu
 260 265 270
 Arg Ala Phe Lys Val Arg Asn Phe Ser Phe Ser Leu Thr Thr Ile Leu
 275 280 285
 Leu Ala Phe Gly Ala Met Leu Gly Thr Val Met Val Leu Pro Ile Tyr
 290 295 300
 Leu Gln Thr Ser Leu Gly Val Thr Ala Leu Val Thr Gly Leu Val Val
 305 310 315 320
 Met Pro Gly Gly Leu Leu Gln Gly Leu Ile Ser Pro Phe Ile Gly Arg
 325 330 335
 Phe Tyr Asp Lys Val Gly Pro Arg Pro Leu Leu Ile Pro Gly Ala Ile
 340 345 350
 Ala Leu Ala Ile Ala Ala Ser Ser Met Thr Phe Leu Asn Glu Asn Ser
 355 360 365
 Pro Val Trp Met Val Val Val Met His Val Val Phe Ser Ile Gly Met
 370 375 380
 Cys Leu Met Met Thr Pro Leu Met Thr Thr Ala Leu Gly Ala Leu Pro
 385 390 395 400
 Lys His Leu Tyr Gly His Gly Ser Ala Ile Leu Asn Thr Phe Gln Gln
 405 410 415
 Leu Ala Gly Ala Ala Gly Thr Ala Ile Met Ile Ala Ala Leu Ser Phe
 420 425 430
 Gly Thr Ser Ile Ala Ala Ser Ser Gly Ser Ala His Ala Glu Ala Val
 435 440 445
 Ala Ala Gly Thr Lys Val Ala Phe Ile Ala Gly Ala Ile Ile Ala Val
 450 455 460
 Ile Ala Leu Val Val Ser Leu Phe Val Thr Arg Val Glu Glu Glu Ala
 465 470 475 480

His

<210> 3

<211> 371

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (52)..(348)

<223> RXA00497

<400> 3

```

tggaaccca caaccggcac acacaaaatt tttctcatgg agggattcac c gtg gca 57
                               Val Ala
                               1

aac gtc aac atc aag ccg ctt gag gac aag atc ctc gtt cag atc aac 105
Asn Val Asn Ile Lys Pro Leu Glu Asp Lys Ile Leu Val Gln Ile Asn
      5                      10                      15

gaa gca gag acc acc acc gct tcc ggc ctg gtc att cca gat tcc gct 153
Glu Ala Glu Thr Thr Thr Ala Ser Gly Leu Val Ile Pro Asp Ser Ala
      20                      25                      30

aag gaa aag cca caa gag gca acc gtt atc gca gtt ggc cca ggc cgc 201
Lys Glu Lys Pro Gln Glu Ala Thr Val Ile Ala Val Gly Pro Gly Arg
      35                      40                      45                      50

ttc gat gac aag ggt aac cgc atc cca ctg gac atc aag gaa gat gac 249
Phe Asp Asp Lys Gly Asn Arg Ile Pro Leu Asp Ile Lys Glu Asp Asp
      55                      60                      65

gtt gtg atc ttc tcc cgt tac ggc ggc acc gag atc aag ttc ggt ggc 297
Val Val Ile Phe Ser Arg Tyr Gly Gly Thr Glu Ile Lys Phe Gly Gly
      70                      75                      80

gtg gag tac ttg ctt ctc tcc gct cgt gac atc ctc gca atc gtc gag 345
Val Glu Tyr Leu Leu Leu Ser Ala Arg Asp Ile Leu Ala Ile Val Glu
      85                      90                      95

aag taggggataa gttcatggca aag 371
Lys

```

<210> 4

<211> 99

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 4

```

Val Ala Asn Val Asn Ile Lys Pro Leu Glu Asp Lys Ile Leu Val Gln
      1                      5                      10                      15

Ile Asn Glu Ala Glu Thr Thr Thr Ala Ser Gly Leu Val Ile Pro Asp
      20                      25                      30

Ser Ala Lys Glu Lys Pro Gln Glu Ala Thr Val Ile Ala Val Gly Pro
      35                      40                      45

Gly Arg Phe Asp Asp Lys Gly Asn Arg Ile Pro Leu Asp Ile Lys Glu
      50                      55                      60

Asp Asp Val Val Ile Phe Ser Arg Tyr Gly Gly Thr Glu Ile Lys Phe
      65                      70                      75                      80

Gly Gly Val Glu Tyr Leu Leu Leu Ser Ala Arg Asp Ile Leu Ala Ile
      85                      90                      95

Val Glu Lys

```

<400> 5															60
cccgttacgg cggcaccgag atcaagttcg gtggcgtgga gtacttgctt ctctccgctc															
gtgacatcct cgcaatcgtc gagaagtagg ggataagttc atg gca aag ctc att															115
Met Ala Lys Leu Ile															
1 5															
gct ttt gac cag gac gcc cgc gaa ggc att ctc cgg ggc gtt gac gct															163
Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu Arg Gly Val Asp Ala															
10 15 20															
ctg gca aac gct gtc aag gta acc ctc ggc cca cgc ggc cgt aac gtg															211
Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Arg Gly Arg Asn Val															
25 30 35															
gtt ctt gat aag gca ttc ggc gga cct ctg gtc acc aac gac ggt gtc															259
Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val Thr Asn Asp Gly Val															
40 45 50															
acc att gcc cgc gac atc gac ctt gag gat cct ttt gag aac ctc ggt															307
Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly															
55 60 65															
gcg cag ctg gtg aag tcc gtt gct gtt aag acc aac gac atc gct ggt															355
Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr Asn Asp Ile Ala Gly															
70 75 80 85															
gac ggc acc acg act gca act ctg ctt gct cag gca ctc att gct gaa															403
Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln Ala Leu Ile Ala Glu															
90 95 100															
ggc ctg cgc aac gtt gct gct ggc gca aac cca atg gag ctc aac aag															451
Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro Met Glu Leu Asn Lys															
105 110 115															
ggt att tct gca gct gca gaa aag acc ttg gaa gag ttg aag gca cgc															499
Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu Glu Leu Lys Ala Arg															
120 125 130															
gca acc gag gtg tct gac acc aag gaa atc gca aac gtc gct acc gtt															547
Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala Asn Val Ala Thr Val															
135 140 145															
tca tcc cgc gat gaa gtt gtc ggc gag atc gtt gct gca gcg atg gaa															595
Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val Ala Ala Ala Met Glu															
150 155 160 165															
aag gtt ggc aag gac ggt gtc gtc acc gtt gag gag tcc cag tcc atc															643
Lys Val Gly Lys Asp Gly Val Val Thr Val Glu Glu Ser Gln Ser Ile															

				170				175				180				
gag	act	gct	ctc	gag	gtc	acc	gaa	ggt	att	tct	ttc	gac	aag	ggc	tac	691
Glu	Thr	Ala	Leu	Glu	Val	Thr	Glu	Gly	Ile	Ser	Phe	Asp	Lys	Gly	Tyr	
185								190				195				
ctt	tcc	cct	tat	ttc	atc	aac	gac	aac	gac	act	cag	cag	gct	gtc	ctg	739
Leu	Ser	Pro	Tyr	Phe	Ile	Asn	Asp	Asn	Asp	Thr	Gln	Gln	Ala	Val	Leu	
200								205				210				
gac	aac	cct	gca	gtg	ctg	ctt	ggt	cgc	aac	aag	att	tct	tcc	ctc	cca	787
Asp	Asn	Pro	Ala	Val	Leu	Leu	Val	Arg	Asn	Lys	Ile	Ser	Ser	Leu	Pro	
215				220				225								
gac	ttc	ctc	cca	ttg	ctg	gag	aag	ggt	gtg	gag	tcc	aac	cgt	cct	ttg	835
Asp	Phe	Leu	Pro	Leu	Leu	Glu	Lys	Val	Val	Glu	Ser	Asn	Arg	Pro	Leu	
230				235				240				245				
ctg	atc	atc	gca	gaa	gac	gtc	gag	ggc	gag	cct	ttg	cag	acc	ctg	ggt	883
Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	Glu	Pro	Leu	Gln	Thr	Leu	Val	
250								255				260				
gtg	aac	tcc	atc	cgc	aag	acc	atc	aag	gtc	ggt	gca	gtg	aag	tcc	cct	931
Val	Asn	Ser	Ile	Arg	Lys	Thr	Ile	Lys	Val	Val	Ala	Val	Lys	Ser	Pro	
265								270				275				
tac	ttc	ggg	gac	cga	cgc	aag	gcg	ttc	atg	gat	gac	ctg	gct	att	gtc	979
Tyr	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Phe	Met	Asp	Asp	Leu	Ala	Ile	Val	
280								285				290				
acc	aag	gca	act	gtc	gtg	gat	cca	gaa	gtg	ggc	atc	aac	ctc	aac	gaa	1027
Thr	Lys	Ala	Thr	Val	Val	Asp	Pro	Glu	Val	Gly	Ile	Asn	Leu	Asn	Glu	
295				300				305								
gct	ggc	gaa	gaa	gtt	ttc	ggg	acc	gca	cgc	cgc	atc	acc	gtt	tcc	aag	1075
Ala	Gly	Glu	Glu	Val	Phe	Gly	Thr	Ala	Arg	Arg	Ile	Thr	Val	Ser	Lys	
310				315				320				325				
gac	gaa	acc	atc	atc	gtt	gat	ggg	gca	ggg	tcc	gca	gaa	gac	gtt	gaa	1123
Asp	Glu	Thr	Ile	Ile	Val	Asp	Gly	Ala	Gly	Ser	Ala	Glu	Asp	Val	Glu	
330								335				340				
gca	cgt	cgc	ggc	cag	atc	cgt	cgc	gaa	atc	gcc	aac	acc	gat	tcc	acc	1171
Ala	Arg	Arg	Gly	Gln	Ile	Arg	Arg	Glu	Ile	Ala	Asn	Thr	Asp	Ser	Thr	
345								350				355				
tgg	gat	cgc	gaa	aag	gca	gaa	gag	cgt	ttg	gct	aag	ctc	tcc	ggg	ggg	1219
Trp	Asp	Arg	Glu	Lys	Ala	Glu	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Gly	Gly	
360				365				370								
att	gct	gtc	atc	cgc	gtt	ggg	gca	gca	act	gaa	acc	gaa	gtc	aac	gac	1267
Ile	Ala	Val	Ile	Arg	Val	Gly	Ala	Ala	Thr	Glu	Thr	Glu	Val	Asn	Asp	
375				380				385								
cgc	aag	ctg	cgt	gtc	gaa	gat	gcc	atc	aac	gct	gct	cgc	gca	gca	gca	1315
Arg	Lys	Leu	Arg	Val	Glu	Asp										

gag act ctg aag gct tac gcc gaa gag ttc gaa ggc gac cag aag gtc 1411
 Glu Thr Leu Lys Ala Tyr Ala Glu Glu Phe Glu Gly Asp Gln Lys Val
 425 430 435

ggc gtt cgc gca ctg gct act gct ttg ggc aag cca gcg tac tgg atc 1459
 Gly Val Arg Ala Leu Ala Thr Ala Leu Gly Lys Pro Ala Tyr Trp Ile
 440 445 450

gcc tcc aac gca ggt ctt gac ggc tct gtt gtt gtt gca cgc act gct 1507
 Ala Ser Asn Ala Gly Leu Asp Gly Ser Val Val Val Ala Arg Thr Ala
 455 460 465

gct ctg cca aac ggc gag ggc ttc aac gct gca act ttg gaa tac gga 1555
 Ala Leu Pro Asn Gly Glu Gly Phe Asn Ala Ala Thr Leu Glu Tyr Gly
 470 475 480 485

aac ctg atc aac gac ggt gtc atc gac cca gtc aag gtc acc cat tcc 1603
 Asn Leu Ile Asn Asp Gly Val Ile Asp Pro Val Lys Val Thr His Ser
 490 495 500

gca gta gtg aat gca acc tct gtt gca cgc atg gtt ctg acc act gag 1651
 Ala Val Val Asn Ala Thr Ser Val Ala Arg Met Val Leu Thr Thr Glu
 505 510 515

gct tct gtt gtt gag aag cct gca gaa gaa gca gcc gat gca cat gca 1699
 Ala Ser Val Val Glu Lys Pro Ala Glu Glu Ala Ala Asp Ala His Ala
 520 525 530

gga cat cat cac cac taaagttctg tgaaaaacac cgt 1737
 Gly His His His His
 535

<210> 6

<211> 538

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 6

Met Ala Lys Leu Ile Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu
1 5 10 15

Arg Gly Val Asp Ala Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro
20 25 30

Arg Gly Arg Asn Val Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val
35 40 45

Thr Asn Asp Gly Val Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro
50 55 60

Phe Glu Asn Leu Gly Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr
65 70 75 80

Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln
85 90 95

Ala Leu Ile Ala Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
100 105 110

Met Glu Leu Asn Lys Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu
 115 120 125
 Glu Leu Lys Ala Arg Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala
 130 135 140
 Asn Val Ala Thr Val Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val
 145 150 155 160
 Ala Ala Ala Met Glu Lys Val Gly Lys Asp Gly Val Val Thr Val Glu
 165 170 175
 Glu Ser Gln Ser Ile Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser
 180 185 190
 Phe Asp Lys Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr
 195 200 205
 Gln Gln Ala Val Leu Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys
 210 215 220
 Ile Ser Ser Leu Pro Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu
 225 230 235 240
 Ser Asn Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro
 245 250 255
 Leu Gln Thr Leu Val Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val
 260 265 270
 Ala Val Lys Ser Pro Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp
 275 280 285
 Asp Leu Ala Ile Val Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly
 290 295 300
 Ile Asn Leu Asn Glu Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg
 305 310 315 320
 Ile Thr Val Ser Lys Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser
 325 330 335
 Ala Glu Asp Val Glu Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala
 340 345 350
 Asn Thr Asp Ser Thr Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala
 355 360 365
 Lys Leu Ser Gly Gly Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu
 370 375 380
 Thr Glu Val Asn Asp Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala
 385 390 395 400
 Ala Arg Ala Ala Ala Gln Glu Gly Val Ile Ala Gly Gly Gly Ser Ala
 405 410 415
 Leu Val Gln Ile Ala Glu Thr Leu Lys Ala Tyr Ala Glu Glu Phe Glu
 420 425 430
 Gly Asp Gln Lys Val Gly Val Arg Ala Leu Ala Thr Ala Leu Gly Lys

435					440					445					
Pro	Ala	Tyr	Trp	Ile	Ala	Ser	Asn	Ala	Gly	Leu	Asp	Gly	Ser	Val	Val
450						455					460				
Val	Ala	Arg	Thr	Ala	Ala	Leu	Pro	Asn	Gly	Glu	Gly	Phe	Asn	Ala	Ala
465					470					475					480
Thr	Leu	Glu	Tyr	Gly	Asn	Leu	Ile	Asn	Asp	Gly	Val	Ile	Asp	Pro	Val
				485					490					495	
Lys	Val	Thr	His	Ser	Ala	Val	Val	Asn	Ala	Thr	Ser	Val	Ala	Arg	Met
			500					505					510		
Val	Leu	Thr	Thr	Glu	Ala	Ser	Val	Val	Glu	Lys	Pro	Ala	Glu	Glu	Ala
			515				520					525			
Ala	Asp	Ala	His	Ala	Gly	His	His	His							
530					535										

<210> 7
 <211> 1339
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1339)
 <223> FRXA00498

<400> 7
 cccggttacgg cggcaccgag atcaagttcg gtggcggtgga gtacttgctt ctctccgctc 60
 gtgacatcct cgcaatcgtc gagaagtagg ggataagttc atg gca aag ctc att 115
 Met Ala Lys Leu Ile 5
 1 5
 gct ttt gac cag gac gcc cgc gaa ggc att ctc cgg ggc gtt gac gct 163
 Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu Arg Gly Val Asp Ala 20
 10 15
 ctg gca aac gct gtc aag gta acc ctc ggc cca cgc ggc cgt aac gtg 211
 Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Arg Gly Arg Asn Val 35
 25 30
 gtt ctt gat aag gca ttc ggc gga cct ctg gtc acc aac gac ggt gtc 259
 Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val Thr Asn Asp Gly Val 50
 40 45
 acc att gcc cgc gac atc gac ctt gag gat cct ttt gag aac ctc ggt 307
 Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly 65
 55 60
 gcg cag ctg gtg aag tcc gtt gct gtt aag acc aac gac atc gct ggt 355
 Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr Asn Asp Ile Ala Gly 85
 70 75 80
 gac ggc acc acg act gca act ctg ctt gct cag gca ctc att gct gaa 403
 Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln Ala Leu Ile Ala Glu 100
 90 95

ggc ctg cgc aac gtt gct gct ggc gca aac cca atg gag ctc aac aag	451
Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro Met Glu Leu Asn Lys	
105 110 115	
ggg att tct gca gct gca gaa aag acc ttg gaa gag ttg aag gca cgc	499
Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu Glu Leu Lys Ala Arg	
120 125 130	
gca acc gag gtg tct gac acc aag gaa atc gca aac gtc gct acc gtt	547
Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala Asn Val Ala Thr Val	
135 140 145	
tca tcc cgc gat gaa gtt gtc ggc gag atc gtt gct gca gcg atg gaa	595
Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val Ala Ala Ala Met Glu	
150 155 160 165	
aag gtt ggc aag gac ggt gtc gtc acc gtt gag gag tcc cag tcc atc	643
Lys Val Gly Lys Asp Gly Val Val Thr Val Glu Glu Ser Gln Ser Ile	
170 175 180	
gag act gct ctc gag gtc acc gaa ggt att tct ttc gac aag ggc tac	691
Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser Phe Asp Lys Gly Tyr	
185 190 195	
ctt tcc cct tat ttc atc aac gac aac gac act cag cag gct gtc ctg	739
Leu Ser Pro Tyr Phe Ile Asn Asp Asn Asp Thr Gln Gln Ala Val Leu	
200 205 210	
gac aac cct gca gtg ctg ctt gtt cgc aac aag att tct tcc ctc cca	787
Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys Ile Ser Ser Leu Pro	
215 220 225	
gac ttc ctc cca ttg ctg gag aag gtt gtg gag tcc aac cgt cct ttg	835
Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu Ser Asn Arg Pro Leu	
230 235 240 245	
ctg atc atc gca gaa gac gtc gag ggc gag cct ttg cag acc ctg gtt	883
Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro Leu Gln Thr Leu Val	
250 255 260	
gtg aac tcc atc cgc aag acc atc aag gtc gtt gca gtg aag tcc cct	931
Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val Ala Val Lys Ser Pro	
265 270 275	
tac ttc ggt gac cga cgc aag gcg ttc atg gat gac ctg gct att gtc	979
Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp Asp Leu Ala Ile Val	
280 285 290	
acc aag gca act gtc gtg gat cca gaa gtg ggc atc aac ctc aac gaa	1027
Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly Ile Asn Leu Asn Glu	
295 300 305	
gct ggc gaa gaa gtt ttc ggt acc gca cgc cgc atc acc gtt tcc aag	1075
Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg Ile Thr Val Ser Lys	
310 315 320 325	
gac gaa acc atc atc gtt gat ggt gca ggt tcc gca gaa gac gtt gaa	1123
Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser Ala Glu Asp Val Glu	
330 335 340	

gca cgt cgc ggc cag atc cgt cgc gaa atc gcc aac acc gat tcc acc 1171
 Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala Asn Thr Asp Ser Thr
 345 350 355

tgg gat cgc gaa aag gca gaa gag cgt ttg gct aag ctc tcc ggt ggt 1219
 Trp Asp Arg Glu Lys Ala Glu Glu Arg Leu Ala Lys Leu Ser Gly Gly
 360 365 370

att gct gtc atc cgc gtt ggt gca gca act gaa acc gaa gtc aac gac 1267
 Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu Thr Glu Val Asn Asp
 375 380 385

cgc aag ctg cgt gtc gaa gat gcc atc aac gct gct cgc gca gca gca 1315
 Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala Ala Arg Ala Ala Ala
 390 395 400 405

caa gaa ggc gtt atc gct ggt ggc 1339
 Gln Glu Gly Val Ile Ala Gly Gly
 410

<210> 8

<211> 413

<212> PRT

<213> Corynebacterium glutamicum

<400> 8

Met Ala Lys Leu Ile Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu
 1 5 10 15

Arg Gly Val Asp Ala Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro
 20 25 30

Arg Gly Arg Asn Val Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val
 35 40 45

Thr Asn Asp Gly Val Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro
 50 55 60

Phe Glu Asn Leu Gly Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr
 65 70 75 80

Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Leu Leu Ala Gln
 85 90 95

Ala Leu Ile Ala Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
 100 105 110

Met Glu Leu Asn Lys Gly Ile Ser Ala Ala Ala Glu Lys Thr Leu Glu
 115 120 125

Glu Leu Lys Ala Arg Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala
 130 135 140

Asn Val Ala Thr Val Ser Ser Arg Asp Glu Val Val Gly Glu Ile Val
 145 150 155 160

Ala Ala Ala Met Glu Lys Val Gly Lys Asp Gly Val Val Thr Val Glu
 165 170 175

Glu Ser Gln Ser Ile Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser

```
<210> 9
<211> 723
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(700)  
<223> RXA01217
```

```

<400> 9
gcgctgcctg cgaagactcg accaagacat tcgagtcggt cgcgggcatt ttttattttc 60

gcggccgagt gtccaccttc atccatgagg agaaatcact atg gca aag tac caa 115
Met Ala Lys Tyr Gln
1 5

```

```

acc att gag gct gct gtc cgc tct gag ttc ggc aag ggc tct gca cgt 163
Thr Ile Glu Ala Val Arg Ser Glu Phe Gly Lys Gly Ser Ala Arg
      10              15              20

cgt gca cgc gtt gct ggc cag atc cct gct gtt gtt tac ggc gca gat 211
Arg Ala Arg Val Ala Gly Gln Ile Pro Ala Val Val Tyr Gly Ala Asp
      25              30              35

gtt gag tcc aac ctg cac gtc acc atc gac cac cgc acc ttc gct gcg 259
Val Glu Ser Asn Leu His Val Thr Ile Asp His Arg Thr Phe Ala Ala
      40              45              50

ctg gtt cgc cag gaa ggc gta aac gct gtt ctt gag ctc gac atc gag 307
Leu Val Arg Gln Glu Gly Val Asn Ala Val Leu Glu Leu Asp Ile Glu
      55              60              65

ggc cag aag cag ctc acc atg atc aag cac atc gac cag aac gtg ctg 355
Gly Gln Lys Gln Leu Thr Met Ile Lys His Ile Asp Gln Asn Val Leu
      70              75              80              85

acc ttc cac atc gac cac ttg gac ctg ctt gcc att aag cgc ggc gaa 403
Thr Phe His Ile Asp His Leu Asp Leu Leu Ala Ile Lys Arg Gly Glu
      90              95              100

aag gtt gag gtt gac gtt cca gtt atc gtc gag ggc gag cca gct cca 451
Lys Val Glu Val Asp Val Pro Val Ile Val Glu Gly Glu Pro Ala Pro
      105              110              115

ggc acc atg tgg gtt cag gat gct gac acc atc aag gtt gag gct gac 499
Gly Thr Met Trp Val Gln Asp Ala Asp Thr Ile Lys Val Glu Ala Asp
      120              125              130

gtt ctg tcc atc cct gaa gag ttc acc gtt tcc atc gaa ggc ctt gag 547
Val Leu Ser Ile Pro Glu Glu Phe Thr Val Ser Ile Glu Gly Leu Glu
      135              140              145

ctc ggc gca cag atc acc gca gct gac atc aag ctc gag ggc gac acc 595
Leu Gly Ala Gln Ile Thr Ala Ala Asp Ile Lys Leu Glu Gly Asp Thr
      150              155              160              165

acc ctg gtt gag gat cct gag acc ctc atc gtc aac atc gtt ctc cca 643
Thr Leu Val Glu Asp Pro Glu Thr Leu Ile Val Asn Ile Val Leu Pro
      170              175              180

gct gtc gag gaa gaa gac acc gaa gag gac gaa gca gct gaa gaa gca 691
Ala Val Glu Glu Glu Asp Thr Glu Glu Asp Glu Ala Ala Glu Glu Ala
      185              190              195

gct act gag taagcttttt tagatagctt tat 723
Ala Thr Glu
      200

```

<210> 10

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 10

Met Ala Lys Tyr Gln Thr Ile Glu Ala Ala Val Arg Ser Glu Phe Gly

1	5	10	15
Lys Gly Ser Ala Arg Arg Ala Arg Val Ala Gly Gln Ile Pro Ala Val	20	25	30
Val Tyr Gly Ala Asp Val Glu Ser Asn Leu His Val Thr Ile Asp His	35	40	45
Arg Thr Phe Ala Ala Leu Val Arg Gln Glu Gly Val Asn Ala Val Leu	50	55	60
Glu Leu Asp Ile Glu Gly Gln Lys Gln Leu Thr Met Ile Lys His Ile	65	70	75
Asp Gln Asn Val Leu Thr Phe His Ile Asp His Leu Asp Leu Leu Ala	85	90	95
Ile Lys Arg Gly Glu Lys Val Glu Val Asp Val Pro Val Ile Val Glu	100	105	110
Gly Glu Pro Ala Pro Gly Thr Met Trp Val Gln Asp Ala Asp Thr Ile	115	120	125
Lys Val Glu Ala Asp Val Leu Ser Ile Pro Glu Glu Phe Thr Val Ser	130	135	140
Ile Glu Gly Leu Glu Leu Gly Ala Gln Ile Thr Ala Ala Asp Ile Lys	145	150	155
Leu Glu Gly Asp Thr Thr Leu Val Glu Asp Pro Glu Thr Leu Ile Val	165	170	175
Asn Ile Val Leu Pro Ala Val Glu Glu Glu Asp Thr Glu Glu Asp Glu	180	185	190
Ala Ala Glu Glu Ala Ala Thr Glu	195	200	

<210> 11
 <211> 1603
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (33)..(1580)
 <223> RXA00605

<400> 11	
ataggttaacc ctcataaaag gaaggaatgc ta atg tct gag aag tca gca gca	53
Met Ser Glu Lys Ser Ala Ala	
1 5	
gac cag atc gta gat cgc gga atg cgt cca aag ctt tct gga aac act	101
Asp Gln Ile Val Asp Arg Gly Met Arg Pro Lys Leu Ser Gly Asn Thr	
10 15 20	
acc cgc cac aac gga gca cca gtt cca tct gag aac atc tcc gca acc	149
Thr Arg His Asn Gly Ala Pro Val Pro Ser Glu Asn Ile Ser Ala Thr	
25 30 35	

gca ggc cca cag ggt cca aac gtt ctc aat gac att cac ctc att gaa	197
Ala Gly Pro Gln Gly Pro Asn Val Leu Asn Asp Ile His Leu Ile Glu	
40 45 50 55	
aag ctc gca cac ttt aac cgc gag aac gtt cca gag cgt atc cct cac	245
Lys Leu Ala His Phe Asn Arg Glu Asn Val Pro Glu Arg Ile Pro His	
60 65 70	
gca aag ggc cac ggc gct ttc ggt gag ctg cac atc acc gag gac gta	293
Ala Lys Gly His Gly Ala Phe Gly Glu Leu His Ile Thr Glu Asp Val	
75 80 85	
tcc gaa tac acc aag gca gac ctg ttc cag cct ggt aag gtc acc ccg	341
Ser Glu Tyr Thr Lys Ala Asp Leu Phe Gln Pro Gly Lys Val Thr Pro	
90 95 100	
ctg gct gtt cgc ttc tct act gtt gct ggt gag cag ggc tcc cca gat	389
Leu Ala Val Arg Phe Ser Thr Val Ala Gly Glu Gln Gly Ser Pro Asp	
105 110 115	
acc tgg cgc gac gtc cac ggc ttc gct ctt cgc ttc tac acc gaa gag	437
Thr Trp Arg Asp Val His Gly Phe Ala Leu Arg Phe Tyr Thr Glu Glu	
120 125 130 135	
ggc aac tac gac atc gtg ggt aac aac acc cca acc ttc ttc ctt cgt	485
Gly Asn Tyr Asp Ile Val Gly Asn Asn Thr Pro Thr Phe Phe Leu Arg	
140 145 150	
gac ggc atg aag ttc ccg gac ttc atc cac tca cag aag cgt ctc aac	533
Asp Gly Met Lys Phe Pro Asp Phe Ile His Ser Gln Lys Arg Leu Asn	
155 160 165	
aag aac ggt ctg cgc gat gca gac atg cag tgg gat ttc tgg acc cgc	581
Lys Asn Gly Leu Arg Asp Ala Asp Met Gln Trp Asp Phe Trp Thr Arg	
170 175 180	
gca cct gaa tct gca cac cag gtg acc tac ctg atg ggt gac cgc ggt	629
Ala Pro Glu Ser Ala His Gln Val Thr Tyr Leu Met Gly Asp Arg Gly	
185 190 195	
acc cct aag acc tcc cgc cac cag gac ggc ttc ggc tcc cac acc ttc	677
Thr Pro Lys Thr Ser Arg His Gln Asp Gly Phe Gly Ser His Thr Phe	
200 205 210 215	
cag tgg atc aac gct gaa ggt aag cca gtt tgg gtt aag tac cac ttc	725
Gln Trp Ile Asn Ala Glu Gly Lys Pro Val Trp Val Lys Tyr His Phe	
220 225 230	
aag acc cgc cag ggc tgg gat tgc ttc acc gat gca gaa gca gca aag	773
Lys Thr Arg Gln Gly Trp Asp Cys Phe Thr Asp Ala Glu Ala Ala Lys	
235 240 245	
gtt gca ggc gag aac gct gac tac cag cgc gaa gac ctc tac aac gct	821
Val Ala Gly Glu Asn Ala Asp Tyr Gln Arg Glu Asp Leu Tyr Asn Ala	
250 255 260	
att gaa aac ggc gac ttc cca atc tgg gac gtc aag gtt cag atc atg	869
Ile Glu Asn Gly Asp Phe Pro Ile Trp Asp Val Lys Val Gln Ile Met	
265 270 275	

cct ttc gag gat gca gag aac tac cgc tgg aac cca ttc gac ctg acc	917
Pro Phe Glu Asp Ala Glu Asn Tyr Arg Trp Asn Pro Phe Asp Leu Thr	
280 285 290 295	
aag acc tgg tcc cag aag gat tac cca ctg atc cca gtc ggt tac ttc	965
Lys Thr Trp Ser Gln Lys Asp Tyr Pro Leu Ile Pro Val Gly Tyr Phe	
300 305 310	
atc ctg aac cgc aac cca cgc aac ttc ttc gct cag atc gag cag ctt	1013
Ile Leu Asn Arg Asn Pro Arg Asn Phe Phe Ala Gln Ile Glu Gln Leu	
315 320 325	
gca ctg gat cca ggc aac atc gtt cct ggc gtc ggc ctg tcc cca gac	1061
Ala Leu Asp Pro Gly Asn Ile Val Pro Gly Val Gly Leu Ser Pro Asp	
330 335 340	
cgc atg ctc cag gca cgt atc ttc gca tac gct gac cag cag cgt tac	1109
Arg Met Leu Gln Ala Arg Ile Phe Ala Tyr Ala Asp Gln Gln Arg Tyr	
345 350 355	
cgc atc ggc gct aac tac cgc gac ctg cca gtg aac cgt cca atc aac	1157
Arg Ile Gly Ala Asn Tyr Arg Asp Leu Pro Val Asn Arg Pro Ile Asn	
360 365 370 375	
gag gtc aac acc tac agc cgc gaa ggt tcc atg cag tac atc ttc gac	1205
Glu Val Asn Thr Tyr Ser Arg Glu Gly Ser Met Gln Tyr Ile Phe Asp	
380 385 390	
gct gag ggc gag cct tcc tac agc cct aac cgc tac gac aag ggc gca	1253
Ala Glu Gly Glu Pro Ser Tyr Ser Pro Asn Arg Tyr Asp Lys Gly Ala	
395 400 405	
ggc tac ctg gat aac ggt acg gat tcc tcc tcc aac cac acc tcc tac	1301
Gly Tyr Leu Asp Asn Gly Thr Asp Ser Ser Ser Asn His Thr Ser Tyr	
410 415 420	
ggc cag gct gat gac atc tac gtc aac cca gac cca cac ggc acc gac	1349
Gly Gln Ala Asp Asp Ile Tyr Val Asn Pro Asp Pro His Gly Thr Asp	
425 430 435	
ctg gtt cgt gct gct tac gtc aag cac cag gat gat gac gac ttc atc	1397
Leu Val Arg Ala Ala Tyr Val Lys His Gln Asp Asp Asp Asp Phe Ile	
440 445 450 455	
cag cca ggc atc cta tac cgc gag gtc ctg gat gag ggc gag aag gag	1445
Gln Pro Gly Ile Leu Tyr Arg Glu Val Leu Asp Glu Gly Glu Lys Glu	
460 465 470	
cga ttg gca gac aac atc tcc aac gca atg cag ggc atc tct gag gca	1493
Arg Leu Ala Asp Asn Ile Ser Asn Ala Met Gln Gly Ile Ser Glu Ala	
475 480 485	
acc gag cca cgc gtc tac gac tac tgg aac aac gtt gat gag aac ctc	1541
Thr Glu Pro Arg Val Tyr Asp Tyr Trp Asn Asn Val Asp Glu Asn Leu	
490 495 500	
ggc gct cgc gtc aag gag ctt tac ctc cag aag aag gct taagtccttc	1590
Gly Ala Arg Val Lys Glu Leu Tyr Leu Gln Lys Lys Ala	
505 510 515	
tgatttaaaa tga	1603

<210> 12

<211> 516

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 12

Met Ser Glu Lys Ser Ala Ala Asp Gln Ile Val Asp Arg Gly Met Arg
 1 5 10 15

Pro Lys Leu Ser Gly Asn Thr Thr Arg His Asn Gly Ala Pro Val Pro
 20 25 30

Ser Glu Asn Ile Ser Ala Thr Ala Gly Pro Gln Gly Pro Asn Val Leu
 35 40 45

Asn Asp Ile His Leu Ile Glu Lys Leu Ala His Phe Asn Arg Glu Asn
 50 55 60

Val Pro Glu Arg Ile Pro His Ala Lys Gly His Gly Ala Phe Gly Glu
 65 70 75 80

Leu His Ile Thr Glu Asp Val Ser Glu Tyr Thr Lys Ala Asp Leu Phe
 85 90 95

Gln Pro Gly Lys Val Thr Pro Leu Ala Val Arg Phe Ser Thr Val Ala
 100 105 110

Gly Glu Gln Gly Ser Pro Asp Thr Trp Arg Asp Val His Gly Phe Ala
 115 120 125

Leu Arg Phe Tyr Thr Glu Glu Gly Asn Tyr Asp Ile Val Gly Asn Asn
 130 135 140

Thr Pro Thr Phe Phe Leu Arg Asp Gly Met Lys Phe Pro Asp Phe Ile
 145 150 155 160

His Ser Gln Lys Arg Leu Asn Lys Asn Gly Leu Arg Asp Ala Asp Met
 165 170 175

Gln Trp Asp Phe Trp Thr Arg Ala Pro Glu Ser Ala His Gln Val Thr
 180 185 190

Tyr Leu Met Gly Asp Arg Gly Thr Pro Lys Thr Ser Arg His Gln Asp
 195 200 205

Gly Phe Gly Ser His Thr Phe Gln Trp Ile Asn Ala Glu Gly Lys Pro
 210 215 220

Val Trp Val Lys Tyr His Phe Lys Thr Arg Gln Gly Trp Asp Cys Phe
 225 230 235 240

Thr Asp Ala Glu Ala Ala Lys Val Ala Gly Glu Asn Ala Asp Tyr Gln
 245 250 255

Arg Glu Asp Leu Tyr Asn Ala Ile Glu Asn Gly Asp Phe Pro Ile Trp
 260 265 270

Asp Val Lys Val Gln Ile Met Pro Phe Glu Asp Ala Glu Asn Tyr Arg
 275 280 285

Trp Asn Pro Phe Asp Leu Thr Lys Thr Trp Ser Gln Lys Asp Tyr Pro
 290 295 300
 Leu Ile Pro Val Gly Tyr Phe Ile Leu Asn Arg Asn Pro Arg Asn Phe
 305 310 315 320
 Phe Ala Gln Ile Glu Gln Leu Ala Leu Asp Pro Gly Asn Ile Val Pro
 325 330 335
 Gly Val Gly Leu Ser Pro Asp Arg Met Leu Gln Ala Arg Ile Phe Ala
 340 345 350
 Tyr Ala Asp Gln Gln Arg Tyr Arg Ile Gly Ala Asn Tyr Arg Asp Leu
 355 360 365
 Pro Val Asn Arg Pro Ile Asn Glu Val Asn Thr Tyr Ser Arg Glu Gly
 370 375 380
 Ser Met Gln Tyr Ile Phe Asp Ala Glu Gly Glu Pro Ser Tyr Ser Pro
 385 390 395 400
 Asn Arg Tyr Asp Lys Gly Ala Gly Tyr Leu Asp Asn Gly Thr Asp Ser
 405 410 415
 Ser Ser Asn His Thr Ser Tyr Gly Gln Ala Asp Asp Ile Tyr Val Asn
 420 425 430
 Pro Asp Pro His Gly Thr Asp Leu Val Arg Ala Ala Tyr Val Lys His
 435 440 445
 Gln Asp Asp Asp Asp Phe Ile Gln Pro Gly Ile Leu Tyr Arg Glu Val
 450 455 460
 Leu Asp Glu Gly Glu Lys Glu Arg Leu Ala Asp Asn Ile Ser Asn Ala
 465 470 475 480
 Met Gln Gly Ile Ser Glu Ala Thr Glu Pro Arg Val Tyr Asp Tyr Trp
 485 490 495
 Asn Asn Val Asp Glu Asn Leu Gly Ala Arg Val Lys Glu Leu Tyr Leu
 500 505 510
 Gln Lys Lys Ala
 515

<210> 13

<211> 2439

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2416)

<223> RXA00404

<400> 13

aagatccgat catcggcata cagaaacacc catctggccg aactttcctt tttctgcatg 60

catttctgca cacagtttct gcccgctggt tctacgcata gtg gct ttg aaa cga 115

												Val	Ala	Leu	Lys	Arg	
												1				5	
ccc	gaa	gag	aaa	aca	gta	aag	atc	gtg	acc	ata	aaa	cag	act	gac	aac		163
Pro	Glu	Glu	Lys	Thr	Val	Lys	Ile	Val	Thr	Ile	Lys	Gln	Thr	Asp	Asn		
				10					15					20			
atc	aat	gac	gat	gat	ttg	gtg	tac	agc	aac	gct	act	gac	ctt	cca	gta		211
Ile	Asn	Asp	Asp	Asp	Leu	Val	Tyr	Ser	Asn	Ala	Thr	Asp	Leu	Pro	Val		
			25					30					35				
ggc	gtg	aag	aag	tcc	cct	aaa	atg	tca	ccg	acc	gcc	cgc	gtt	ggg	ctc		259
Gly	Val	Lys	Lys	Ser	Pro	Lys	Met	Ser	Pro	Thr	Ala	Arg	Val	Gly	Leu		
		40					45					50					
ctt	gtc	ttt	ggg	gtt	atc	gcg	gcg	gtg	ggg	tgg	gga	gca	atc	gct	ttc		307
Leu	Val	Phe	Gly	Val	Ile	Ala	Ala	Val	Gly	Trp	Gly	Ala	Ile	Ala	Phe		
	55					60				65							
tcc	cgt	ggc	gaa	aca	atc	aac	tct	gtg	tgg	ctg	gtt	ttg	gcg	gca	gtt		355
Ser	Arg	Gly	Glu	Thr	Ile	Asn	Ser	Val	Trp	Leu	Val	Leu	Ala	Ala	Val		
70					75					80					85		
ggg	tcc	tat	atc	att	gcg	ttt	tct	ttc	tat	gcc	cga	ctg	att	gaa	tac		403
Gly	Ser	Tyr	Ile	Ile	Ala	Phe	Ser	Phe	Tyr	Ala	Arg	Leu	Ile	Glu	Tyr		
			90					95					100				
aaa	gtt	gtt	aag	ccg	aaa	gat	cag	cga	gca	acc	ccg	gcg	gaa	tac	gtt		451
Lys	Val	Val	Lys	Pro	Lys	Asp	Gln	Arg	Ala	Thr	Pro	Ala	Glu	Tyr	Val		
			105				110					115					
aat	gac	ggc	aag	gac	tat	gtc	cca	acg	gat	cgt	cgt	gtg	ctt	ttt	ggc		499
Asn	Asp	Gly	Lys	Asp	Tyr	Val	Pro	Thr	Asp	Arg	Arg	Val	Leu	Phe	Gly		
	120						125					130					
cac	cac	ttt	gca	gct	att	gca	ggg	gcc	ggg	cca	ttg	gtt	gga	cct	gtc		547
His	His	Phe	Ala	Ala	Ile	Ala	Gly	Ala	Gly	Pro	Leu	Val	Gly	Pro	Val		
	135					140					145						
atg	gcc	gcg	cag	atg	ggc	tac	ctg	cca	ggc	acc	ttg	tgg	att	atc	ctc		595
Met	Ala	Ala	Gln	Met	Gly	Tyr	Leu	Pro	Gly	Thr	Leu	Trp	Ile	Ile	Leu		
150					155					160					165		
ggg	gtg	att	ttc	gcc	ggg	gca	gtg	cag	gac	tac	cta	gtg	ctg	tgg	gtg		643
Gly	Val	Ile	Phe	Ala	Gly	Ala	Val	Gln	Asp	Tyr	Leu	Val	Leu	Trp	Val		
			170						175				180				
tct	act	cgt	agg	cgt	gga	cgc	tca	ctt	ggc	cag	atg	gtt	cgt	gat	gaa		691
Ser	Thr	Arg	Arg	Arg	Gly	Arg	Ser	Leu	Gly	Gln	Met	Val	Arg	Asp	Glu		
		185						190					195				
atg	ggc	acg	gtc	ggg	gga	gct	gcc	ggg	atc	ttg	gcg	acc	atc	tcc	atc		739
Met	Gly	Thr	Val	Gly	Gly	Ala	Ala	Gly	Ile	Leu	Ala	Thr	Ile	Ser	Ile		
		200				205						210					
atg	atc	atc	att	atc	gcg	gtg	ctc	gca	ttg	atc	gtg	gtt	aat	gca	ctg		787
Met	Ile	Ile	Ile	Ile	Ala	Val	Leu	Ala	Leu	Ile	Val	Val	Asn	Ala	Leu		
	215					220					225						
gct	gat	tca	cca	tgg	ggc	gtt	ttc	tcc	atc	acc	atg	acc	atc	cca	att		835
Ala	Asp	Ser	Pro	Trp	Gly	Val	Phe	Ser	Ile	Thr	Met	Thr	Ile	Pro	Ile		

230	235	240	245	
gca ctg ttc atg ggt gtg tac ttg cgt tac ctg cgc cca ggt cgt gtt Ala Leu Phe Met Gly Val Tyr Leu Arg Tyr Leu Arg Pro Gly Arg Val 250 255 260				883
act gaa gtg tcc atc atc ggt gtg gca ctg ctc ctg ctg gct atc gtt Thr Glu Val Ser Ile Ile Gly Val Ala Leu Leu Leu Leu Ala Ile Val 265 270 275				931
gct ggt ggt tgg gtt gca gac acc tca tgg ggc gtg gaa tgg ttc acc Ala Gly Gly Trp Val Ala Asp Thr Ser Trp Gly Val Glu Trp Phe Thr 280 285 290				979
tgg tct aag acc act ttg gcg ttg gcc ttg atc ggt tac gga atc atg Trp Ser Lys Thr Thr Leu Ala Leu Ala Leu Ile Gly Tyr Gly Ile Met 295 300 305				1027
gct gcg att ttg ccg gtg tgg ctg ctg ctt gca ccg cgc gat tac ctg Ala Ala Ile Leu Pro Val Trp Leu Leu Leu Ala Pro Arg Asp Tyr Leu 310 315 320 325				1075
tct acc ttt atg aag atc ggc gtc atc ggt ctg ttg gca gtg ggt att Ser Thr Phe Met Lys Ile Gly Val Ile Gly Leu Leu Ala Val Gly Ile 330 335 340				1123
ttg ttc gca cgt cct gag gtg cag atg cct tcc gtg acc tcc ttc gca Leu Phe Ala Arg Pro Glu Val Gln Met Pro Ser Val Thr Ser Phe Ala 345 350 355				1171
ctt gag ggc aac ggt ccg gtg ttc tct gga agt ctg ttc cca ttc ctg Leu Glu Gly Asn Gly Pro Val Phe Ser Gly Ser Leu Phe Pro Phe Leu 360 365 370				1219
ttc atc acg att gcc tgt ggt gca ctg tct ggt ttc cac gca ctg att Phe Ile Thr Ile Ala Cys Gly Ala Leu Ser Gly Phe His Ala Leu Ile 375 380 385				1267
tct tca gga acc aca cca aag ctt gtg gag aag gaa tcc cag atg cgc Ser Ser Gly Thr Thr Pro Lys Leu Val Glu Lys Glu Ser Gln Met Arg 390 395 400 405				1315
atg ctc ggc tac ggc ggc atg ttg atg gaa tct ttc gtg gcg atg atg Met Leu Gly Tyr Gly Gly Met Leu Met Glu Ser Phe Val Ala Met Met 410 415 420				1363
gca ctg atc acc gct gtt att ctg gat cgt cac ctg tac ttc tcc atg Ala Leu Ile Thr Ala Val Ile Leu Asp Arg His Leu Tyr Phe Ser Met 425 430 435				1411
aac gct ccg ctg gca ctg act ggt gga gat cca gca acc gca gct gag Asn Ala Pro Leu Ala Leu Thr Gly Gly Asp Pro Ala Thr Ala Ala Glu 440 445 450				1459
tgg gtt aac tcc att ggg ctg aca ggt gcg gat atc acc ccg gaa cag Trp Val Asn Ser Ile Gly Leu Thr Gly Ala Asp Ile Thr Pro Glu Gln 455 460 465				1507
ctg tcg gaa gct gct gaa agt gtc gga gaa tcc act gtt att tcc cgt Leu Ser Glu Ala Ala Glu Ser Val Gly Glu Ser Thr Val Ile Ser Arg 470 475 480 485				1555

acc ggt ggc gca cca acc ttg gcg ttc ggt atg tct gaa atc ctc tcc	1603
Thr Gly Gly Ala Pro Thr Leu Ala Phe Gly Met Ser Glu Ile Leu Ser	
490 495 500	
gga ttc atc ggc ggc gct gga atg aag gcg ttc tgg tac cac ttc gcc	1651
Gly Phe Ile Gly Gly Ala Gly Met Lys Ala Phe Trp Tyr His Phe Ala	
505 510 515	
atc atg ttt gag gct ctg ttc atc ctc act act gtg gat gca ggt act	1699
Ile Met Phe Glu Ala Leu Phe Ile Leu Thr Thr Val Asp Ala Gly Thr	
520 525 530	
cgt gtg gct cgc ttt atg atg acc gat acc ttg ggc aat gtt cca ggt	1747
Arg Val Ala Arg Phe Met Met Thr Asp Thr Leu Gly Asn Val Pro Gly	
535 540 545	
ctg cgc cgt ttc aag gat cct tca tgg act gtc ggt aac tgg att tct	1795
Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val Gly Asn Trp Ile Ser	
550 555 560 565	
acc gtg ttt gtg tgt gct cta tgg ggt gct att ttg ctc atg ggt gtt	1843
Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile Leu Leu Met Gly Val	
570 575 580	
acc gat cca ctg ggc ggc atc aac gtg ctt ttc cca cta ttc ggt atc	1891
Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe Pro Leu Phe Gly Ile	
585 590 595	
gct aac cag ctg ctc gcc gct att gca ctt gct ctc gtg ctg gtt gtt	1939
Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala Leu Val Leu Val Val	
600 605 610	
gtg gtg aag aag ggc ctg tac aag tgg gcg tgg att cca gct gtt cct	1987
Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp Ile Pro Ala Val Pro	
615 620 625	
ttg gca tgg gat ctc att gtc acg atg act gcg tca tgg cag aag att	2035
Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala Ser Trp Gln Lys Ile	
630 635 640 645	
ttc cac tct gat ccg gct att ggc tac tgg gct cag aac gcg aac ttc	2083
Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala Gln Asn Ala Asn Phe	
650 655 660	
cgc gat gca aag tct caa ggc ctt acc gaa ttt ggt gcc gct aaa tct	2131
Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe Gly Ala Ala Lys Ser	
665 670 675	
cct gag gca atc gat gcg gtt atc cga aac acc atg att cag ggc atc	2179
Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr Met Ile Gln Gly Ile	
680 685 690	
ttg tcc atc ctg ttc gcg gtg ctc gtc ctc gtt gtt gtc ggc gca gcc	2227
Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val Val Gly Ala Ala	
695 700 705	
att gcg gtg tgc atc aag tcc atc agg gct cgt gca gcc gga aca cct	2275
Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg Ala Ala Gly Thr Pro	
710 715 720 725	

ttg gag acc act gaa gag cct gat act gaa tct gag ttc ttc gcc cca 2323
 Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser Glu Phe Phe Ala Pro
 730 735 740

act gga ttc ctt gca tct tcc agg gat aag gaa gtc cag gcc atg tgg 2371
 Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu Val Gln Ala Met Trp
 745 750 755

gac gag cgc tac cca ggc ggt gcg ccc gtg tct tct gga ggg cac 2416
 Asp Glu Arg Tyr Pro Gly Gly Ala Pro Val Ser Ser Gly Gly His
 760 765 770

taaaacatga tggctcttac tca 2439

<210> 14
 <211> 772
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 14
 Val Ala Leu Lys Arg Pro Glu Glu Lys Thr Val Lys Ile Val Thr Ile
 1 5 10 15

Lys Gln Thr Asp Asn Ile Asn Asp Asp Asp Leu Val Tyr Ser Asn Ala
 20 25 30

Thr Asp Leu Pro Val Gly Val Lys Lys Ser Pro Lys Met Ser Pro Thr
 35 40 45

Ala Arg Val Gly Leu Leu Val Phe Gly Val Ile Ala Ala Val Gly Trp
 50 55 60

Gly Ala Ile Ala Phe Ser Arg Gly Glu Thr Ile Asn Ser Val Trp Leu
 65 70 75 80

Val Leu Ala Ala Val Gly Ser Tyr Ile Ile Ala Phe Ser Phe Tyr Ala
 85 90 95

Arg Leu Ile Glu Tyr Lys Val Val Lys Pro Lys Asp Gln Arg Ala Thr
 100 105 110

Pro Ala Glu Tyr Val Asn Asp Gly Lys Asp Tyr Val Pro Thr Asp Arg
 115 120 125

Arg Val Leu Phe Gly His His Phe Ala Ala Ile Ala Gly Ala Gly Pro
 130 135 140

Leu Val Gly Pro Val Met Ala Ala Gln Met Gly Tyr Leu Pro Gly Thr
 145 150 155 160

Leu Trp Ile Ile Leu Gly Val Ile Phe Ala Gly Ala Val Gln Asp Tyr
 165 170 175

Leu Val Leu Trp Val Ser Thr Arg Arg Arg Gly Arg Ser Leu Gly Gln
 180 185 190

Met Val Arg Asp Glu Met Gly Thr Val Gly Gly Ala Ala Gly Ile Leu
 195 200 205

Ala Thr Ile Ser Ile Met Ile Ile Ile Ile Ala Val Leu Ala Leu Ile

210					215					220					
Val	Val	Asn	Ala	Leu	Ala	Asp	Ser	Pro	Trp	Gly	Val	Phe	Ser	Ile	Thr
225					230					235					240
Met	Thr	Ile	Pro	Ile	Ala	Leu	Phe	Met	Gly	Val	Tyr	Leu	Arg	Tyr	Leu
				245					250					255	
Arg	Pro	Gly	Arg	Val	Thr	Glu	Val	Ser	Ile	Ile	Gly	Val	Ala	Leu	Leu
			260					265					270		
Leu	Leu	Ala	Ile	Val	Ala	Gly	Gly	Trp	Val	Ala	Asp	Thr	Ser	Trp	Gly
		275					280					285			
Val	Glu	Trp	Phe	Thr	Trp	Ser	Lys	Thr	Thr	Leu	Ala	Leu	Ala	Leu	Ile
	290					295					300				
Gly	Tyr	Gly	Ile	Met	Ala	Ala	Ile	Leu	Pro	Val	Trp	Leu	Leu	Leu	Ala
305					310					315					320
Pro	Arg	Asp	Tyr	Leu	Ser	Thr	Phe	Met	Lys	Ile	Gly	Val	Ile	Gly	Leu
				325					330					335	
Leu	Ala	Val	Gly	Ile	Leu	Phe	Ala	Arg	Pro	Glu	Val	Gln	Met	Pro	Ser
			340					345					350		
Val	Thr	Ser	Phe	Ala	Leu	Glu	Gly	Asn	Gly	Pro	Val	Phe	Ser	Gly	Ser
		355					360					365			
Leu	Phe	Pro	Phe	Leu	Phe	Ile	Thr	Ile	Ala	Cys	Gly	Ala	Leu	Ser	Gly
	370					375					380				
Phe	His	Ala	Leu	Ile	Ser	Ser	Gly	Thr	Thr	Pro	Lys	Leu	Val	Glu	Lys
385					390					395					400
Glu	Ser	Gln	Met	Arg	Met	Leu	Gly	Tyr	Gly	Gly	Met	Leu	Met	Glu	Ser
				405					410					415	
Phe	Val	Ala	Met	Met	Ala	Leu	Ile	Thr	Ala	Val	Ile	Leu	Asp	Arg	His
			420					425					430		
Leu	Tyr	Phe	Ser	Met	Asn	Ala	Pro	Leu	Ala	Leu	Thr	Gly	Gly	Asp	Pro
		435					440					445			
Ala	Thr	Ala	Ala	Glu	Trp	Val	Asn	Ser	Ile	Gly	Leu	Thr	Gly	Ala	Asp
	450					455					460				
Ile	Thr	Pro	Glu	Gln	Leu	Ser	Glu	Ala	Ala	Glu	Ser	Val	Gly	Glu	Ser
465					470					475					480
Thr	Val	Ile	Ser	Arg	Thr	Gly	Gly	Ala	Pro	Thr	Leu	Ala	Phe	Gly	Met
				485					490					495	
Ser	Glu	Ile	Leu	Ser	Gly	Phe	Ile	Gly	Gly	Ala	Gly	Met	Lys	Ala	Phe
			500					505					510		
Trp	Tyr	His	Phe	Ala	Ile	Met	Phe	Glu	Ala	Leu	Phe	Ile	Leu	Thr	Thr
		515					520					525			
Val	Asp	Ala	Gly	Thr	Arg	Val	Ala	Arg	Phe	Met	Met	Thr	Asp	Thr	Leu
	530					535					540				

Gly Asn Val Pro Gly Leu Arg Arg Phe Lys Asp Pro Ser Trp Thr Val
 545 550 555 560
 Gly Asn Trp Ile Ser Thr Val Phe Val Cys Ala Leu Trp Gly Ala Ile
 565 570 575
 Leu Leu Met Gly Val Thr Asp Pro Leu Gly Gly Ile Asn Val Leu Phe
 580 585 590
 Pro Leu Phe Gly Ile Ala Asn Gln Leu Leu Ala Ala Ile Ala Leu Ala
 595 600 605
 Leu Val Leu Val Val Val Val Lys Lys Gly Leu Tyr Lys Trp Ala Trp
 610 615 620
 Ile Pro Ala Val Pro Leu Ala Trp Asp Leu Ile Val Thr Met Thr Ala
 625 630 635 640
 Ser Trp Gln Lys Ile Phe His Ser Asp Pro Ala Ile Gly Tyr Trp Ala
 645 650 655
 Gln Asn Ala Asn Phe Arg Asp Ala Lys Ser Gln Gly Leu Thr Glu Phe
 660 665 670
 Gly Ala Ala Lys Ser Pro Glu Ala Ile Asp Ala Val Ile Arg Asn Thr
 675 680 685
 Met Ile Gln Gly Ile Leu Ser Ile Leu Phe Ala Val Leu Val Leu Val
 690 695 700
 Val Val Gly Ala Ala Ile Ala Val Cys Ile Lys Ser Ile Arg Ala Arg
 705 710 715 720
 Ala Ala Gly Thr Pro Leu Glu Thr Thr Glu Glu Pro Asp Thr Glu Ser
 725 730 735
 Glu Phe Phe Ala Pro Thr Gly Phe Leu Ala Ser Ser Arg Asp Lys Glu
 740 745 750
 Val Gln Ala Met Trp Asp Glu Arg Tyr Pro Gly Gly Ala Pro Val Ser
 755 760 765
 Ser Gly Gly His
 770

<210> 15
 <211> 255
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(232)
 <223> RXN03119

<400> 15
 tgggaggtgt cgcaccaagt acttttgcga agcgccatct gacggatttt caaaagatgt 60
 atatgctcgg tgcggaaacc tacgaaagga tttttttaccc atg gct gta tac gaa 115

Met Ala Val Tyr Glu
1 5

ctc cca gaa ctc gac tac gca tac gac gct ctc gag cca cac atc gtc 163
Leu Pro Glu Leu Asp Tyr Ala Tyr Asp Ala Leu Glu Pro His Ile Val
10 15 20

gct gaa atc atg gag ctt gac cag tcc aag gac cac gca acc tac gtt 211
Ala Glu Ile Met Glu Leu Asp Gln Ser Lys Asp His Ala Thr Tyr Val
25 30 35

gcg ggc gca aat gca gca ctc taggcactag agaaggcacg cga 255
Ala Gly Ala Asn Ala Ala Leu
40

<210> 16
<211> 44
<212> PRT
<213> Corynebacterium glutamicum

<400> 16
Met Ala Val Tyr Glu Leu Pro Glu Leu Asp Tyr Ala Tyr Asp Ala Leu
1 5 10 15

Glu Pro His Ile Val Ala Glu Ile Met Glu Leu Asp Gln Ser Lys Asp
20 25 30

His Ala Thr Tyr Val Ala Gly Ala Asn Ala Ala Leu
35 40

<210> 17
<211> 249
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(226)
<223> RXN03120

<400> 17
ctgggcagtt cttgggtacg accacatc cggtcgcctg gttatcgagc agctcaccga 60

ccaggagggc aacatctcct tcgacatcac ccagttctg atg ctc gat atg tgg 115
Met Leu Asp Met Trp
1 5

gag cac gct ttc tac ctg cag tac atg aac gtt aag gca gat tac gtc 163
Glu His Ala Phe Tyr Leu Gln Tyr Met Asn Val Lys Ala Asp Tyr Val
10 15 20

aag gct gtt tgg aac gtc ttc aac tgg gac gac gca aga gca cgc ttc 211
Lys Ala Val Trp Asn Val Phe Asn Trp Asp Asp Ala Arg Ala Arg Phe
25 30 35

gca gca gct tcc aag taagcatttt tagtccgtgc aat 249
Ala Ala Ala Ser Lys
40

<400> 19															60
gaagcggtccg caggcaagaa aacgtcccgg aaaacggcga taggggtcac ccgcgcatgt															
ccggttgccg atctattttaa ataccaggac aattgcgtgc															115
Met Val Glu Arg Asp															5
1															
ttc act atc cga cca atc cgc gag ggt gat ttc cct cag gtg agg gac															163
Phe Thr Ile Arg Pro Ile Arg Glu Gly Asp Phe Pro Gln Val Arg Asp															20
10 15															
atc tac gaa ttg ggc ctg gag acg gga cat gcg act tat gag act tct															211
Ile Tyr Glu Leu Gly Leu Glu Thr Gly His Ala Thr Tyr Glu Thr Ser															35
25 30															
ggg ccc acg tgg gac cag ttc tcc caa tct aaa atc atg gat acc gtc															259
Gly Pro Thr Trp Asp Gln Phe Ser Ser Gln Ser Lys Ile Met Asp Thr Val															50
40 45															
atg gtg gcg gta gaa aac aac gac ccg gac ttc atc ctc gga tgg gtg															307
Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu Gly Trp Val															65
55 60															
tct gct gct cca att tca agc cga cag gtt ttc cat gga gtg gtg gaa															355
Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly Val Val Glu															85
70 75 80															
gat tcc atc tat atc cac ccc cag ggc caa ggc cga gga atc ggc ggc															403
Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly Ile Gly Gly															100
90 95															
gct ttg ctc gac gcc ctt atc acc tac tgc gaa agc aac ggc atc tgg															451
Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn Gly Ile Trp															115
105 110															

tcg atc cac tcc tgg atc ttc ccg gaa aac ctc ggt tct gcg aaa ctg 499
 Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser Ala Lys Leu
 120 125 130

cat gaa tgc aag ggc ttc gtg aag gtg ggc acc atg cac caa atg gca 547
 His Glu Ser Lys Gly Phe Val Lys Val Gly Thr Met His Gln Met Ala
 135 140 145

agg atg ccc tac ggc gag atg gaa gga caa tgg cgc gat tgt gat ctg 595
 Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp Cys Asp Leu
 150 155 160 165

tgg gag tgc ctc tta tcc gtt cca gag caa gct caa agt tcc 637
 Trp Glu Cys Leu Leu Ser Val Pro Glu Gln Ala Gln Ser Ser
 170 175

taaagcaatt taaatctgac ttt 660

<210> 20

<211> 179

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 20

Met Val Glu Arg Asp Phe Thr Ile Arg Pro Ile Arg Glu Gly Asp Phe
 1 5 10 15

Pro Gln Val Arg Asp Ile Tyr Glu Leu Gly Leu Glu Thr Gly His Ala
 20 25 30

Thr Tyr Glu Thr Ser Gly Pro Thr Trp Asp Gln Phe Ser Gln Ser Lys
 35 40 45

Ile Met Asp Thr Val Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe
 50 55 60

Ile Leu Gly Trp Val Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe
 65 70 75 80

His Gly Val Val Glu Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly
 85 90 95

Arg Gly Ile Gly Gly Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu
 100 105 110

Ser Asn Gly Ile Trp Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu
 115 120 125

Gly Ser Ala Lys Leu His Glu Ser Lys Gly Phe Val Lys Val Gly Thr
 130 135 140

Met His Gln Met Ala Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp
 145 150 155 160

Arg Asp Cys Asp Leu Trp Glu Cys Leu Leu Ser Val Pro Glu Gln Ala
 165 170 175

Gln Ser Ser

<400> 21																60
gcatgtccgg ttgccgatct atttaaatac caggacaatt gcgtgcatgg ttgaaagaga																
cttcactatc cgaccaatcc gcgagggtga tttccctcag																115
Val Arg Asp Ile Tyr																1 5
gaa ttg ggc ctg gag acg gga cat gcg act tat gag act tct ggt ccc																163
Glu Leu Gly Leu Glu Thr Gly His Ala Thr Tyr Glu Thr Ser Gly Pro																10 15 20
acg tgg gac cag ttc tcc caa tct aaa atc atg gat acc gtc atg gtg																211
Thr Trp Asp Gln Phe Ser Gln Ser Lys Ile Met Asp Thr Val Met Val																25 30 35
gcg gta gaa aac aac gac ccg gac ttc atc ctc gga tgg gtg tct gct																259
Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu Gly Trp Val Ser Ala																40 45 50
gct cca att tca agc cga cag gtt ttc cat gga gtg gtg gaa gat tcc																307
Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly Val Val Glu Asp Ser																55 60 65
atc tat atc cac ccc cag ggc caa ggc cga gga atc ggc ggc gct ttg																355
Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly Ile Gly Gly Ala Leu																70 75 80 85
ctc gac gcc ctt atc acc tac tgc gaa agc aac ggc atc tgg tcg atc																403
Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn Gly Ile Trp Ser Ile																90 95 100
cac tcc tgg atc ttc ccg gaa aac ctc ggt tct gcg aaa ctg cat gaa																451
His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser Ala Lys Leu His Glu																105 110 115
tcg aag ggc ttc gtg aag gtg ggc acc atg cac caa atg gca agg atg																499
Ser Lys Gly Phe Val Lys Val Gly Thr Met His Gln Met Ala Arg Met																120 125 130
ccc tac ggc gag atg gaa gga caa tgg cgc gat tgt gat ctg tgg gag																547
Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp Cys Asp Leu Trp Glu																135 140 145
tgc ctc tta tcc gtt cca gag caa gct caa agt tcc taaagcaatt																593
Cys Leu Leu Ser Val Pro Glu Gln Ala Gln Ser Ser																150 155 160
taaattctgac ttt																606

<210> 22
 <211> 161
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 22
 Val Arg Asp Ile Tyr Glu Leu Gly Leu Glu Thr Gly His Ala Thr Tyr
 1 5 10 15
 Glu Thr Ser Gly Pro Thr Trp Asp Gln Phe Ser Gln Ser Lys Ile Met
 20 25 30
 Asp Thr Val Met Val Ala Val Glu Asn Asn Asp Pro Asp Phe Ile Leu
 35 40 45
 Gly Trp Val Ser Ala Ala Pro Ile Ser Ser Arg Gln Val Phe His Gly
 50 55 60
 Val Val Glu Asp Ser Ile Tyr Ile His Pro Gln Gly Gln Gly Arg Gly
 65 70 75 80
 Ile Gly Gly Ala Leu Leu Asp Ala Leu Ile Thr Tyr Cys Glu Ser Asn
 85 90 95
 Gly Ile Trp Ser Ile His Ser Trp Ile Phe Pro Glu Asn Leu Gly Ser
 100 105 110
 Ala Lys Leu His Glu Ser Lys Gly Phe Val Lys Val Gly Thr Met His
 115 120 125
 Gln Met Ala Arg Met Pro Tyr Gly Glu Met Glu Gly Gln Trp Arg Asp
 130 135 140
 Cys Asp Leu Trp Glu Cys Leu Leu Ser Val Pro Glu Gln Ala Gln Ser
 145 150 155 160
 Ser

<210> 23
 <211> 1575
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1552)
 <223> RXN01345

<400> 23
 cataacctca ttgaacatgc aaaactaatg cttttggggg gtatgcataa attcgtttcg 60
 ttccactgca cagcccgaaa atgctgctag ggtcaagttc atg cgt ttt gga ctt 115
 Met Arg Phe Gly Leu
 1 5
 gac ttg gga act acc cgc aca atc gcg gcc gcc gtg gac cgc gga aac 163
 Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala Val Asp Arg Gly Asn
 10 15 20

tat	ccc	atc	gtc	act	gtg	gaa	gat	tct	tta	ggc	gac	acc	cac	gat	ttc	211
Tyr	Pro	Ile	Val	Thr	Val	Glu	Asp	Ser	Leu	Gly	Asp	Thr	His	Asp	Phe	
			25					30					35			
att	cca	tct	gtg	gtg	gcc	ctc	aag	gca	gat	agg	att	gtc	gcg	ggg	tgg	259
Ile	Pro	Ser	Val	Val	Ala	Leu	Lys	Ala	Asp	Arg	Ile	Val	Ala	Gly	Trp	
		40					45					50				
gat	gct	att	gag	gtt	ggg	cag	gac	cac	cct	tcc	ttc	gta	cgt	tct	ttc	307
Asp	Ala	Ile	Glu	Val	Gly	Gln	Asp	His	Pro	Ser	Phe	Val	Arg	Ser	Phe	
	55					60					65					
aaa	cgc	cta	ctc	tct	gaa	ccc	aat	gtc	acg	gaa	gcc	acc	ccg	gtc	tac	355
Lys	Arg	Leu	Leu	Ser	Glu	Pro	Asn	Val	Thr	Glu	Ala	Thr	Pro	Val	Tyr	
70					75				80						85	
ttg	ggc	gat	cat	gta	cac	cct	ttg	ggc	gcc	gtc	ctg	gag	gct	ttt	gcg	403
Leu	Gly	Asp	His	Val	His	Pro	Leu	Gly	Ala	Val	Leu	Glu	Ala	Phe	Ala	
				90				95						100		
gaa	aac	gtg	gtc	act	gcg	ctg	cgt	gca	ttt	cag	acg	caa	ttg	gga	gat	451
Glu	Asn	Val	Val	Thr	Ala	Leu	Arg	Ala	Phe	Gln	Thr	Gln	Leu	Gly	Asp	
			105					110					115			
acc	tcc	ccg	atc	gaa	gta	gtc	att	ggg	gtg	ccc	gcc	aac	tcc	cac	agc	499
Thr	Ser	Pro	Ile	Glu	Val	Val	Ile	Gly	Val	Pro	Ala	Asn	Ser	His	Ser	
		120					125					130				
gcc	cag	cga	ctg	ctc	acc	atg	tcc	gcc	ttc	agc	gcc	aca	ggc	atc	acc	547
Ala	Gln	Arg	Leu	Leu	Thr	Met	Ser	Ala	Phe	Ser	Ala	Thr	Gly	Ile	Thr	
	135					140					145					
gtt	gtc	ggg	ttg	gtc	aat	gag	ccc	agc	gcc	gca	gct	ttc	gag	tac	acc	595
Val	Val	Gly	Leu	Val	Asn	Glu	Pro	Ser	Ala	Ala	Ala	Phe	Glu	Tyr	Thr	
150					155				160					165		
cac	cgc	cac	gcc	cgc	acc	tta	aac	tcc	aag	cgc	caa	gcc	atc	gtg	gtt	643
His	Arg	His	Ala	Arg	Thr	Leu	Asn	Ser	Lys	Arg	Gln	Ala	Ile	Val	Val	
			170					175						180		
tat	gat	ttg	gga	ggc	gga	aca	ttc	gac	tcc	tcg	ctc	atc	cgc	atc	gac	691
Tyr	Asp	Leu	Gly	Gly	Gly	Thr	Phe	Asp	Ser	Ser	Leu	Ile	Arg	Ile	Asp	
			185					190					195			
ggc	acc	cac	cac	gag	gtt	gtg	tcc	tcc	att	ggc	att	tca	cgc	ctt	ggg	739
Gly	Thr	His	His	Glu	Val	Val	Ser	Ser	Ile	Gly	Ile	Ser	Arg	Leu	Gly	
		200					205					210				
ggc	gat	gat	ttc	gat	gaa	atc	ctc	ctc	caa	tgc	gcg	ctc	aag	gcc	gca	787
Gly	Asp	Asp	Phe	Asp	Glu	Ile	Leu	Leu	Gln	Cys	Ala	Leu	Lys	Ala	Ala	
	215					220					225					
ggc	aga	cag	cac	gat	gcg	ttt	ggc	aag	cgt	gct	aaa	aac	acg	ctt	ctc	835
Gly	Arg	Gln	His	Asp	Ala	Phe	Gly	Lys	Arg	Ala	Lys	Asn	Thr	Leu	Leu	
230					235				240					245		
gac	gaa	tcc	cgc	aac	gcg	aag	gaa	gct	ctt	gtt	ccg	caa	tcc	cgt	cgc	883
Asp	Glu	Ser	Arg	Asn	Ala	Lys	Glu	Ala	Leu	Val	Pro	Gln	Ser	Arg	Arg	
				250				255						260		

ttg gtt cta gaa att ggc gac gac gac atc acc gtt cca gtg aac aag	931
Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr Val Pro Val Asn Lys	
265 270 275	
ttc tac gag gct gcc act ccc ctg gtg gaa aaa tcc ttg tcc atc atg	979
Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys Ser Leu Ser Ile Met	
280 285 290	
gaa ccc ctc atc ggc gtc gat gat ctt aaa gat tcc gac atc gca ggc	1027
Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp Ser Asp Ile Ala Gly	
295 300 305	
atc tac ctt gtt ggt gga gga tcc tcg ctc cca ctc gtt tcc agg ttg	1075
Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro Leu Val Ser Arg Leu	
310 315 320 325	
ctc cgc gag cgt ttc ggc cgc cgt gtc cac cgc tcc cca ttc ccc tca	1123
Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg Ser Pro Phe Pro Ser	
330 335 340	
ggt tcc act gcg gtg ggt ctg gcc atc gcg gct gac cct tcc tct ggt	1171
Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala Asp Pro Ser Ser Gly	
345 350 355	
ttc cac cta agg gac cgc gtt gcg cga ggc atc ggt gtg ttc cgt gag	1219
Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile Gly Val Phe Arg Glu	
360 365 370	
cac gat tct ggt cgt gcc gtg agc ttt gac ccg ctg atc gcc ccg gac	1267
His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro Leu Ile Ala Pro Asp	
375 380 385	
acc gat tct gcg acc gtg gcg aaa cga tgc tac aag gcg gtg cac aac	1315
Thr Asp Ser Ala Thr Val Ala Lys Arg Cys Tyr Lys Ala Val His Asn	
390 395 400 405	
att ggt tgg ttc agg ttc gtg gaa tac tcc acc gtg tcc gag gat ggc	1363
Ile Gly Trp Phe Arg Phe Val Glu Tyr Ser Thr Val Ser Glu Asp Gly	
410 415 420	
agc ccc gga gat att tcc ctg ctc agt gaa atc aag att cct ttt gat	1411
Ser Pro Gly Asp Ile Ser Leu Leu Ser Glu Ile Lys Ile Pro Phe Asp	
425 430 435	
agc tcc atc acc gat gtg gat gct acc gag att tca cgt ttc gat ggc	1459
Ser Ser Ile Thr Asp Val Asp Ala Thr Glu Ile Ser Arg Phe Asp Gly	
440 445 450	
cca gaa gta gaa gaa acc atc aca gtc aat gac aac ggc gtg gct tcc	1507
Pro Glu Val Glu Glu Thr Ile Thr Val Asn Asp Asn Gly Val Ala Ser	
455 460 465	
att tcc atc aag ata ctc ggc ggc gtt acc gtc gag cac aca att	1552
Ile Ser Ile Lys Ile Leu Gly Gly Val Thr Val Glu His Thr Ile	
470 475 480	
tagttaccat tttggtgctg gtg	1575

<210> 24

<211> 484

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 24

```

Met Arg Phe Gly Leu Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala
 1           5           10           15

Val Asp Arg Gly Asn Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly
          20           25           30

Asp Thr His Asp Phe Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg
          35           40           45

Ile Val Ala Gly Trp Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser
 50           55           60

Phe Val Arg Ser Phe Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu
 65           70           75           80

Ala Thr Pro Val Tyr Leu Gly Asp His Val His Pro Leu Gly Ala Val
          85           90           95

Leu Glu Ala Phe Ala Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln
          100          105          110

Thr Gln Leu Gly Asp Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro
          115          120          125

Ala Asn Ser His Ser Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser
          130          135          140

Ala Thr Gly Ile Thr Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala
          145          150          155          160

Ala Phe Glu Tyr Thr His Arg His Ala Arg Thr Leu Asn Ser Lys Arg
          165          170          175

Gln Ala Ile Val Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser
          180          185          190

Leu Ile Arg Ile Asp Gly Thr His His Glu Val Val Ser Ser Ile Gly
          195          200          205

Ile Ser Arg Leu Gly Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys
          210          215          220

Ala Leu Lys Ala Ala Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala
          225          230          235          240

Lys Asn Thr Leu Leu Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val
          245          250          255

Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr
          260          265          270

Val Pro Val Asn Lys Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys
          275          280          285

Ser Leu Ser Ile Met Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp
          290          295          300

```

Ser Asp Ile Ala Gly Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro
 305 310 315 320
 Leu Val Ser Arg Leu Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg
 325 330 335
 Ser Pro Phe Pro Ser Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala
 340 345 350
 Asp Pro Ser Ser Gly Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile
 355 360 365
 Gly Val Phe Arg Glu His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro
 370 375 380
 Leu Ile Ala Pro Asp Thr Asp Ser Ala Thr Val Ala Lys Arg Cys Tyr
 385 390 395 400
 Lys Ala Val His Asn Ile Gly Trp Phe Arg Phe Val Glu Tyr Ser Thr
 405 410 415
 Val Ser Glu Asp Gly Ser Pro Gly Asp Ile Ser Leu Leu Ser Glu Ile
 420 425 430
 Lys Ile Pro Phe Asp Ser Ser Ile Thr Asp Val Asp Ala Thr Glu Ile
 435 440 445
 Ser Arg Phe Asp Gly Pro Glu Val Glu Glu Thr Ile Thr Val Asn Asp
 450 455 460
 Asn Gly Val Ala Ser Ile Ser Ile Lys Ile Leu Gly Gly Val Thr Val
 465 470 475 480
 Glu His Thr Ile

<210> 25
 <211> 1267
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1267)
 <223> FRXA01345

<400> 25
 cataacctca ttgaacatgc aaaactaatg cttttggggg gtatgcataa attcgtttcg 60
 ttccactgca cagcccgaaa atgctgctag ggtcaagttc atg cgt ttt gga ctt 115
 Met Arg Phe Gly Leu
 1 5
 gac ttg gga act acc cgc aca atc gcg gcc gcc gtg gac cgc gga aac 163
 Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala Val Asp Arg Gly Asn
 10 15 20
 tat ccc atc gtc act gtg gaa gat tct tta ggc gac acc cac gat ttc 211
 Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly Asp Thr His Asp Phe
 25 30 35

att cca tct gtg gtg gcc ctc aag gca gat agg att gtc gcg ggt tgg	259
Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg Ile Val Ala Gly Trp	
40 45 50	
gat gct att gag gtt ggg cag gac cac cct tcc ttc gta cgt tct ttc	307
Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser Phe Val Arg Ser Phe	
55 60 65	
aaa cgc cta ctc tct gaa ccc aat gtc acg gaa gcc acc ccg gtc tac	355
Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu Ala Thr Pro Val Tyr	
70 75 80 85	
ttg ggc gat cat gta cac cct ttg ggc gcc gtc ctg gag gct ttt gcg	403
Leu Gly Asp His Val His Pro Leu Gly Ala Val Leu Glu Ala Phe Ala	
90 95 100	
gaa aac gtg gtc act gcg ctg cgt gca ttt cag acg caa ttg gga gat	451
Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln Thr Gln Leu Gly Asp	
105 110 115	
acc tcc ccg atc gaa gta gtc att ggt gtg ccc gcc aac tcc cac agc	499
Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro Ala Asn Ser His Ser	
120 125 130	
gcc cag cga ctg ctc acc atg tcc gcc ttc agc gcc aca ggc atc acc	547
Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser Ala Thr Gly Ile Thr	
135 140 145	
gtt gtc ggt ttg gtc aat gag ccc agc gcc gca gct ttc gag tac acc	595
Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala Phe Glu Tyr Thr	
150 155 160 165	
cac cgc cac gcc cgc acc tta aac tcc aag cgc caa gcc atc gtg gtt	643
His Arg His Ala Arg Thr Leu Asn Ser Lys Arg Gln Ala Ile Val Val	
170 175 180	
tat gat ttg gga ggc gga aca ttc gac tcc tcg ctc atc cgc atc gac	691
Tyr Asp Leu Gly Gly Thr Phe Asp Ser Ser Leu Ile Arg Ile Asp	
185 190 195	
ggc acc cac cac gag gtt gtg tcc tcc att ggc att tca cgc ctt ggt	739
Gly Thr His His Glu Val Val Ser Ser Ile Gly Ile Ser Arg Leu Gly	
200 205 210	
ggc gat gat ttc gat gaa atc ctc ctc caa tgc gcg ctc aag gcc gca	787
Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys Ala Leu Lys Ala Ala	
215 220 225	
ggc aga cag cac gat gcg ttt ggc aag cgt gct aaa aac acg ctt ctc	835
Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala Lys Asn Thr Leu Leu	
230 235 240 245	
gac gaa tcc cgc aac gcg aag gaa gct ctt gtt ccg caa tcc cgt cgc	883
Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val Pro Gln Ser Arg Arg	
250 255 260	
ttg gtt cta gaa att ggc gac gac gac atc acc gtt cca gtg aac aag	931
Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr Val Pro Val Asn Lys	
265 270 275	

ttc tac gag gct gcc act ccc ctg gtg gaa aaa tcc ttg tcc atc atg 979
 Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys Ser Leu Ser Ile Met
 280 285 290

gaa ccc ctc atc ggc gtc gat gat ctt aaa gat tcc gac atc gca ggc 1027
 Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp Ser Asp Ile Ala Gly
 295 300 305

atc tac ctt gtt ggt gga gga tcc tcg ctc cca ctc gtt tcc agg ttg 1075
 Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro Leu Val Ser Arg Leu
 310 315 320 325

ctc cgc gag cgt ttc ggc cgc cgt gtc cac cgc tcc cca ttc ccc tca 1123
 Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg Ser Pro Phe Pro Ser
 330 335 340

ggt tcc act gcg gtg ggt ctg gcc atc gcg gct gac cct tcc tct ggt 1171
 Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala Asp Pro Ser Ser Gly
 345 350 355

ttc cac cta agg gac cgc gtt gcg cga ggc atc ggt gtg ttc cgt gag 1219
 Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile Gly Val Phe Arg Glu
 360 365 370

cac gat tct ggt cgt gcc gtg agc ttt gac ccg ctg atc gcc ccg gac 1267
 His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro Leu Ile Ala Pro Asp
 375 380 385

<210> 26
 <211> 389
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 26
 Met Arg Phe Gly Leu Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala
 1 5 10 15

Val Asp Arg Gly Asn Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly
 20 25 30

Asp Thr His Asp Phe Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg
 35 40 45

Ile Val Ala Gly Trp Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser
 50 55 60

Phe Val Arg Ser Phe Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu
 65 70 75 80

Ala Thr Pro Val Tyr Leu Gly Asp His Val His Pro Leu Gly Ala Val
 85 90 95

Leu Glu Ala Phe Ala Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln
 100 105 110

Thr Gln Leu Gly Asp Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro
 115 120 125

Ala Asn Ser His Ser Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser
 130 135 140

Ala Thr Gly Ile Thr Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala
 145 150 155 160
 Ala Phe Glu Tyr Thr His Arg His Ala Arg Thr Leu Asn Ser Lys Arg
 165 170 175
 Gln Ala Ile Val Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser
 180 185 190
 Leu Ile Arg Ile Asp Gly Thr His His Glu Val Val Ser Ser Ile Gly
 195 200 205
 Ile Ser Arg Leu Gly Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys
 210 215 220
 Ala Leu Lys Ala Ala Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala
 225 230 235 240
 Lys Asn Thr Leu Leu Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val
 245 250 255
 Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr
 260 265 270
 Val Pro Val Asn Lys Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys
 275 280 285
 Ser Leu Ser Ile Met Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp
 290 295 300
 Ser Asp Ile Ala Gly Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro
 305 310 315 320
 Leu Val Ser Arg Leu Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg
 325 330 335
 Ser Pro Phe Pro Ser Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala
 340 345 350
 Asp Pro Ser Ser Gly Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile
 355 360 365
 Gly Val Phe Arg Glu His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro
 370 375 380
 Leu Ile Ala Pro Asp
 385

<210> 27
 <211> 1308
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1285)
 <223> RXA02541

<400> 27

atccgccggt gtccggacaa caaaacttgc aacacaagat aacttaagaa attgcataca 60

attcaccgca tataagactc atggaaggag gggatgccca gtg aac aac agc gaa 115
Val Asn Asn Ser Glu
1 5

tgg gca aat aag aac tat tac gca gac ctg ggg gtc tcc tcg tcc gct 163
Trp Ala Asn Lys Asn Tyr Tyr Ala Asp Leu Gly Val Ser Ser Ser Ala
10 15 20

tca gaa gat gag atc aaa aag gct tac cgc aag ctc gcc agg gaa aat 211
Ser Glu Asp Glu Ile Lys Lys Ala Tyr Arg Lys Leu Ala Arg Glu Asn
25 30 35

cac cca gat aaa aat cca ggt gac aag gcc gct gaa gat cga ttc aaa 259
His Pro Asp Lys Asn Pro Gly Asp Lys Ala Ala Glu Asp Arg Phe Lys
40 45 50

aaa gcg gcc gag gca tat gac gta ctt ggt gat gac aag aaa cga aaa 307
Lys Ala Ala Glu Ala Tyr Asp Val Leu Gly Asp Asp Lys Lys Arg Lys
55 60 65

gaa tac gac gag ctc aaa gca ctt cta gct tct ggt gga atc cgc gga 355
Glu Tyr Asp Glu Leu Lys Ala Leu Leu Ala Ser Gly Gly Ile Arg Gly
70 75 80 85

gga ttc gga agc gga ggt gcg gga ttc ccc ggc ggg ttt cgc acg tcg 403
Gly Phe Gly Ser Gly Gly Ala Gly Phe Pro Gly Gly Phe Arg Thr Ser
90 95 100

acg gga gga ttc gac acc tca gac ctc ttc gga gga gga caa ggt gga 451
Thr Gly Gly Phe Asp Thr Ser Asp Leu Phe Gly Gly Gly Gln Gly Gly
105 110 115

ggg ttt tct acg gac ggc ggt ttg ggc gat atc ttc ggt ggc ctt ttc 499
Gly Phe Ser Thr Asp Gly Gly Leu Gly Asp Ile Phe Gly Gly Leu Phe
120 125 130

aac cgc ggc gct ggt tct cac cag tca gct agg ccg acg cgg ggg gcg 547
Asn Arg Gly Ala Gly Ser His Gln Ser Ala Arg Pro Thr Arg Gly Ala
135 140 145

gat gta caa acc gaa ata act ctc tcg ttt gtt gag gca gcg aaa ggc 595
Asp Val Gln Thr Glu Ile Thr Leu Ser Phe Val Glu Ala Ala Lys Gly
150 155 160 165

acg acc atc cca gtg gaa ctc acc ggc gat gcg ccc tgc aac acc tgc 643
Thr Thr Ile Pro Val Glu Leu Thr Gly Asp Ala Pro Cys Asn Thr Cys
170 175 180

cac gga tcg ggc tcc aaa tca ggc cac ccc gca aaa tgt gga acc tgt 691
His Gly Ser Gly Ser Lys Ser Gly His Pro Ala Lys Cys Gly Thr Cys
185 190 195

gat gga acc gga ttc acc tct gag aac aag ggt gct ttc gga ttc tcc 739
Asp Gly Thr Gly Phe Thr Ser Glu Asn Lys Gly Ala Phe Gly Phe Ser
200 205 210

gct cca tgt gca acc tgt ggt ggc act ggt gaa ata atc act gat cct 787
Ala Pro Cys Ala Thr Cys Gly Gly Thr Gly Glu Ile Ile Thr Asp Pro
215 220 225

tgc gat aac tgc cac ggc cga ggc acc gtc cgg aag tct cgt tcc atc 835
 Cys Asp Asn Cys His Gly Arg Gly Thr Val Arg Lys Ser Arg Ser Ile
 230 235 240 245

acc gtg cgt atc cca act ggt gtg gaa gat gga cag aaa gtt cgt ctt 883
 Thr Val Arg Ile Pro Thr Gly Val Glu Asp Gly Gln Lys Val Arg Leu
 250 255 260

gca ggc caa ggc gaa gca gga cca aat ggc aaa cca gcg ggc gat ctc 931
 Ala Gly Gln Gly Glu Ala Gly Pro Asn Gly Lys Pro Ala Gly Asp Leu
 265 270 275

ttt gtg aaa gtc cac gtg aaa aag gac gat gtg ttc aca cgc gac ggc 979
 Phe Val Lys Val His Val Lys Lys Asp Asp Val Phe Thr Arg Asp Gly
 280 285 290

agc aac att ttg atc acc att ccc gtg agc ttc agc gag ctg gct ttg 1027
 Ser Asn Ile Leu Ile Thr Ile Pro Val Ser Phe Ser Glu Leu Ala Leu
 295 300 305

ggt ggc gct att tct gtg cca acg ctc aac aag cct gta aaa ctc aag 1075
 Gly Gly Ala Ile Ser Val Pro Thr Leu Asn Lys Pro Val Lys Leu Lys
 310 315 320 325

cta cct gcg gga acg cca gat ggt cgt act ttg cgt gta cgc ggt cgc 1123
 Leu Pro Ala Gly Thr Pro Asp Gly Arg Thr Leu Arg Val Arg Gly Arg
 330 335 340

ggt atc gaa gca cgt gat tcc act ggt gat ctg ctg gtt aca gtc cag 1171
 Gly Ile Glu Ala Arg Asp Ser Thr Gly Asp Leu Leu Val Thr Val Gln
 345 350 355

gtt tct gtc ccg aag aat ctg gat gac aac gct gcg gaa gct ctc cgc 1219
 Val Ser Val Pro Lys Asn Leu Asp Asp Asn Ala Ala Glu Ala Leu Arg
 360 365 370

gca tat gct gaa gca gaa act aat tca ggt ttt gat ccc cgc gct aac 1267
 Ala Tyr Ala Glu Ala Glu Thr Asn Ser Gly Phe Asp Pro Arg Ala Asn
 375 380 385

tgg gcg ggc cag aac cgc tagacgttct ctttgagaaa gga 1308
 Trp Ala Gly Gln Asn Arg
 390 395

<210> 28

<211> 395

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 28

Val Asn Asn Ser Glu Trp Ala Asn Lys Asn Tyr Tyr Ala Asp Leu Gly
 1 5 10 15

Val Ser Ser Ser Ala Ser Glu Asp Glu Ile Lys Lys Ala Tyr Arg Lys
 20 25 30

Leu Ala Arg Glu Asn His Pro Asp Lys Asn Pro Gly Asp Lys Ala Ala
 35 40 45

Glu Asp Arg Phe Lys Lys Ala Ala Glu Ala Tyr Asp Val Leu Gly Asp
 50 55 60
 Asp Lys Lys Arg Lys Glu Tyr Asp Glu Leu Lys Ala Leu Leu Ala Ser
 65 70 75 80
 Gly Gly Ile Arg Gly Gly Phe Gly Ser Gly Gly Ala Gly Phe Pro Gly
 85 90 95
 Gly Phe Arg Thr Ser Thr Gly Gly Phe Asp Thr Ser Asp Leu Phe Gly
 100 105 110
 Gly Gly Gln Gly Gly Gly Phe Ser Thr Asp Gly Gly Leu Gly Asp Ile
 115 120 125
 Phe Gly Gly Leu Phe Asn Arg Gly Ala Gly Ser His Gln Ser Ala Arg
 130 135 140
 Pro Thr Arg Gly Ala Asp Val Gln Thr Glu Ile Thr Leu Ser Phe Val
 145 150 155 160
 Glu Ala Ala Lys Gly Thr Thr Ile Pro Val Glu Leu Thr Gly Asp Ala
 165 170 175
 Pro Cys Asn Thr Cys His Gly Ser Gly Ser Lys Ser Gly His Pro Ala
 180 185 190
 Lys Cys Gly Thr Cys Asp Gly Thr Gly Phe Thr Ser Glu Asn Lys Gly
 195 200 205
 Ala Phe Gly Phe Ser Ala Pro Cys Ala Thr Cys Gly Gly Thr Gly Glu
 210 215 220
 Ile Ile Thr Asp Pro Cys Asp Asn Cys His Gly Arg Gly Thr Val Arg
 225 230 235 240
 Lys Ser Arg Ser Ile Thr Val Arg Ile Pro Thr Gly Val Glu Asp Gly
 245 250 255
 Gln Lys Val Arg Leu Ala Gly Gln Gly Glu Ala Gly Pro Asn Gly Lys
 260 265 270
 Pro Ala Gly Asp Leu Phe Val Lys Val His Val Lys Lys Asp Asp Val
 275 280 285
 Phe Thr Arg Asp Gly Ser Asn Ile Leu Ile Thr Ile Pro Val Ser Phe
 290 295 300
 Ser Glu Leu Ala Leu Gly Gly Ala Ile Ser Val Pro Thr Leu Asn Lys
 305 310 315 320
 Pro Val Lys Leu Lys Leu Pro Ala Gly Thr Pro Asp Gly Arg Thr Leu
 325 330 335
 Arg Val Arg Gly Arg Gly Ile Glu Ala Arg Asp Ser Thr Gly Asp Leu
 340 345 350
 Leu Val Thr Val Gln Val Ser Val Pro Lys Asn Leu Asp Asp Asn Ala
 355 360 365
 Ala Glu Ala Leu Arg Ala Tyr Ala Glu Ala Glu Thr Asn Ser Gly Phe

370 375 380

Asp Pro Arg Ala Asn Trp Ala Gly Gln Asn Arg
 385 390 395

<210> 29
 <211> 777
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(754)
 <223> RXA02542

<400> 29
 ccaggctgac gcaggtgcag aaggcgcctgc agatgacaat gttgttgacg ctgaagttgt 60

cgaagacgac gcagctgaca atggtgagga caagaagtaa atg act acc cct aac 115
 Met Thr Thr Pro Asn
 1 5

gga atg ccc gac aat cct ggg gat cct gaa aat acc gat cca gag gca 163
 Gly Met Pro Asp Asn Pro Gly Asp Pro Glu Asn Thr Asp Pro Glu Ala
 10 15 20

acc tct gct gat cgt gct gag cag gca gct gaa gaa gca gct gcc cgc 211
 Thr Ser Ala Asp Arg Ala Glu Gln Ala Ala Glu Glu Ala Ala Arg
 25 30 35

caa gcg gag gaa tct cca ttt gga cag gcc tca gag gaa gaa att tct 259
 Gln Ala Glu Glu Ser Pro Phe Gly Gln Ala Ser Glu Glu Glu Ile Ser
 40 45 50

cca gag ctc gaa gca gag atc aat gat ctt cta tca gat gtt gat cca 307
 Pro Glu Leu Glu Ala Glu Ile Asn Asp Leu Leu Ser Asp Val Asp Pro
 55 60 65

gat ttg gat ggc gat ggt gaa gtg tcc gct gta gaa aca cag ctt gcc 355
 Asp Leu Asp Gly Asp Gly Glu Val Ser Ala Val Glu Thr Gln Leu Ala
 70 75 80 85

gaa cgc act gag gat ctg cag cga gtc acc gct gag tac gcc aac tac 403
 Glu Arg Thr Glu Asp Leu Gln Arg Val Thr Ala Glu Tyr Ala Asn Tyr
 90 95 100

cgt cga cgt acc gag cgt gaa cgc cag ggc atc atc gac acc gca cgc 451
 Arg Arg Arg Thr Glu Arg Glu Arg Gln Gly Ile Ile Asp Thr Ala Arg
 105 110 115

gca ggt gtt gtt acc caa ctt ctg ccg ttg ctc gac gat ctt gac ctg 499
 Ala Gly Val Val Thr Gln Leu Leu Pro Leu Leu Asp Asp Leu Asp Leu
 120 125 130

gct gaa cag cac ggt gac ctt aac gaa ggt ccg ctg aag tca ctg tct 547
 Ala Glu Gln His Gly Asp Leu Asn Glu Gly Pro Leu Lys Ser Leu Ser
 135 140 145

gac aag ctg atc aac atc ctg ggt gga ttg aag gtg gaa tcc ttc ggc 595
 Asp Lys Leu Ile Asn Ile Leu Gly Gly Leu Lys Val Glu Ser Phe Gly

150	155	160	165	
gag atc ggc gaa gca ttc gat cca gag atc cac gaa gca gta cag gat				643
Glu Ile Gly Glu Ala Phe Asp Pro Glu Ile His Glu Ala Val Gln Asp				
	170	175	180	
ctc tca cag ggt gat gtc aag gtt ctg gga acg gta ctc cgc aag gga				691
Leu Ser Gln Gly Asp Val Lys Val Leu Gly Thr Val Leu Arg Lys Gly				
	185	190	195	
tac cgc ctc ggc gac cgc gtc atc cgc acc gca atg gtc ctc att ggg				739
Tyr Arg Leu Gly Asp Arg Val Ile Arg Thr Ala Met Val Leu Ile Gly				
	200	205	210	
gat cca gag gag agc tagagagact aagtctctta gtg				777
Asp Pro Glu Glu Ser				
	215			
<210> 30				
<211> 218				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 30				
Met Thr Thr Pro Asn Gly Met Pro Asp Asn Pro Gly Asp Pro Glu Asn				
1	5	10	15	
Thr Asp Pro Glu Ala Thr Ser Ala Asp Arg Ala Glu Gln Ala Ala Glu				
	20	25	30	
Glu Ala Ala Ala Arg Gln Ala Glu Glu Ser Pro Phe Gly Gln Ala Ser				
	35	40	45	
Glu Glu Glu Ile Ser Pro Glu Leu Glu Ala Glu Ile Asn Asp Leu Leu				
	50	55	60	
Ser Asp Val Asp Pro Asp Leu Asp Gly Asp Gly Glu Val Ser Ala Val				
	65	70	75	80
Glu Thr Gln Leu Ala Glu Arg Thr Glu Asp Leu Gln Arg Val Thr Ala				
	85	90	95	
Glu Tyr Ala Asn Tyr Arg Arg Arg Thr Glu Arg Glu Arg Gln Gly Ile				
	100	105	110	
Ile Asp Thr Ala Arg Ala Gly Val Val Thr Gln Leu Leu Pro Leu Leu				
	115	120	125	
Asp Asp Leu Asp Leu Ala Glu Gln His Gly Asp Leu Asn Glu Gly Pro				
	130	135	140	
Leu Lys Ser Leu Ser Asp Lys Leu Ile Asn Ile Leu Gly Gly Leu Lys				
	145	150	155	160
Val Glu Ser Phe Gly Glu Ile Gly Glu Ala Phe Asp Pro Glu Ile His				
	165	170	175	
Glu Ala Val Gln Asp Leu Ser Gln Gly Asp Val Lys Val Leu Gly Thr				
	180	185	190	

Val Leu Arg Lys Gly Tyr Arg Leu Gly Asp Arg Val Ile Arg Thr Ala
 195 200 205

Met Val Leu Ile Gly Asp Pro Glu Glu Ser
 210 215

<210> 31
 <211> 1977
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1954)
 <223> RXN02543

<400> 31
 ctcaatgagg agtttttctt accggcgaaa gtcggtggga agcaagtcaa agctcaagcc 60
 gtggacagta ctaaaatcac ctaaaacagg aggcaccatt atg gga cgt gca gta 115
 Met Gly Arg Ala Val
 1 5
 gga att gac ctt gga acc acc aac tct gtg gtt tcc gta ctt gaa ggc 163
 Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val Ser Val Leu Glu Gly
 10 15 20
 ggc gag cca gta gtt atc gca aac gca gaa ggc tca cgc acc acc cct 211
 Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly Ser Arg Thr Thr Pro
 25 30 35
 tcc gtc gtt gca ttc gca aag aac ggt gaa gtt cta gtc ggc cag tcc 259
 Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val Leu Val Gly Gln Ser
 40 45 50
 gct aag aac cag gcg gtc acc aac gtt gac cgc acc att cgc tcc gtc 307
 Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg Thr Ile Arg Ser Val
 55 60 65
 aag cgc cac atc ggc acc gac tgg tcc gtt gct atc gat gac aag aac 355
 Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala Ile Asp Asp Lys Asn
 70 75 80 85
 tac acc tca cag gaa atc tcg gct cgt acc ctg atg aag ctg aag cgc 403
 Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu Met Lys Leu Lys Arg
 90 95 100
 gac gct gaa gca tac ctg ggc gag gac gtc act gat gct gtt att acc 451
 Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr Asp Ala Val Ile Thr
 105 110 115
 gtt cct gca tac ttc gag gac tca cag cgc cag gca acc aag gaa gct 499
 Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln Ala Thr Lys Glu Ala
 120 125 130
 ggt cag atc gca ggc ctt aac gtt ctg cgt att gtt aac gag cca acc 547
 Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile Val Asn Glu Pro Thr
 135 140 145
 gcg gct gca ctt gca tac ggc ctt gag aag ggc gag cag gag cag acc 595

Ala 150	Ala	Ala	Leu	Ala	Tyr 155	Gly	Leu	Glu	Lys	Gly 160	Glu	Gln	Glu	Gln	Thr 165	
att	ctg	gta	ttc	gac	ctc	ggg	ggc	ggc	acc	ttc	gac	gtc	tcc	ctc	cta	643
Ile	Leu	Val	Phe	Asp 170	Leu	Gly	Gly	Gly	Thr 175	Phe	Asp	Val	Ser	Leu	Leu 180	
gag	atc	ggc	gac	ggg	gtt	gtt	gag	gtt	cgc	gca	acc	tcc	ggc	gat	aac	691
Glu	Ile	Gly	Asp 185	Gly	Val	Val	Glu	Val	Arg 190	Ala	Thr	Ser	Gly	Asp	Asn 195	
gag	ctc	ggg	ggc	gac	gac	tgg	gat	cag	cgt	atc	gtt	gac	tgg	ctg	gta	739
Glu	Leu	Gly 200	Gly	Asp	Asp	Trp	Asp 205	Gln	Arg	Ile	Val	Asp 210	Trp	Leu	Val	
gag	aag	ttc	cag	tcc	tcc	aac	ggc	att	gac	ctg	acc	aag	gac	aag	atg	787
Glu	Lys 215	Phe	Gln	Ser	Ser	Asn 220	Gly	Ile	Asp	Leu	Thr 225	Lys	Asp	Lys	Met	
gcc	ctg	cag	cgt	ctg	cgt	gag	gca	gct	gag	aag	gca	aag	atc	gag	ctg	835
Ala	Leu	Gln	Arg	Leu	Arg 235	Glu	Ala	Ala	Glu	Lys 240	Ala	Lys	Ile	Glu	Leu 245	
tcc	tct	tcc	cag	agt	gca	aac	atc	aac	ctt	cct	tac	atc	acc	gtt	gat	883
Ser	Ser	Ser	Gln 250	Ser	Ala	Asn	Ile	Asn	Leu 255	Pro	Tyr	Ile	Thr	Val	Asp 260	
gca	gac	aag	aac	cca	ctg	ttc	ttg	gat	gag	acc	ctt	tcc	cgt	gcc	gag	931
Ala	Asp	Lys 265	Asn	Pro	Leu	Phe	Leu	Asp 270	Glu	Thr	Leu	Ser	Arg 275	Ala	Glu	
ttc	cag	cgc	atc	acc	cag	gac	ctc	ctg	gcc	cgc	acc	aag	act	cct	ttc	979
Phe	Gln 280	Arg	Ile	Thr	Gln	Asp	Leu 285	Leu	Ala	Arg	Thr	Lys 290	Thr	Pro	Phe	
aac	cag	gtt	gtt	aag	gac	gct	ggc	gtg	tcc	gtc	tcg	gag	atc	gac	cac	1027
Asn 295	Gln	Val	Val	Lys	Asp 300	Ala	Gly	Val	Ser	Val 305	Ser	Glu	Ile	Asp	His	
gtt	gtt	ctc	gtc	ggg	ggg	tcc	acc	cgt	atg	cct	gct	gtt	acc	gaa	ctg	1075
Val	Val	Leu	Val	Gly 315	Gly	Ser	Thr	Arg	Met	Pro 320	Ala	Val	Thr	Glu	Leu 325	
gtc	aag	gaa	ctg	acc	ggg	gga	cgt	gag	cca	aac	aag	ggg	gtt	aac	cca	1123
Val	Lys	Glu	Leu 330	Thr	Gly	Gly	Arg	Glu	Pro 335	Asn	Lys	Gly	Val	Asn 340	Pro	
gat	gag	gtt	gtt	gca	gtt	ggg	gca	gca	ctt	cag	gcc	ggg	gtt	ctc	cgc	1171
Asp	Glu	Val 345	Val	Ala	Val	Gly	Ala	Ala	Leu 350	Gln	Ala	Gly	Val	Leu	Arg 355	
ggc	gag	gtc	aag	gat	gtt	ctt	ctt	ctt	gac	gtc	acc	cca	ctg	tcc	ctc	1219
Gly	Glu	Val 360	Lys	Asp	Val	Leu	Leu	Leu	Asp 365	Val	Thr	Pro 370	Leu	Ser	Leu	
ggc	att	gag	acc	aag	ggg	ggc	gtg	atg	acc	aag	ctc	atc	gag	cgc	aac	1267
Gly 375	Ile	Glu	Thr	Lys	Gly 380	Gly	Val	Met	Thr	Lys 385	Leu	Ile	Glu	Arg	Asn	
acc	acc	atc	cct	acc	aag	cgt	tcc	gag	acc	ttc	acc	acc	gca	gag	gac	1315
Thr	Thr	Ile	Pro	Thr	Lys	Arg	Ser	Glu	Thr	Phe	Thr	Thr	Ala	Glu	Asp	

390	395	400	405	
aac cag cct tct gtt	cag atc cag gtc	ttc cag ggc gag	cgt gaa atc	1363
Asn Gln Pro Ser Val	Gln Ile Gln Val Phe	Gln Gly Glu Arg Glu	Ile	
410	415	420		
gca acc gcc aac aag	ctg ctc gga tcc	ttc gag ctc ggc ggc	atc gca	1411
Ala Thr Ala Asn Lys	Leu Leu Gly Ser Phe	Glu Leu Gly Gly Ile	Ala	
425	430	435		
cct gca cca cgt ggc	gtc cca cag atc	gag gtc act ttc	gac atc gac	1459
Pro Ala Pro Arg Gly	Val Pro Gln Ile	Glu Val Thr Phe	Asp Ile Asp	
440	445	450		
gcc aac ggc atc gtc	cac gtc acc gca	aag gac aag ggt	act ggc aag	1507
Ala Asn Gly Ile Val	His Val Thr Ala	Lys Asp Lys Gly	Thr Gly Lys	
455	460	465		
gaa aac acc atc acc	att cag gac ggc	tcc ggt ctc tcc	cag gat gaa	1555
Glu Asn Thr Ile Thr	Ile Gln Asp Gly	Ser Gly Leu Ser	Gln Asp Glu	
470	475	480	485	
att gat cgc atg atc	aag gat gct gaa	gct cac gct gat	gag gac aag	1603
Ile Asp Arg Met Ile	Lys Asp Ala Glu	Ala His Ala Asp	Glu Asp Lys	
490	495	500		
aag cgc cgc gag gag	cag gaa gtc cgc	aac aac gct gag	tcc ctg gtt	1651
Lys Arg Arg Glu	Glu Gln Glu Val	Arg Asn Asn Ala	Glu Ser Leu	
505	510	515		
tac cag acc cgc aag	ttc gtt gaa gag	aac tcc gag aag	gtc tcc gaa	1699
Tyr Gln Thr Arg Lys	Phe Val Glu Glu	Asn Ser Glu Lys	Val Ser Glu	
520	525	530		
gac ctc aag gca aag	gtc gaa gag gca	gcc aag ggc gtt	gaa gaa gca	1747
Asp Leu Lys Ala Lys	Val Glu Glu Ala	Ala Lys Gly Val	Glu Glu Ala	
535	540	545		
ctc aag ggc gag gac	ctc gag gca atc	aag gct gca gtt	gag aag ctg	1795
Leu Lys Gly Glu Asp	Leu Glu Ala Ile	Lys Ala Ala Val	Glu Lys Leu	
550	555	560	565	
aac acc gag tcc cag	gaa atg ggt aag	gct atc tac gag	gct gac gct	1843
Asn Thr Glu Ser Gln	Glu Met Gly Lys	Ala Ile Tyr Glu	Ala Asp Ala	
570	575	580		
gct gct ggt gca acc	cag gct gac gca	ggt gca gaa ggc	gct gca gat	1891
Ala Ala Gly Ala Thr	Gln Ala Asp Ala	Gly Ala Glu Gly	Ala Ala Asp	
585	590	595		
gac aat gtt gtt gac	gct gaa gtt gtc	gaa gac gac gca	gct gac aat	1939
Asp Asn Val Val Asp	Ala Glu Val Val	Glu Asp Asp Ala	Ala Asp Asn	
600	605	610		
ggt gag gac aag aag	taaataccta	cccctaacgg	aat	1977
Gly Glu Asp Lys Lys				
615				

<210> 32

<211> 618

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 32

```

Met Gly Arg Ala Val Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val
 1              5              10              15

Ser Val Leu Glu Gly Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly
          20              25              30

Ser Arg Thr Thr Pro Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val
          35              40              45

Leu Val Gly Gln Ser Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
          50              55              60

Thr Ile Arg Ser Val Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala
          65              70              75              80

Ile Asp Asp Lys Asn Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu
          85              90              95

Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr
          100              105              110

Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln
          115              120              125

Ala Thr Lys Glu Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
          130              135              140

Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly
          145              150              155              160

Glu Gln Glu Gln Thr Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
          165              170              175

Asp Val Ser Leu Leu Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala
          180              185              190

Thr Ser Gly Asp Asn Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile
          195              200              205

Val Asp Trp Leu Val Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu
          210              215              220

Thr Lys Asp Lys Met Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys
          225              230              235              240

Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro
          245              250              255

Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr
          260              265              270

Leu Ser Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Ala Arg
          275              280              285

Thr Lys Thr Pro Phe Asn Gln Val Val Lys Asp Ala Gly Val Ser Val
          290              295              300

```

Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
 305 310 315 320
 Ala Val Thr Glu Leu Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn
 325 330 335
 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
 340 345 350
 Ala Gly Val Leu Arg Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
 355 360 365
 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys
 370 375 380
 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
 385 390 395 400
 Thr Thr Ala Glu Asp Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln
 405 410 415
 Gly Glu Arg Glu Ile Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu
 420 425 430
 Leu Gly Gly Ile Ala Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val
 435 440 445
 Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp
 450 455 460
 Lys Gly Thr Gly Lys Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly
 465 470 475 480
 Leu Ser Gln Asp Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His
 485 490 495
 Ala Asp Glu Asp Lys Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn
 500 505 510
 Ala Glu Ser Leu Val Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser
 515 520 525
 Glu Lys Val Ser Glu Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys
 530 535 540
 Gly Val Glu Glu Ala Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala
 545 550 555 560
 Ala Val Glu Lys Leu Asn Thr Glu Ser Gln Glu Met Gly Lys Ala Ile
 565 570 575
 Tyr Glu Ala Asp Ala Ala Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala
 580 585 590
 Glu Gly Ala Ala Asp Asp Asn Val Val Asp Ala Glu Val Val Glu Asp
 595 600 605
 Asp Ala Ala Asp Asn Gly Glu Asp Lys Lys
 610 615

<210> 33
 <211> 1977
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1954)
 <223> FRXA02543

<220>
 <223> All occurrences of n indicate any nucleotide

<220>
 <223> All occurrences of Xaa indicate any amino acid

<400> 33
 ctcaatgagg agtttttctt accggcgaaa gtcggtggga agcaagtcaa agctcaagcc 60
 gtggacagta ctaaaatcac ctaaaacagg aggcaccatt atg gga cgt gca gta 115
 Met Gly Arg Ala Val
 1 5
 gga att gac ctt gga acc acc aac tct gtg gtt tcc gta ctt gaa ggc 163
 Gly Ile Asp Leu Gly Thr Thr Asn Ser Val Val Ser Val Leu Glu Gly
 10 15 20
 ggc gag cca gta gtt atc gca aac gca gaa ggc tca cgc acc acc cct 211
 Gly Glu Pro Val Val Ile Ala Asn Ala Glu Gly Ser Arg Thr Thr Pro
 25 30 35
 tcc gtc gtt gca ttc gca aag aac ggt gaa gtt cta gtc ggc cag tcc 259
 Ser Val Val Ala Phe Ala Lys Asn Gly Glu Val Leu Val Gly Gln Ser
 40 45 50
 gct aag aac cag gcg gtc acc aac gtt gac cgc acc att cgc tcc gtc 307
 Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg Thr Ile Arg Ser Val
 55 60 65
 aag cgc cac atc ggc acc gac tgg tcc gtt gct atc gat gac aag aac 355
 Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala Ile Asp Asp Lys Asn
 70 75 80 85
 tac acc tca cag gaa atc tcg gct cgt acc ctg atg aag ctg aag cgc 403
 Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu Met Lys Leu Lys Arg
 90 95 100
 gac gct gaa gca tac ctg ggc gag gac gtc act gat gct gtt att acc 451
 Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr Asp Ala Val Ile Thr
 105 110 115
 gtt cct gca tac ttc gag gac tca cag cgc cag gca acc aag gaa gct 499
 Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln Ala Thr Lys Glu Ala
 120 125 130
 ggt cag atc gca ggc ctt aac gtt ctg cgt att gtt aac gag cca acc 547
 Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile Val Asn Glu Pro Thr
 135 140 145
 gcg gct gca ctt gca tac ggc ctt gag aag ggc gag cag gag cag acc 595
 Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly Glu Gln Glu Gln Thr

150	155	160	165	
att ctg gta ttc gac ctc ggt ggc ggc acc ttc gac gtc tcc ctc cta				643
Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu	170	175	180	
gag atc ggc gac ggt gtt gtt gag gtt cgc gca acc tcc ggc gat aac				691
Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala Thr Ser Gly Asp Asn	185	190	195	
gag ctc ggt ggc gac gac tgg gat cag cgt atc gtt gac tgg ctg gta				739
Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile Val Asp Trp Leu Val	200	205	210	
gag aag ttc cag tcc tcc aac ggc att gac ctg acc aag gac aag atg				787
Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu Thr Lys Asp Lys Met	215	220	225	
gcc ctg cag cgt ctg cgt gag gca gct gag aag gca aag atc gag ctg				835
Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys Ala Lys Ile Glu Leu	230	235	240	245
tcc tct tcc cag agt gca aac atc aac ctt cct tac atc acc gtt gat				883
Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro Tyr Ile Thr Val Asp	250	255	260	
gca gac aag aac cca ctg ttc ttg gat gag acc ctt tcc cgt gcc gag				931
Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr Leu Ser Arg Ala Glu	265	270	275	
ttc cag cgc atc acc cag gac ctc ctg gcc cgc acc aag act cct ttc				979
Phe Gln Arg Ile Thr Gln Asp Leu Leu Ala Arg Thr Lys Thr Pro Phe	280	285	290	
aac cag gtt gtt aag gac gct ggc gtg tcc gtc tcg gag atc gac cac				1027
Asn Gln Val Val Lys Asp Ala Gly Val Ser Val Ser Glu Ile Asp His	295	300	305	
gtt gtt ctc gtc ggt ggt tcc acc cgt atg cct gct gtt acc gaa ctg				1075
Val Val Leu Val Gly Gly Ser Thr Arg Met Pro Ala Val Thr Glu Leu	310	315	320	325
gtc aag gaa ctg acc ggt gga cgt gag cca aac aag ggt gtt aac cca				1123
Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn Lys Gly Val Asn Pro	330	335	340	
gat gag gtt gtt gca gtt ggt gca gca ctt cag gcc ggt gtt ctc cgc				1171
Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln Ala Gly Val Leu Arg	345	350	355	
ggc gag gtc aag gat gtt ctt ctt ctt gac gtc acc cca ctg tcc ctc				1219
Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val Thr Pro Leu Ser Leu	360	365	370	
ggc att gag acc aag ggt ggc gtg atg acc aag ctc atc gag cgc aac				1267
Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys Leu Ile Glu Arg Asn	375	380	385	
acc acc atc cct acc aag cgt tcc gag acc ttc acc acc gca gag gac				1315
Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe Thr Thr Ala Glu Asp	390	395	400	405

aac cag cct tct gtt cag atc cag gtc ttc cag ggc gag cgt gaa atc	1363
Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln Gly Glu Arg Glu Ile	
410 415 420	
gca acc gcc aac aag ctg ctc gga tcc ttc gag ctc ggc ggc atc gca	1411
Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu Leu Gly Gly Ile Ala	
425 430 435	
cct gca cca cgt ggc gtc cca cag atc gag gtc act ttc gac atc gac	1459
Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val Thr Phe Asp Ile Asp	
440 445 450	
gcc aac ggc atc gtc cac gtc acc gca aag gac aag ggt act ggc aag	1507
Ala Asn Gly Ile Val His Val Thr Ala Lys Asp Lys Gly Thr Gly Lys	
455 460 465	
gaa aac acc atc acc att cag gac ggc tcc ggt ctc tcc cag gat gaa	1555
Glu Asn Thr Ile Thr Ile Gln Asp Gly Ser Gly Leu Ser Gln Asp Glu	
470 475 480 485	
att gat cgc atg atc aag gat gct gaa gct cac gct gat gag gac aag	1603
Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His Ala Asp Glu Asp Lys	
490 495 500	
aag cgc cgc gag gag cag gaa gtc cgc aac aac gct gag tcc ctg gtt	1651
Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn Ala Glu Ser Leu Val	
505 510 515	
tac cag acc cgc aag ttc gtt gaa gag aac tcc gag aag gtc tcc gaa	1699
Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser Glu Lys Val Ser Glu	
520 525 530	
gac ctc aag gca aag gtc gaa gag gca gcc aag ggc gtt gaa gaa gca	1747
Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys Gly Val Glu Glu Ala	
535 540 545	
ctc aag ggc gag gac ctc gag gca atc aag gct gca gtt gag aag ctg	1795
Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala Ala Val Glu Lys Leu	
550 555 560 565	
aac acc gag tcc cag gaa atg ggt aag gnt atc tnc gag gct gac gct	1843
Asn Thr Glu Ser Gln Glu Met Gly Lys Xaa Ile Xaa Glu Ala Asp Ala	
570 575 580	
nct gct ggt gca acc cag gct gac gca ggt gca gaa ggc gct gca gat	1891
Xaa Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala Glu Gly Ala Ala Asp	
585 590 595	
gac aat gtt gtt gac gct gaa gtt gtc gaa gac gac gca gct gac aat	1939
Asp Asn Val Val Asp Ala Glu Val Val Glu Asp Asp Ala Ala Asp Asn	
600 605 610	
ggt gag gac aag aag taaatgacta cccctaacgg aat	1977
Gly Glu Asp Lys Lys	
615	

<210> 34
 <211> 618
 <212> PRT

<213> *Corynebacterium glutamicum*

<220>

<223> All occurrences of Xaa indicate any amino acid

<400> 34

Met	Gly	Arg	Ala	Val	Gly	Ile	Asp	Leu	Gly	Thr	Thr	Asn	Ser	Val	Val	1	5	10	15
Ser	Val	Leu	Glu	Gly	Gly	Glu	Pro	Val	Val	Ile	Ala	Asn	Ala	Glu	Gly	20	25	30	
Ser	Arg	Thr	Thr	Pro	Ser	Val	Val	Ala	Phe	Ala	Lys	Asn	Gly	Glu	Val	35	40	45	
Leu	Val	Gly	Gln	Ser	Ala	Lys	Asn	Gln	Ala	Val	Thr	Asn	Val	Asp	Arg	50	55	60	
Thr	Ile	Arg	Ser	Val	Lys	Arg	His	Ile	Gly	Thr	Asp	Trp	Ser	Val	Ala	65	70	75	80
Ile	Asp	Asp	Lys	Asn	Tyr	Thr	Ser	Gln	Glu	Ile	Ser	Ala	Arg	Thr	Leu	85	90	95	
Met	Lys	Leu	Lys	Arg	Asp	Ala	Glu	Ala	Tyr	Leu	Gly	Glu	Asp	Val	Thr	100	105	110	
Asp	Ala	Val	Ile	Thr	Val	Pro	Ala	Tyr	Phe	Glu	Asp	Ser	Gln	Arg	Gln	115	120	125	
Ala	Thr	Lys	Glu	Ala	Gly	Gln	Ile	Ala	Gly	Leu	Asn	Val	Leu	Arg	Ile	130	135	140	
Val	Asn	Glu	Pro	Thr	Ala	Ala	Ala	Leu	Ala	Tyr	Gly	Leu	Glu	Lys	Gly	145	150	155	160
Glu	Gln	Glu	Gln	Thr	Ile	Leu	Val	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe	165	170	175	
Asp	Val	Ser	Leu	Leu	Glu	Ile	Gly	Asp	Gly	Val	Val	Glu	Val	Arg	Ala	180	185	190	
Thr	Ser	Gly	Asp	Asn	Glu	Leu	Gly	Gly	Asp	Asp	Trp	Asp	Gln	Arg	Ile	195	200	205	
Val	Asp	Trp	Leu	Val	Glu	Lys	Phe	Gln	Ser	Ser	Asn	Gly	Ile	Asp	Leu	210	215	220	
Thr	Lys	Asp	Lys	Met	Ala	Leu	Gln	Arg	Leu	Arg	Glu	Ala	Ala	Glu	Lys	225	230	235	240
Ala	Lys	Ile	Glu	Leu	Ser	Ser	Ser	Gln	Ser	Ala	Asn	Ile	Asn	Leu	Pro	245	250	255	
Tyr	Ile	Thr	Val	Asp	Ala	Asp	Lys	Asn	Pro	Leu	Phe	Leu	Asp	Glu	Thr	260	265	270	
Leu	Ser	Arg	Ala	Glu	Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	Ala	Arg	275	280	285	
Thr	Lys	Thr	Pro	Phe	Asn	Gln	Val	Val	Lys	Asp	Ala	Gly	Val	Ser	Val				

290					295					300					
Ser	Glu	Ile	Asp	His	Val	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	Met	Pro
305					310					315					320
Ala	Val	Thr	Glu	Leu	Val	Lys	Glu	Leu	Thr	Gly	Gly	Arg	Glu	Pro	Asn
				325					330					335	
Lys	Gly	Val	Asn	Pro	Asp	Glu	Val	Val	Ala	Val	Gly	Ala	Ala	Leu	Gln
			340					345					350		
Ala	Gly	Val	Leu	Arg	Gly	Glu	Val	Lys	Asp	Val	Leu	Leu	Leu	Asp	Val
		355					360					365			
Thr	Pro	Leu	Ser	Leu	Gly	Ile	Glu	Thr	Lys	Gly	Gly	Val	Met	Thr	Lys
		370				375						380			
Leu	Ile	Glu	Arg	Asn	Thr	Thr	Ile	Pro	Thr	Lys	Arg	Ser	Glu	Thr	Phe
385					390					395					400
Thr	Thr	Ala	Glu	Asp	Asn	Gln	Pro	Ser	Val	Gln	Ile	Gln	Val	Phe	Gln
				405					410					415	
Gly	Glu	Arg	Glu	Ile	Ala	Thr	Ala	Asn	Lys	Leu	Leu	Gly	Ser	Phe	Glu
			420					425					430		
Leu	Gly	Gly	Ile	Ala	Pro	Ala	Pro	Arg	Gly	Val	Pro	Gln	Ile	Glu	Val
		435					440					445			
Thr	Phe	Asp	Ile	Asp	Ala	Asn	Gly	Ile	Val	His	Val	Thr	Ala	Lys	Asp
	450					455					460				
Lys	Gly	Thr	Gly	Lys	Glu	Asn	Thr	Ile	Thr	Ile	Gln	Asp	Gly	Ser	Gly
465					470					475					480
Leu	Ser	Gln	Asp	Glu	Ile	Asp	Arg	Met	Ile	Lys	Asp	Ala	Glu	Ala	His
			485					490						495	
Ala	Asp	Glu	Asp	Lys	Lys	Arg	Arg	Glu	Glu	Gln	Glu	Val	Arg	Asn	Asn
			500					505					510		
Ala	Glu	Ser	Leu	Val	Tyr	Gln	Thr	Arg	Lys	Phe	Val	Glu	Glu	Asn	Ser
		515					520					525			
Glu	Lys	Val	Ser	Glu	Asp	Leu	Lys	Ala	Lys	Val	Glu	Glu	Ala	Ala	Lys
		530				535					540				
Gly	Val	Glu	Glu	Ala	Leu	Lys	Gly	Glu	Asp	Leu	Glu	Ala	Ile	Lys	Ala
545					550					555					560
Ala	Val	Glu	Lys	Leu	Asn	Thr	Glu	Ser	Gln	Glu	Met	Gly	Lys	Xaa	Ile
			565						570					575	
Xaa	Glu	Ala	Asp	Ala	Xaa	Ala	Gly	Ala	Thr	Gln	Ala	Asp	Ala	Gly	Ala
			580					585					590		
Glu	Gly	Ala	Ala	Asp	Asp	Asn	Val	Val	Asp	Ala	Glu	Val	Val	Glu	Asp
		595					600					605			
Asp	Ala	Ala	Asp	Asn	Gly	Glu	Asp	Lys	Lys						
		610				615									

<400> 35																60
cgcgattgcg tcatcgatcg ttgttgcttc catgcgcacc acactatctt tctgcacgcc																
ctgatgccct gtggattcaa aactgtgctt ttataggcgt atg caa gaa tcc tca																115
Met Gln Glu Ser Ser																5
cgt gat aat ttc caa gtt gac ctc ggc ggc gtt gtt gat ctt ttg agt																163
Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val Val Asp Leu Leu Ser																20
cgc cac att tat tcc ggt ccg agg gtg tat gtg cgt gag ttg ctg cag																211
Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val Arg Glu Leu Leu Gln																35
aat gcg gtt gat gct tgt act gca cgt tct gaa cag ggt gag gag ggc																259
Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu Gln Gly Glu Glu Gly																50
tac gag ccg agt att cgt att ccg ccg gtg acc aag gat cgt gcc acg																307
Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr Lys Asp Arg Ala Thr																65
ttt tca ctg gtt gat aat ggt acg ggc ctg acc gcg cag gag gcg cgg																355
Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr Ala Gln Glu Ala Arg																85
gaa ttg ctg gcg acg gtg ggg ccg acg tcg aaa cgc gat gaa ttc ggt																403
Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys Arg Asp Glu Phe Gly																100
ctg cag cgg gaa ggt cgc ctg ggg caa ttt ggc atc ggg ctg ctt agt																451
Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly Ile Gly Leu Leu Ser																115
tgt ttc atg gtg gcg gat gag atc acc atg gtg tcg cat gcg gag ggt																499
Cys Phe Met Val Ala Asp Glu Ile Thr Met Val Ser His Ala Glu Gly																130
gcg tcg gcg att ccg tgg act ggt cat gcg gat ggc acc ttt aac ctg																547
Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp Gly Thr Phe Asn Leu																145
gag att ctt ggg gat gac gca acg gat gtc att ccg gtg ggc acg act																595
Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile Pro Val Gly Thr Thr																165
gtg cac ctg act ccg cgc cct gat gag cgc acg ttg ctg acg gaa aat																643
Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr Leu Leu Thr Glu Asn																

				170				175				180				
tcc	gtg	gtc	acc	att	gct	agt	aat	tat	ggc	cgc	tac	ctg	ccg	att	cct	691
Ser	Val	Val	Thr	Ile	Ala	Ser	Asn	Tyr	Gly	Arg	Tyr	Leu	Pro	Ile	Pro	
185								190				195				
att	gtg	gtg	cag	ggg	gag	aaa	aac	acc	acc	atc	act	aca	tcg	ccg	gtg	739
Ile	Val	Val	Gln	Gly	Glu	Lys	Asn	Thr	Thr	Ile	Thr	Thr	Ser	Pro	Val	
200								205				210				
ttt	gca	aag	gat	act	gat	cag	cag	cac	agg	ctg	tat	gcc	ggc	cgg	gag	787
Phe	Ala	Lys	Asp	Thr	Asp	Gln	Gln	His	Arg	Leu	Tyr	Ala	Gly	Arg	Glu	
215				220				225								
cgc	ctt	ggg	aaa	act	cct	ttt	gat	gtc	atc	gat	ctc	acc	ggg	cct	ggc	835
Arg	Leu	Gly	Lys	Thr	Pro	Phe	Asp	Val	Ile	Asp	Leu	Thr	Gly	Pro	Gly	
230				235				240				245				
atc	gag	ggg	gtg	gct	tat	gta	ttg	ccg	gag	gcc	cag	gct	ccg	cat	atg	883
Ile	Glu	Gly	Val	Ala	Tyr	Val	Leu	Pro	Glu	Ala	Gln	Ala	Pro	His	Met	
250								255				260				
tcc	agg	cgt	cac	agt	att	tat	gtc	aac	cgc	atg	ttg	gtc	tct	gat	ggg	931
Ser	Arg	Arg	His	Ser	Ile	Tyr	Val	Asn	Arg	Met	Leu	Val	Ser	Asp	Gly	
265								270				275				
cct	tcc	acg	gtg	ctg	ccc	aac	tgg	gcg	ttc	ttt	gtg	gaa	tgt	gaa	atc	979
Pro	Ser	Thr	Val	Leu	Pro	Asn	Trp	Ala	Phe	Phe	Val	Glu	Cys	Glu	Ile	
280								285				290				
aat	tca	acc	gat	ttg	gaa	ccc	acc	gca	tcg	cgt	gaa	gcg	ctc	atg	gat	1027
Asn	Ser	Thr	Asp	Leu	Glu	Pro	Thr	Ala	Ser	Arg	Glu	Ala	Leu	Met	Asp	
295				300				305								
gac	acc	gcg	ttc	gcg	gca	acc	agg	gaa	cat	atc	ggg	gag	tgc	att	aaa	1075
Asp	Thr	Ala	Phe	Ala	Ala	Thr	Arg	Glu	His	Ile	Gly	Glu	Cys	Ile	Lys	
310				315				320				325				
tcg	tgg	ctg	att	aat	ctc	gcc	atg	acc	aag	cct	cac	cgc	gtg	cgg	gaa	1123
Ser	Trp	Leu	Ile	Asn	Leu	Ala	Met	Thr	Lys	Pro	His	Arg	Val	Arg	Glu	
330								335				340				
ttt	act	gcg	att	cat	gat	ctt	gcc	ctg	cgc	gag	ctg	tgc	caa	tcg	gac	1171
Phe	Thr	Ala	Ile	His	Asp	Leu	Ala	Leu	Arg	Glu	Leu	Cys	Gln	Ser	Asp	
345								350				355				
gcg	gac	ctg	gct	gaa	acc	atg	ttg	ggg	ctt	ctc	acc	ttg	gag	acc	tcc	1219
Ala	Asp	Leu	Ala	Glu	Thr	Met	Leu	Gly	Leu	Leu	Thr	Leu	Glu	Thr	Ser	
360				365				370								
cgt	ggg	cgc	atc	tcg	atc	ggg	gag	atc	acc	acg	ttg	tcc	atc	acc	gag	1267
Arg	Gly	Arg	Ile	Ser	Ile	Gly	Glu	Ile	Thr	Thr	Leu	Ser	Ile	Thr	Glu	
375				380				385								
gat	gtg	tcg	ctg	cag	ctg	gct	acc	acg	ttg	gat	gat	ttc	agg	cag	ctc	1315
Asp	Val	Ser	Leu	Gln	Leu	Ala	Thr	Thr	Leu</							

cac gac agc gat ctg gct cgg ctc att ccc gtt cac tac cca ccg ctt 1411
 His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu
 425 430 435

acg gta tct act gct gac ctg cgc gaa tcc atg gat ctg atg gag ctt 1459
 Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu
 440 445 450

ccg ccg ctg cag gac att gag aaa gcc aag gca ctg gat gcg cag gtc 1507
 Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val
 455 460 465

acg gaa tca ttg aag gat ttt cag atc aag ggc gca acg agg gtt ttt 1555
 Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe
 470 475 480 485

gaa ccc gca gat gtt cct gcc gtg gtg atc att gat tcc aag gcg cag 1603
 Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln
 490 495 500

gcc tca cgg gat cgc aat gaa aca caa agc gca acc act gat cgt tgg 1651
 Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp
 505 510 515

gct gac att ttg gca acg gtg gat aac acg ttg agc cgt caa aca gcc 1699
 Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala
 520 525 530

aac att cca cag gat cag gga ctg tcg gcg ttg tgc ttg aat tgg aac 1747
 Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn
 535 540 545

aat tcg ctg gtc agg aaa ttg gcg tcc act gat gac acc gcc gtg gtg 1795
 Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val
 550 555 560 565

tcg cgc acg gtg cgt ttg ctc tac gtt cag gca ttg ttg tcc agc aag 1843
 Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys
 570 575 580

agg cca ctg cgg gtg aag gaa cgc gcg ctg ctt aat gat tcg ctg gca 1891
 Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala
 585 590 595

gat ctg gtt tct ttg tct ttg tca tcc gat atc taagacaatc ctccgctaata 1944
 Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile
 600 605

ctt 1947

<210> 36

<211> 608

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Gln Glu Ser Ser Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val
 1 5 10 15

Val Asp Leu Leu Ser Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val
 20 25 30
 Arg Glu Leu Leu Gln Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu
 35 40 45
 Gln Gly Glu Glu Gly Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr
 50 55 60
 Lys Asp Arg Ala Thr Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr
 65 70 75 80
 Ala Gln Glu Ala Arg Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys
 85 90 95
 Arg Asp Glu Phe Gly Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly
 100 105 110
 Ile Gly Leu Leu Ser Cys Phe Met Val Ala Asp Glu Ile Thr Met Val
 115 120 125
 Ser His Ala Glu Gly Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp
 130 135 140
 Gly Thr Phe Asn Leu Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile
 145 150 155 160
 Pro Val Gly Thr Thr Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr
 165 170 175
 Leu Leu Thr Glu Asn Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg
 180 185 190
 Tyr Leu Pro Ile Pro Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile
 195 200 205
 Thr Thr Ser Pro Val Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu
 210 215 220
 Tyr Ala Gly Arg Glu Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp
 225 230 235 240
 Leu Thr Gly Pro Gly Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala
 245 250 255
 Gln Ala Pro His Met Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met
 260 265 270
 Leu Val Ser Asp Gly Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe
 275 280 285
 Val Glu Cys Glu Ile Asn Ser Thr Asp Leu Glu Pro Thr Ala Ser Arg
 290 295 300
 Glu Ala Leu Met Asp Asp Thr Ala Phe Ala Ala Thr Arg Glu His Ile
 305 310 315 320
 Gly Glu Cys Ile Lys Ser Trp Leu Ile Asn Leu Ala Met Thr Lys Pro
 325 330 335
 His Arg Val Arg Glu Phe Thr Ala Ile His Asp Leu Ala Leu Arg Glu

340					345					350					
Leu	Cys	Gln	Ser	Asp	Ala	Asp	Leu	Ala	Glu	Thr	Met	Leu	Gly	Leu	Leu
		355					360					365			
Thr	Leu	Glu	Thr	Ser	Arg	Gly	Arg	Ile	Ser	Ile	Gly	Glu	Ile	Thr	Thr
		370				375					380				
Leu	Ser	Ile	Thr	Glu	Asp	Val	Ser	Leu	Gln	Leu	Ala	Thr	Thr	Leu	Asp
385					390					395					400
Asp	Phe	Arg	Gln	Leu	Asn	Thr	Ile	Ala	Arg	Pro	Asp	Thr	Leu	Ile	Ile
				405					410					415	
Asn	Gly	Gly	Tyr	Ile	His	Asp	Ser	Asp	Leu	Ala	Arg	Leu	Ile	Pro	Val
			420					425					430		
His	Tyr	Pro	Pro	Leu	Thr	Val	Ser	Thr	Ala	Asp	Leu	Arg	Glu	Ser	Met
		435					440					445			
Asp	Leu	Met	Glu	Leu	Pro	Pro	Leu	Gln	Asp	Ile	Glu	Lys	Ala	Lys	Ala
		450				455					460				
Leu	Asp	Ala	Gln	Val	Thr	Glu	Ser	Leu	Lys	Asp	Phe	Gln	Ile	Lys	Gly
465					470					475					480
Ala	Thr	Arg	Val	Phe	Glu	Pro	Ala	Asp	Val	Pro	Ala	Val	Val	Ile	Ile
				485					490					495	
Asp	Ser	Lys	Ala	Gln	Ala	Ser	Arg	Asp	Arg	Asn	Glu	Thr	Gln	Ser	Ala
			500					505					510		
Thr	Thr	Asp	Arg	Trp	Ala	Asp	Ile	Leu	Ala	Thr	Val	Asp	Asn	Thr	Leu
		515					520						525		
Ser	Arg	Gln	Thr	Ala	Asn	Ile	Pro	Gln	Asp	Gln	Gly	Leu	Ser	Ala	Leu
		530				535					540				
Cys	Leu	Asn	Trp	Asn	Asn	Ser	Leu	Val	Arg	Lys	Leu	Ala	Ser	Thr	Asp
545					550					555					560
Asp	Thr	Ala	Val	Val	Ser	Arg	Thr	Val	Arg	Leu	Leu	Tyr	Val	Gln	Ala
				565					570					575	
Leu	Leu	Ser	Ser	Lys	Arg	Pro	Leu	Arg	Val	Lys	Glu	Arg	Ala	Leu	Leu
			580					585					590		
Asn	Asp	Ser	Leu	Ala	Asp	Leu	Val	Ser	Leu	Ser	Leu	Ser	Ser	Asp	Ile
			595				600						605		

<210> 37

<211> 436

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(436)

<223> FRXA02282

```

<400> 38
Met Gln Glu Ser Ser Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val
  1                    5                10              15

Val Asp Leu Leu Ser Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val
                20                25              30

Arg Glu Leu Leu Gln Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu
          35                40              45

Gln Gly Glu Glu Gly Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr
  50                55              60

Lys Asp Arg Ala Thr Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr
  65                70              75              80

Ala Gln Glu Ala Arg Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys
                85                90              95

Arg Asp Glu Phe Gly Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly

```


100
 105
 110

<210> 39
 <211> 1269
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(1246)
 <223> RXA00886

<400> 39
 taagtatggt ggtcgtgtgc tcgctggcga atagctgcgg gtatagttgg ccatttggtt 60
 tgattaatct gtttagaagc taaaggaagt atcacccacc gtg gca cgt gac tat 115
 Val Ala Arg Asp Tyr
 1 5
 tac ggc att ctc ggc gtc gat cgc aat gca acc gaa tca gag atc aaa 163
 Tyr Gly Ile Leu Gly Val Asp Arg Asn Ala Thr Glu Ser Glu Ile Lys
 10 15 20
 aag gca tac cga aag ctt gcc cgc aaa tac cac ccg gac gta aac cca 211
 Lys Ala Tyr Arg Lys Leu Ala Arg Lys Tyr His Pro Asp Val Asn Pro
 25 30 35
 ggt gag gaa gca gcg gag aaa ttc cgc gag gct tct gtt gcg cat gag 259
 Gly Glu Glu Ala Ala Glu Lys Phe Arg Glu Ala Ser Val Ala His Glu
 40 45 50
 gta ctc act gat ccg gat aag cgc cgc att gtt gat atg ggc ggt gac 307
 Val Leu Thr Asp Pro Asp Lys Arg Arg Ile Val Asp Met Gly Gly Asp
 55 60 65
 cca atg gag caa ggc ggc gga gct ggc gct ggt ggc ttc ggt gga ggc 355
 Pro Met Glu Gln Gly Gly Gly Ala Gly Ala Gly Gly Phe Gly Gly Gly
 70 75 80 85
 ttc ggc ggc agc ggt gga ctg ggc gat atc ttc gat gcc ttc ttc ggc 403
 Phe Gly Gly Ser Gly Gly Leu Gly Asp Ile Phe Asp Ala Phe Phe Gly
 90 95 100
 ggt ggc gcg ggc ggt tcc cgt gga cca cgt tcc cgc gtg cag cca ggc 451
 Gly Gly Ala Gly Gly Ser Arg Gly Pro Arg Ser Arg Val Gln Pro Gly
 105 110 115
 agt gac acc ttg tgg cgc acc tcc atc acc ttg gaa gag gct tac aag 499
 Ser Asp Thr Leu Trp Arg Thr Ser Ile Thr Leu Glu Glu Ala Tyr Lys
 120 125 130
 ggc gct aag aaa gat ctc acc ctt gac acc gca gtg ctg tgt acc aag 547
 Gly Ala Lys Lys Asp Leu Thr Leu Asp Thr Ala Val Leu Cys Thr Lys
 135 140 145
 tgt cat ggt tct gga tct gca tcc gac aag aag cct gtt acc tgt ggc 595
 Cys His Gly Ser Gly Ser Ala Ser Asp Lys Lys Pro Val Thr Cys Gly
 150 155 160 165
 acc tgt aat ggc gct ggt gaa att cag gaa gtg cag cgc agc ttc ctg 643

Thr	Cys	Asn	Gly	Ala	Gly	Glu	Ile	Gln	Glu	Val	Gln	Arg	Ser	Phe	Leu		
				170					175					180			
ggc	aac	gtc	atg	acg	tcc	cgc	cca	tgc	cac	acc	tgc	gat	ggc	acc	ggc	691	
Gly	Asn	Val	Met	Thr	Ser	Arg	Pro	Cys	His	Thr	Cys	Asp	Gly	Thr	Gly		
			185					190					195				
gag	atc	atc	cca	gat	cct	tgc	act	gag	tgt	gca	gca	gat	ggc	cgt	gtg	739	
Glu	Ile	Ile	Pro	Asp	Pro	Cys	Thr	Glu	Cys	Ala	Ala	Asp	Gly	Arg	Val		
		200					205					210					
cgt	gct	cgc	cgc	gac	atc	gtg	gcc	aac	atc	cca	gct	ggc	atc	cag	tcc	787	
Arg	Ala	Arg	Arg	Asp	Ile	Val	Ala	Asn	Ile	Pro	Ala	Gly	Ile	Gln	Ser		
	215					220					225						
ggc	atg	cgc	atc	cgc	atg	gca	ggc	caa	ggc	gag	gtt	ggc	gct	ggc	ggc	835	
Gly	Met	Arg	Ile	Arg	Met	Ala	Gly	Gln	Gly	Glu	Val	Gly	Ala	Gly	Gly		
230					235					240					245		
ggc	cct	gcg	ggc	gac	ctc	tac	att	gaa	gtc	atg	gtg	cgc	ccg	cac	gcc	883	
Gly	Pro	Ala	Gly	Asp	Leu	Tyr	Ile	Glu	Val	Met	Val	Arg	Pro	His	Ala		
			250					255						260			
atc	ttc	acc	cgc	gat	ggc	gac	gat	ctg	cac	gcc	agc	atc	aag	gtt	cca	931	
Ile	Phe	Thr	Arg	Asp	Gly	Asp	Asp	Leu	His	Ala	Ser	Ile	Lys	Val	Pro		
			265					270					275				
atg	ttc	gat	gca	gcg	ctt	ggc	acc	gaa	ttg	gac	gtg	gaa	tcc	ctc	acc	979	
Met	Phe	Asp	Ala	Ala	Leu	Gly	Thr	Glu	Leu	Asp	Val	Glu	Ser	Leu	Thr		
		280					285					290					
ggc	gaa	gag	gtg	aaa	att	acc	atc	cct	gca	ggc	act	cag	ccc	aac	gat	1027	
Gly	Glu	Glu	Val	Lys	Ile	Thr	Ile	Pro	Ala	Gly	Thr	Gln	Pro	Asn	Asp		
	295					300					305						
gtg	atc	acc	ttg	gat	ggc	gaa	ggc	atg	ccg	aag	ctg	cgc	gca	gaa	ggc	1075	
Val	Ile	Thr	Leu	Asp	Gly	Glu	Gly	Met	Pro	Lys	Leu	Arg	Ala	Glu	Gly		
310					315				320						325		
cac	ggc	aac	ctc	atg	gcg	cat	gtc	gat	cta	ttt	gtg	cca	acc	gat	ttg	1123	
His	Gly	Asn	Leu	Met	Ala	His	Val	Asp	Leu	Phe	Val	Pro	Thr	Asp	Leu		
			330					335						340			
gat	gac	cgc	acc	cgc	gaa	ttg	ctt	gaa	gaa	atc	cgc	aac	cat	cgc	agc	1171	
Asp	Asp	Arg	Thr	Arg	Glu	Leu	Leu	Glu	Glu	Ile	Arg	Asn	His	Arg	Ser		
			345					350					355				
gac	aac	gct	tcc	gtg	cat	cgc	gaa	ggc	gga	gaa	gaa	tcc	ggc	ttc	ttt	1219	
Asp	Asn	Ala	Ser	Val	His	Arg	Glu	Gly	Gly	Glu	Glu	Ser	Gly	Phe	Phe		
		360					365					370					
gac	aag	ctc	cga	aac	aag	ttc	cgc	aaa	taatgtcact	gccagtat	ttt					1266	
Asp	Lys	Leu	Arg	Asn	Lys	Phe	Arg	Lys									
	375					380											
atc																1269	

<210> 40
 <211> 382
 <212> PRT

<213> *Corynebacterium glutamicum*

<400> 40

Val Ala Arg Asp Tyr Tyr Gly Ile Leu Gly Val Asp Arg Asn Ala Thr
 1 5 10 15
 Glu Ser Glu Ile Lys Lys Ala Tyr Arg Lys Leu Ala Arg Lys Tyr His
 20 25 30
 Pro Asp Val Asn Pro Gly Glu Glu Ala Ala Glu Lys Phe Arg Glu Ala
 35 40 45
 Ser Val Ala His Glu Val Leu Thr Asp Pro Asp Lys Arg Arg Ile Val
 50 55 60
 Asp Met Gly Gly Asp Pro Met Glu Gln Gly Gly Gly Ala Gly Ala Gly
 65 70 75 80
 Gly Phe Gly Gly Gly Phe Gly Gly Ser Gly Gly Leu Gly Asp Ile Phe
 85 90 95
 Asp Ala Phe Phe Gly Gly Gly Ala Gly Gly Ser Arg Gly Pro Arg Ser
 100 105 110
 Arg Val Gln Pro Gly Ser Asp Thr Leu Trp Arg Thr Ser Ile Thr Leu
 115 120 125
 Glu Glu Ala Tyr Lys Gly Ala Lys Lys Asp Leu Thr Leu Asp Thr Ala
 130 135 140
 Val Leu Cys Thr Lys Cys His Gly Ser Gly Ser Ala Ser Asp Lys Lys
 145 150 155 160
 Pro Val Thr Cys Gly Thr Cys Asn Gly Ala Gly Glu Ile Gln Glu Val
 165 170 175
 Gln Arg Ser Phe Leu Gly Asn Val Met Thr Ser Arg Pro Cys His Thr
 180 185 190
 Cys Asp Gly Thr Gly Glu Ile Ile Pro Asp Pro Cys Thr Glu Cys Ala
 195 200 205
 Ala Asp Gly Arg Val Arg Ala Arg Arg Asp Ile Val Ala Asn Ile Pro
 210 215 220
 Ala Gly Ile Gln Ser Gly Met Arg Ile Arg Met Ala Gly Gln Gly Glu
 225 230 235 240
 Val Gly Ala Gly Gly Gly Pro Ala Gly Asp Leu Tyr Ile Glu Val Met
 245 250 255
 Val Arg Pro His Ala Ile Phe Thr Arg Asp Gly Asp Asp Leu His Ala
 260 265 270
 Ser Ile Lys Val Pro Met Phe Asp Ala Ala Leu Gly Thr Glu Leu Asp
 275 280 285
 Val Glu Ser Leu Thr Gly Glu Glu Val Lys Ile Thr Ile Pro Ala Gly
 290 295 300
 Thr Gln Pro Asn Asp Val Ile Thr Leu Asp Gly Glu Gly Met Pro Lys

305		310		315		320
Leu Arg Ala Glu Gly His Gly Asn Leu Met Ala His Val Asp Leu Phe						
		325		330		335
Val Pro Thr Asp Leu Asp Asp Arg Thr Arg Glu Leu Leu Glu Glu Ile						
		340		345		350
Arg Asn His Arg Ser Asp Asn Ala Ser Val His Arg Glu Gly Gly Glu						
		355		360		365
Glu Ser Gly Phe Phe Asp Lys Leu Arg Asn Lys Phe Arg Lys						
		370		375		380

<210> 41

<211> 1470

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1447)

<223> RXS00568

<400> 41

```

gttttcggacg acgcgagaaa tcgcattaat cgctcggaac cgggcttggt tttgtaatat 60

ctgaaacttt ccctttcccg atcatccagg agatttactc gtg aag agt tct gtc 115
                               Val Lys Ser Ser Val
                               1                               5

gag aag ctg agc gac acc cgt tca aag atc acc gtt gag gtt cca ttt 163
Glu Lys Leu Ser Asp Thr Arg Ser Lys Ile Thr Val Glu Val Pro Phe
                               10                               15                               20

tct gaa ctg aag cca gag atc gac cag gca tac gcc gct cta gcg cag 211
Ser Glu Leu Lys Pro Glu Ile Asp Gln Ala Tyr Ala Ala Leu Ala Gln
                               25                               30                               35

caa gtc cag atc cct ggt ttc cgt aag ggc aag gca ccg cgt cag ctt 259
Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys Ala Pro Arg Gln Leu
                               40                               45                               50

atc gac gca cgc ttc ggc cgt ggt gcg gtt ctg gag cag gtt gtc aac 307
Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu Glu Gln Val Val Asn
                               55                               60                               65

gac atg ctt cct aac cgc tac gca cag gca atc gaa gct gag ggc atc 355
Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile Glu Ala Glu Gly Ile
                               70                               75                               80                               85

aag gca atc ggc cag cct aac gta gag gtc acc aag atc gaa gac aac 403
Lys Ala Ile Gly Gln Pro Asn Val Glu Val Thr Lys Ile Glu Asp Asn
                               90                               95                               100

gag ctc gtt gag ttc gtc gct gag gtt gac gtt cgc cca gag ttc gag 451
Glu Leu Val Glu Phe Val Ala Glu Val Asp Val Arg Pro Glu Phe Glu
                               105                               110                               115

ctt cct aag ttc gag gac atc act gtt gag gtc cca gct atc aag gct 499

```

Leu	Pro	Lys	Phe	Glu	Asp	Ile	Thr	Val	Glu	Val	Pro	Ala	Ile	Lys	Ala		
		120					125					130					
gac	gaa	gag	gca	atc	gaa	gca	gag	ctc	gag	acc	ctg	cgt	gca	cgt	ttc	547	
Asp	Glu	Glu	Ala	Ile	Glu	Ala	Glu	Leu	Glu	Thr	Leu	Arg	Ala	Arg	Phe		
	135					140					145						
tcc	acc	ttg	aag	gat	cac	aac	cac	aag	ctg	aag	aag	ggt	gag	ttc	gtc	595	
Ser	Thr	Leu	Lys	Asp	His	Asn	His	Lys	Leu	Lys	Lys	Gly	Glu	Phe	Val		
150					155					160					165		
acc	atc	aac	atc	acc	gca	agc	att	gac	ggt	gag	aag	att	gaa	gag	gca	643	
Thr	Ile	Asn	Ile	Thr	Ala	Ser	Ile	Asp	Gly	Glu	Lys	Ile	Glu	Glu	Ala		
				170					175					180			
acc	act	gag	ggt	ctg	tcc	tac	gaa	atc	gga	tct	gac	gat	ctg	att	gac	691	
Thr	Thr	Glu	Gly	Leu	Ser	Tyr	Glu	Ile	Gly	Ser	Asp	Asp	Leu	Ile	Asp		
		185					190						195				
ggc	ctg	gac	aag	gct	ctg	atc	ggc	gct	aag	aag	gat	gaa	acc	gta	gag	739	
Gly	Leu	Asp	Lys	Ala	Leu	Ile	Gly	Ala	Lys	Lys	Asp	Glu	Thr	Val	Glu		
	200						205					210					
ttc	acc	tct	gag	ctg	gca	aac	ggc	gag	cac	aag	ggc	aag	gaa	gct	caa	787	
Phe	Thr	Ser	Glu	Leu	Ala	Asn	Gly	Glu	His	Lys	Gly	Lys	Glu	Ala	Gln		
	215					220					225						
atc	agc	gtt	gag	atc	acc	gca	acc	aag	cag	cgc	gag	ctg	cct	gag	ctg	835	
Ile	Ser	Val	Glu	Ile	Thr	Ala	Thr	Lys	Gln	Arg	Glu	Leu	Pro	Glu	Leu		
230					235					240					245		
gat	gat	gag	ttc	gca	cag	ctg	gct	tct	gag	ttc	gac	acc	atc	gaa	gag	883	
Asp	Asp	Glu	Phe	Ala	Gln	Leu	Ala	Ser	Glu	Phe	Asp	Thr	Ile	Glu	Glu		
				250					255					260			
ctt	cgt	gag	tcc	acc	gtg	tct	gac	gtt	gag	gct	aag	cag	aag	aac	gag	931	
Leu	Arg	Glu	Ser	Thr	Val	Ser	Asp	Val	Glu	Ala	Lys	Gln	Lys	Asn	Glu		
			265					270					275				
cag	gct	gct	gca	atc	cgc	gac	gaa	gtt	ctc	gct	gcg	gct	ctt	ggc	gag	979	
Gln	Ala	Ala	Ala	Ile	Arg	Asp	Glu	Val	Leu	Ala	Ala	Ala	Leu	Gly	Glu		
	280						285					290					
gct	gac	ttc	gct	ctg	cca	cag	tcc	atc	gtt	gac	gag	cag	gca	cac	tcc	1027	
Ala	Asp	Phe	Ala	Leu	Pro	Gln	Ser	Ile	Val	Asp	Glu	Gln	Ala	His	Ser		
	295					300					305						
cag	ctg	cac	cag	ctc	ctc	ggc	gag	ctt	gca	cac	gac	gat	gct	gca	ctg	1075	
Gln	Leu	His	Gln	Leu	Leu	Gly	Glu	Leu	Ala	His	Asp	Asp	Ala	Ala	Leu		
	310				315					320					325		
aac	tcc	ctc	ctt	gag	gct	cag	ggc	acc	act	cgt	gaa	gag	ttc	gac	aag	1123	
Asn	Ser	Leu	Leu	Glu	Ala	Gln	Gly	Thr	Thr	Arg	Glu	Glu	Phe	Asp	Lys		
				330					335					340			
aag	aac	gtc	gaa	gat	gct	gag	aag	gct	gtt	cgc	acc	cag	ctg	ttc	ctg	1171	
Lys	Asn	Val	Glu	Asp	Ala	Glu	Lys	Ala	Val	Arg	Thr	Gln	Leu	Phe	Leu		
		345					350						355				
gac	acc	ctc	tct	gag	gtt	gag	gag	cct	gag	gtt	tcc	cag	cag	gag	ctc	1219	
Asp	Thr	Leu	Ser	Glu	Val	Glu	Glu	Pro	Glu	Val	Ser	Gln	Gln	Glu	Leu		

360	365	370	
acc gac cac atc ctg ttc acc gca cag tct tac ggc atg gac cca aac			1267
Thr Asp His Ile Leu Phe	Thr Ala Gln Ser Tyr	Gly Met Asp Pro Asn	
375	380	385	
cag ttc atc ggt cag ctg cag cag tcc ggc cag atc gcg aac ctc ttc			1315
Gln Phe Ile Gly Gln Leu Gln Gln Ser Gly Gln Ile Ala Asn Leu Phe			
390	395	400	405
tcc gac gtt cgc cgt ggc aag gct ctt gca cag gct atc tgc cgc gta			1363
Ser Asp Val Arg Arg Gly Lys Ala Leu Ala Gln Ala Ile Cys Arg Val			
410	415	420	
aac gtg aag gac tcc gag ggt aac gag atc gac cct aag gaa tac ttc			1411
Asn Val Lys Asp Ser Glu Gly Asn Glu Ile Asp Pro Lys Glu Tyr Phe			
425	430	435	
ggt gaa gaa gaa gta gct gag act gag tct gaa gct taaaaacttt			1457
Gly Glu Glu Glu Val Ala Glu Thr Glu Ser Glu Ala			
440	445		
aaagaaataa cgc			1470
<210> 42			
<211> 449			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 42			
Val Lys Ser Ser Val Glu Lys Leu Ser Asp Thr Arg Ser Lys Ile Thr			
1	5	10	15
Val Glu Val Pro Phe Ser Glu Leu Lys Pro Glu Ile Asp Gln Ala Tyr			
20	25	30	
Ala Ala Leu Ala Gln Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys			
35	40	45	
Ala Pro Arg Gln Leu Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu			
50	55	60	
Glu Gln Val Val Asn Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile			
65	70	75	80
Glu Ala Glu Gly Ile Lys Ala Ile Gly Gln Pro Asn Val Glu Val Thr			
85	90	95	
Lys Ile Glu Asp Asn Glu Leu Val Glu Phe Val Ala Glu Val Asp Val			
100	105	110	
Arg Pro Glu Phe Glu Leu Pro Lys Phe Glu Asp Ile Thr Val Glu Val			
115	120	125	
Pro Ala Ile Lys Ala Asp Glu Glu Ala Ile Glu Ala Glu Leu Glu Thr			
130	135	140	
Leu Arg Ala Arg Phe Ser Thr Leu Lys Asp His Asn His Lys Leu Lys			
145	150	155	160

Lys Gly Glu Phe Val Thr Ile Asn Ile Thr Ala Ser Ile Asp Gly Glu
 165 170 175
 Lys Ile Glu Glu Ala Thr Thr Glu Gly Leu Ser Tyr Glu Ile Gly Ser
 180 185 190
 Asp Asp Leu Ile Asp Gly Leu Asp Lys Ala Leu Ile Gly Ala Lys Lys
 195 200 205
 Asp Glu Thr Val Glu Phe Thr Ser Glu Leu Ala Asn Gly Glu His Lys
 210 215 220
 Gly Lys Glu Ala Gln Ile Ser Val Glu Ile Thr Ala Thr Lys Gln Arg
 225 230 235 240
 Glu Leu Pro Glu Leu Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe
 245 250 255
 Asp Thr Ile Glu Glu Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala
 260 265 270
 Lys Gln Lys Asn Glu Gln Ala Ala Ala Ile Arg Asp Glu Val Leu Ala
 275 280 285
 Ala Ala Leu Gly Glu Ala Asp Phe Ala Leu Pro Gln Ser Ile Val Asp
 290 295 300
 Glu Gln Ala His Ser Gln Leu His Gln Leu Leu Gly Glu Leu Ala His
 305 310 315 320
 Asp Asp Ala Ala Leu Asn Ser Leu Leu Glu Ala Gln Gly Thr Thr Arg
 325 330 335
 Glu Glu Phe Asp Lys Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg
 340 345 350
 Thr Gln Leu Phe Leu Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val
 355 360 365
 Ser Gln Gln Glu Leu Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr
 370 375 380
 Gly Met Asp Pro Asn Gln Phe Ile Gly Gln Leu Gln Gln Ser Gly Gln
 385 390 395 400
 Ile Ala Asn Leu Phe Ser Asp Val Arg Arg Gly Lys Ala Leu Ala Gln
 405 410 415
 Ala Ile Cys Arg Val Asn Val Lys Asp Ser Glu Gly Asn Glu Ile Asp
 420 425 430
 Pro Lys Glu Tyr Phe Gly Glu Glu Glu Val Ala Glu Thr Glu Ser Glu
 435 440 445
 Ala

<210> 43
 <211> 826
 <212> DNA

<223> RXN03038

gcgcggaataa caccaagtaa gccttacagt ccgacagcct catagcggat gggataagtt 60

gag tta aca gtg cgt aaa gga att tcc cgc gtc ctc tcg gta gcg gtt 163
Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val Leu Ser Val Ala Val
10 15 20

gct agt tca atc gga ttc gga act gta ctg aca ggc acc ggc atc gca 211
Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr Gly Thr Gly Ile Ala
25 30 35

gca gct caa gac tct gca ttt gac tac ggt atg gat cca aac atg aac 259
Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Asn Met Asn
40 45 50

tac aac ccg atc gat gac atc aag gat cgt ccc gaa gga ttg tcc aat 307
 Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro Glu Gly Leu Ser Asn
 55 60 65

ctt ccc tac ttc gga agt aaa ttg acc agc tgg ggc tca tca tat gcc 355
 Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Tyr Ala
 70 75 80 85

acc gcc tca tcc ggc gtc gtg acc tcc gcg ctc ccg cag tac acc gat 403
Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu Pro Gln Tyr Thr Asp
90 95 100

ccg cgc tac ccc ctc ggc aaa gac gac ctg ccc aag gca acc atc gac 451
Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr Ile Asp
105 110 115

atg gag cca gaa gtt ctt gcg cgc ctt gag cga ttc gtc ggc gtt gac 499
Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg Phe Val Gly Val Asp
120 125 130

ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg gga cgc 547
Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met Gly Arg
135 140 145

acc att cct cta gtc tgg gtt gtt cca gaa gac aac acc gtg cct ggc 595
Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp Asn Thr Val Pro Gly
150 155 160 165

c c a a c g t c t a c g c a c t c g g a g g c g g t g a c g g t g g a c a a g g c g g c c a g 643
Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gly Gln Gly Gly Gln
170 175 180

aac tgg gtc acc cgc acc gac ctt gag gaa tta acc agt gac aac aac 691
Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu Thr Ser Asp Asn Asn
185 190 195

atc aac ctc atc atg ccg atg ctc gga tct ttt agt ttc tac tct gac 739
 Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr Ser Asp
 200 205 210

tgg gca cgc gaa agc caa tcc atg ggt tgt gcg caa cag tgg gaa aca 787
 Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala Gln Gln Trp Glu Thr
 215 220 225

ttg ctc atg cac gaa ctg cct gag ccg ctt gta gcg gcc 826
 Leu Leu Met His Glu Leu Pro Glu Pro Leu Val Ala Ala
 230 235 240

<210> 44
 <211> 242
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 44
 Met His Ser Lys Glu Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val
 1 5 10 15

Leu Ser Val Ala Val Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr
 20 25 30

Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met
 35 40 45

Asp Pro Asn Met Asn Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro
 50 55 60

Glu Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp
 65 70 75 80

Gly Ser Ser Tyr Ala Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu
 85 90 95

Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro
 100 105 110

Lys Ala Thr Ile Asp Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg
 115 120 125

Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser
 130 135 140

Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp
 145 150 155 160

Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly
 165 170 175

Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu
 180 185 190

Thr Ser Asp Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe
 195 200 205

Ser Phe Tyr Ser Asp Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala
 210 215 220

Gln Gln Trp Glu Thr Leu Leu Met His Glu Leu Pro Glu Pro Leu Val
 225 230 235 240

Ala Ala

<210> 45

<211> 653

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(630)

<223> RXN03039

<220>

<223> All occurrences of Xaa indicate any amino acid

<400> 45

gca ctc ccg caa tac acc gac cca cgc tac ccc ctc ggc aaa gac gac 48
 Ala Leu Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp
 1 5 10 15

ctg ccc aaa gca acc atc gac atg gag cca gaa gct ctt gcg cgc ctt 96
 Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu
 20 25 30

gag cga ttc gtc ggc gtt gac ggt gat cgc atc cgc caa atc aac gcg 144
 Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala
 35 40 45

tac tcg cca tca atg gga cgc acc att cct cta gtc tgg gtc gtg cca 192
 Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro
 50 55 60

gaa gac aac acc gtg cct ggc cca acg gtc tac gca ctc ggc ggc ggc 240
 Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly
 65 70 75 80

gac ggt ggc caa ggc ggc caa aac tgg gtc acc cgc acc gac ctt gat 288
 Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp
 85 90 95

gag ttg acc agt gaa aac aac atc aac ctc atc atg ccc atg ctc gga 336
 Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly
 100 105 110

tct ttt agt ttc tac gct gac tgg gca ggc gaa agc gaa tcc atg ggt 384
 Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly
 115 120 125

ggt gcg caa cag tgg gaa aca ttc ctc atg cac gaa ctr ccm gag ccg 432
 Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro
 130 135 140

cta gaa gcg gcc atc ggc gca gac ggg caa cgc agc atc gtc ggc atg 480
 Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met
 145 150 155 160

```

tcc atg tcc ggg gga tcr gtg ctg aac ttt gcg acg cat gac ccc aac 528
Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn
      165                      170                      175

ttt tay tcc tck gtc ggc tca ttt tct gga tgt gcc gaa acc aac tcc 576
Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser
      180                      185                      190

tgg atg ggr cgc cgn tgg cat cgc agc cac tgc cta caa cgg caa tgt 624
Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys
      195                      200                      205

cgt gcc tgagcaaatac tttggtgaag tag 653
Arg Ala
      210

```

<210> 46

<211> 210

<212> PRT

<213> *Corynebacterium glutamicum*

<220>

<223> All occurrences of Xaa indicate any amino acid

<400> 46

```

Ala Leu Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp
  1              5              10              15

Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu
      20              25              30

Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala
  35              40              45

Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro
  50              55              60

Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly
  65              70              75              80

Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp
      85              90              95

Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly
  100              105              110

Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly
  115              120              125

Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro
  130              135              140

Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met
  145              150              155              160

Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn
      165              170              175

Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser

```

180185190

Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys
 195 200 205

Arg Ala
 210

<210> 47
<211> 432
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(409)
<223> RXN03040

<220>
<223> All occurrences of n indicate any nucleotide

<220>
<223> All occurrences of Xaa indicate any amino acid

<400> 47
attactctcg ctataacgat ccttntgctc aacgctgcga agctcgaaga acaagacaac 60

ctctacatct tcgccgggttc cggtgtgttc tctgaactag atg tca tnc ggt gac 115
 Met Ser Xaa Gly Asp
 1 5

aac gca ccg att gat gag gat gcg ttc aaa aac cgc gtc ttg gtt ggg 163
Asn Ala Pro Ile Asp Glu Asp Ala Phe Lys Asn Arg Val Leu Val Gly
 10 15 20

ttt gaa atc gaa gct atg tcc aac acc tgc acc cat aac ctc aag gct 211
Phe Glu Ile Glu Ala Met Ser Asn Thr Cys Thr His Asn Leu Lys Ala
 25 30 35

gcg acc gat caa atg ggc atc gac aac atc aac tac gat ttc cga cca 259
Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn Tyr Asp Phe Arg Pro
 40 45 50

acc gga acc cac gcc tgg gat tac tgg aac gaa gcg ctc cac cgc ttc 307
Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu Ala Leu His Arg Phe
 55 60 65

ttc ccg ttg atg atg cag ggc ttc ggc ctc gac ggt ggt ccc atc ccg 355
Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp Gly Gly Pro Ile Pro
 70 75 80 85

atc tat aac cct aac ggt gtg acc tcc agc gag tct tct ntc aga act 403
Ile Tyr Asn Pro Asn Gly Val Thr Ser Ser Glu Ser Ser Xaa Arg Thr
 90 95 100

gtc ttc tgatgtgagc cttggcaccn gtg 432
Val Phe

<210> 48

<211> 103

<212> PRT

<213> Corynebacterium glutamicum

<220>

<223> All occurrences of Xaa indicate any amino acid

<400> 48

Met Ser Xaa Gly Asp Asn Ala Pro Ile Asp Glu Asp Ala Phe Lys Asn
 1 5 10 15

Arg Val Leu Val Gly Phe Glu Ile Glu Ala Met Ser Asn Thr Cys Thr
 20 25 30

His Asn Leu Lys Ala Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn
 35 40 45

Tyr Asp Phe Arg Pro Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu
 50 55 60

Ala Leu His Arg Phe Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp
 65 70 75 80

Gly Gly Pro Ile Pro Ile Tyr Asn Pro Asn Gly Val Thr Ser Ser Glu
 85 90 95

Ser Ser Xaa Arg Thr Val Phe
 100

<210> 49

<211> 835

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(835)

<223> RXN03051

<400> 49

acatccagaa gtagtcgttg agtatcacga gcaagtcaac gatagtaaag ataatgtcga 60

ggaactcccg ctgcctaagc gggacatagt tgcaggggac atg cgt tca gat gtt 115
 Met Arg Ser Asp Val
 1 5

atc gag tta ccg gag ggg gta agc aag gag aaa gct gac cag cta gaa 163
 Ile Glu Leu Pro Glu Gly Val Ser Lys Glu Lys Ala Asp Gln Leu Glu
 10 15 20

gtt gcg gaa gcg cga ctt aac gag ggt gca cga ctg atg gca acc acc 211
 Val Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg Leu Met Ala Thr Thr
 25 30 35

ggg tgt gag gtt atg tgg cca acg ggc ttc tca gtt tgt ggc cga att 259
 Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile
 40 45 50

ctt gac acc tat cgc cag gtt gga ggt cag ttg tca tgg ctt ggg cca 307

Leu	Asp	Thr	Tyr	Arg	Gln	Val	Gly	Gly	Gln	Leu	Ser	Trp	Leu	Gly	Pro		
55						60					65						
ccg	aag	tca	aac	gag	ttg	acc	aat	ccc	gac	ggg	gtt	ggc	aaa	aga	agt	355	
Pro	Lys	Ser	Asn	Glu	Leu	Thr	Asn	Pro	Asp	Gly	Val	Gly	Lys	Arg	Ser		
70					75				80						85		
gaa	ttt	ttt	ggg	gga	gcc	atc	tat	tgg	cac	cca	gac	aca	ggc	gct	tat	403	
Glu	Phe	Phe	Gly	Gly	Ala	Ile	Tyr	Trp	His	Pro	Asp	Thr	Gly	Ala	Tyr		
				90					95					100			
gca	gtg	acc	ttg	gac	ggg	ttg	cga	cag	tgg	ggg	acc	ttg	aac	tgg	gaa	451	
Ala	Val	Thr	Leu	Asp	Gly	Leu	Arg	Gln	Trp	Gly	Thr	Leu	Asn	Trp	Glu		
			105					110					115				
tca	ggg	cca	ttg	ggg	tac	cca	acc	tct	ggg	ccg	atg	gat	aca	aac	tat	499	
Ser	Gly	Pro	Leu	Gly	Tyr	Pro	Thr	Ser	Gly	Pro	Met	Asp	Thr	Asn	Tyr		
		120					125					130					
ccc	ctt	act	cag	cga	cag	act	ttt	caa	ggg	ggg	gac	aac	tac	tac	aac	547	
Pro	Leu	Thr	Gln	Arg	Gln	Thr	Phe	Gln	Gly	Gly	Asp	Asn	Tyr	Tyr	Asn		
	135					140					145						
cca	ttg	act	ggc	ggg	gct	gtg	tgg	ggc	gat	att	aaa	cag	cgc	tac	gaa	595	
Pro	Leu	Thr	Gly	Gly	Ala	Val	Trp	Gly	Asp	Ile	Lys	Gln	Arg	Tyr	Glu		
	150				155				160						165		
gaa	ctt	ggc	ggc	tcg	aat	cat	gcc	att	ggc	atc	ccg	atc	act	aat	gag	643	
Glu	Leu	Gly	Gly	Ser	Asn	His	Ala	Ile	Gly	Ile	Pro	Ile	Thr	Asn	Glu		
				170					175					180			
cta	cct	agc	ggg	act	gag	tat	ttt	tac	aat	aat	ttc	tcc	aat	gga	aca	691	
Leu	Pro	Ser	Gly	Thr	Glu	Tyr	Phe	Tyr	Asn	Asn	Phe	Ser	Asn	Gly	Thr		
			185					190					195				
att	tcg	tgg	cga	aat	gat	cgt	cag	aca	cgg	ttt	atg	tat	ttg	gct	acg	739	
Ile	Ser	Trp	Arg	Asn	Asp	Arg	Gln	Thr	Arg	Phe	Met	Tyr	Leu	Ala	Thr		
		200					205					210					
cag	cgg	gtg	tgg	gat	gcg	ttg	ggg	cgg	gag	acg	ggg	cgt	tta	ggg	ttt	787	
Gln	Arg	Val	Trp	Asp	Ala	Leu	Gly	Arg	Glu	Thr	Gly	Arg	Leu	Gly	Phe		
	215					220					225						
cct	gaa	gca	gat	gaa	aca	cct	gag	gtt	tct	ggg	cta	ttc	cat	gtg	gcg	835	
Pro	Glu	Ala	Asp	Glu	Thr	Pro	Glu	Val	Ser	Gly	Leu	Phe	His	Val	Ala		
	230				235					240					245		

<210> 50

<211> 245

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

Met	Arg	Ser	Asp	Val	Ile	Glu	Leu	Pro	Glu	Gly	Val	Ser	Lys	Glu	Lys
1				5					10					15	

Ala	Asp	Gln	Leu	Glu	Val	Ala	Glu	Ala	Arg	Leu	Asn	Glu	Gly	Ala	Arg
			20					25					30		

Leu	Met	Ala	Thr	Thr	Gly	Cys	Glu	Val	Met	Trp	Pro	Thr	Gly	Phe	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Val Cys Gly Arg Ile Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu		
50	55	60
Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly		
65	70	75 80
Val Gly Lys Arg Ser Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro		
	85	90 95
Asp Thr Gly Ala Tyr Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly		
	100	105 110
Thr Leu Asn Trp Glu Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro		
	115	120 125
Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly		
	130	135 140
Asp Asn Tyr Tyr Asn Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile		
	145	150 155 160
Lys Gln Arg Tyr Glu Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile		
	165	170 175
Pro Ile Thr Asn Glu Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn		
	180	185 190
Phe Ser Asn Gly Thr Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe		
	195	200 205
Met Tyr Leu Ala Thr Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr		
	210	215 220
Gly Arg Leu Gly Phe Pro Glu Ala Asp Glu Thr Pro Glu Val Ser Gly		
	225	230 235 240
Leu Phe His Val Ala		
	245	

<210> 51
 <211> 1704
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1681)
 <223> RXN03054

<400> 51
 ggtggaaata cgcgcaaac aattttattc acagaactta tgattttttc gggtaggggt 60
 cagtttggtc acatcaacta gtaacgaaag gatcatgtga atg aaa ctg ttt tcc 115
 Met Lys Leu Phe Ser
 1 5

aag gct gca ggc gtc att gct gca gca ctt ctt gtt gca ggt ggt ata 163
 Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu Val Ala Gly Gly Ile

10										15										20										
gca	cct	gtg	gca	cag	ggg	caa	gct	agt	cag	gtg	gtc	aca	cct	gaa	gac	211														
Ala	Pro	Val	Ala	Gln	Gly	Gln	Ala	Ser	Gln	Val	Val	Thr	Pro	Glu	Asp															
			25						30			35																		
caa	gat	gcg	tat	gtt	caa	cag	ttc	cac	cac	gaa	ggg	aat	acc	cca	cct	259														
Gln	Asp	Ala	Tyr	Val	Gln	Gln	Phe	His	His	Glu	Gly	Asn	Thr	Pro	Pro															
			40						45			50																		
gtg	gta	gac	ggg	gtg	ggg	ggc	tac	act	gag	caa	gaa	atc	gcc	gag	atc	307														
Val	Val	Asp	Gly	Val	Gly	Gly	Tyr	Thr	Glu	Gln	Glu	Ile	Ala	Glu	Ile															
			55						60			65																		
cac	gag	gct	atc	cga	caa	gcc	caa	gaa	tct	ggc	gca	cct	aat	gaa	gag	355														
His	Glu	Ala	Ile	Arg	Gln	Ala	Gln	Glu	Ser	Gly	Ala	Pro	Asn	Glu	Glu															
			70			75			80						85															
ctc	att	ccg	ggg	gag	atg	tgg	tca	gat	aag	gtg	gag	ctg	cca	gta	act	403														
Leu	Ile	Pro	Gly	Glu	Met	Trp	Ser	Asp	Lys	Val	Glu	Leu	Pro	Val	Thr															
			90						95						100															
att	gat	aaa	gca	gcc	gct	gat	gag	gca	gag	ata	gct	att	gca	cag	caa	451														
Ile	Asp	Lys	Ala	Ala	Ala	Asp	Glu	Ala	Glu	Ile	Ala	Ile	Ala	Gln	Gln															
			105						110						115															
caa	tct	cag	cca	cag	acg	cga	ggc	ctt	gct	gcg	gct	gcg	gcg	tgt	cag	499														
Gln	Ser	Gln	Pro	Gln	Thr	Arg	Gly	Leu	Ala	Ala	Ala	Ala	Ala	Cys	Gln															
			120			125						130																		
acg	ttt	tgg	ccg	tca	cct	cat	cag	gtt	tgt	ggg	gct	att	tta	gag	cgc	547														
Thr	Phe	Trp	Pro	Ser	Pro	His	Gln	Val	Cys	Gly	Ala	Ile	Leu	Glu	Arg															
			135			140						145																		
tat	att	cag	cag	ggg	gcc	cag	ttt	ggg	tgg	atg	ttg	ttt	ccg	agt	gaa	595														
Tyr	Ile	Gln	Gln	Gly	Ala	Gln	Phe	Gly	Trp	Met	Leu	Phe	Pro	Ser	Glu															
150						155			160						165															
ggc	caa	acg	tta	aat	cct	gat	ggg	cag	ggg	tat	cgt	cag	cgg	ttt	atg	643														
Gly	Gln	Thr	Leu	Asn	Pro	Asp	Gly	Gln	Gly	Tyr	Arg	Gln	Arg	Phe	Met															
			170						175						180															
aat	ggg	ttt	gtt	tat	tgg	cat	ccg	aca	act	ggg	gcg	cat	gct	gtt	aat	691														
Asn	Gly	Phe	Val	Tyr	Trp	His	Pro	Thr	Thr	Gly	Ala	His	Ala	Val	Asn															
			185						190						195															
aat	tac	agt	gcg	cag	gtg	tgg	gag	cgt	aat	ggg	tgg	gag	tct	ggg	tgg	739														
Asn	Tyr	Ser	Ala	Gln	Val	Trp	Glu	Arg	Asn	Gly	Trp	Glu	Ser	Gly	Trp															
			200			205						210																		
atg	ggg	tat	ccc	act	ggg	ggg	gaa	gtc	cct	gtg	aat	ggg	tcc	aat	ccg	787														
Met	Gly	Tyr	Pro	Thr	Gly	Gly	Glu	Val	Pro	Val	Asn	Gly	Ser	Asn	Pro															
215						220						225																		
att	gat	ggg	gag	ttg	agt	ggg	tgg	gtg	caa	act	ttc	caa	ggg	ggg	cga	835														
Ile	Asp	Gly	Glu	Leu	Ser	Gly	Trp	Val	Gln	Thr	Phe	Gln	Gly	Gly	Arg															
230						235			240						245															
gtg	tat	cgc	agt	ccg	gta	ttg	gac	ggg	ttc	cag	gtg	gcc	agt	att	aat	883														
Val	Tyr	Arg	Ser	Pro	Val	Leu	Asp	Gly	Phe	Gln	Val	Ala	Ser	Ile	Asn															
			250						255						260															

ggg ctg atc ttg gat aaa tgg ctt gaa ttg ggt ggt cct gat agt gac	931
Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp	
265 270 275	
ctt ggt ttt ccc att gcg gat gag gct gtg aca gct gac ggt gtg ggt	979
Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr Ala Asp Gly Val Gly	
280 285 290	
aga ttt tct gtt ttc cag aac gga gtt gtc tac tgg cat ccg caa cac	1027
Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr Trp His Pro Gln His	
295 300 305	
gga gct cac cct ata tta ggg aat ata tac agt atc tgg aga gaa gaa	1075
Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser Ile Trp Arg Glu Glu	
310 315 320 325	
gga gct gag agt ggg gaa ttc ggt tac cct atc ggc gat cca gaa aag	1123
Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile Gly Asp Pro Glu Lys	
330 335 340	
tat aca gaa aac atg gct aat cag gta ttc gaa aaa ggc gaa ctt gca	1171
Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu Lys Gly Glu Leu Ala	
345 350 355	
gct aac cta tac ccc aat cct ctt gag gct ttt att gag ttt tta ccc	1219
Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe Ile Glu Phe Leu Pro	
360 365 370	
ttt gct aat ctt gag gaa gca ata gag tat ttt gag aac gga ttg tca	1267
Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe Glu Asn Gly Leu Ser	
375 380 385	
aat tct cgt gta gag gcg aat tca ctt aac gcc aag aaa gat tcg att	1315
Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala Lys Lys Asp Ser Ile	
390 395 400 405	
caa tgt caa tcg caa tcc gct aac att cat gtg aga acg aag agt gac	1363
Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val Arg Thr Lys Ser Asp	
410 415 420	
gga gtc ggg att agg gtt cca aag att ggg ttt aag gct agg atg gat	1411
Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp	
425 430 435	
tgc gac ctt cct gga act gtc tca gat gta gtg ggg tat gga tgg att	1459
Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val Gly Tyr Gly Trp Ile	
440 445 450	
tac tac gac tat tgg gga cga tgg gct caa gca gca tat gca caa caa	1507
Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala Ala Tyr Ala Gln Gln	
455 460 465	
ttc ttc ggt aat agg aat tct gtt gtg caa acc aat tta gag gcg ggt	1555
Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly	
470 475 480 485	
tgc agc ggg gag aag aat aca tta ttt tgg ggt act tca tat ttt cag	1603
Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln	
490 495 500	

gtg act tat gaa ggt cag ccg tat ttc ggt cag tca gca act aat tac 1651
 Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr
 505 510 515

gct tat ctt ccg tgt acg ata gac cgt agt taacataagg aatggaatag 1701
 Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser
 520 525

gag 1704

<210> 52

<211> 527

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

Met Lys Leu Phe Ser Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu
 1 5 10 15

Val Ala Gly Gly Ile Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val
 20 25 30

Val Thr Pro Glu Asp Gln Asp Ala Tyr Val Gln Gln Phe His His Glu
 35 40 45

Gly Asn Thr Pro Pro Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln
 50 55 60

Glu Ile Ala Glu Ile His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly
 65 70 75 80

Ala Pro Asn Glu Glu Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val
 85 90 95

Glu Leu Pro Val Thr Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile
 100 105 110

Ala Ile Ala Gln Gln Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala
 115 120 125

Ala Ala Ala Cys Gln Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly
 130 135 140

Ala Ile Leu Glu Arg Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met
 145 150 155 160

Leu Phe Pro Ser Glu Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr
 165 170 175

Arg Gln Arg Phe Met Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly
 180 185 190

Ala His Ala Val Asn Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly
 195 200 205

Trp Glu Ser Gly Trp Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val
 210 215 220

Asn Gly Ser Asn Pro Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr
 225 230 235 240

```
<210> 53
<211> 456
<212> DNA
<213> Corynebacterium glutamicum
```

<220>

<221> CDS

<222> (101)..(433)

<223> RXN02949

<400> 53

```

actctcgaag gttgaacaca gggctgcgat tgtgctggat caaatgtctg cacgaaaaat 60

tggtatcgcc cctggatgag tagtgattta gaggagtgct  gtg agc gac gag cag 115
                                         Val Ser Asp Glu Gln
                                         1           5

aat tct ggc gta ggc gga acg tct cgc cca acg ggt aaa cgc cag ctg 163
Asn Ser Gly Val Gly Gly Thr Ser Arg Pro Thr Gly Lys Arg Gln Leu
                        10                15                20

tcg ggt gct tcc act acc tct acc tct tct tat gag gct aag cag gta 211
Ser Gly Ala Ser Thr Thr Ser Thr Ser Ser Tyr Glu Ala Lys Gln Val
                        25                30                35

tct aca cag aag aag tca tcc ggt tcg gat tct aag cct ggc ggc ggt 259
Ser Thr Gln Lys Lys Ser Ser Gly Ser Asp Ser Lys Pro Gly Gly Gly
                        40                45                50

gtt att tct ttt ctg cct gag gtt gtg gga gaa gtc cgt aag gtt att 307
Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu Val Arg Lys Val Ile
                        55                60                65

tgg cct act gcg cgc cag atg gtc acg tac acc ctt gtc gtt ttg gga 355
Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr Leu Val Val Leu Gly
70                75                80                85

ttc ttg att gtt ttg acc gct ttg gtg tct ggt gtg gat ttc cta gct 403
Phe Leu Ile Val Leu Thr Ala Leu Val Ser Gly Val Asp Phe Leu Ala
                        90                95                100

ggt ctt gga gtt gag aag att ctg act ccg taggtaggat gtgtaacatc 453
Gly Leu Gly Val Glu Lys Ile Leu Thr Pro
                        105                110

ttt 456

```

<210> 54

<211> 111

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 54

```

Val Ser Asp Glu Gln Asn Ser Gly Val Gly Gly Thr Ser Arg Pro Thr
1           5           10           15

Gly Lys Arg Gln Leu Ser Gly Ala Ser Thr Thr Ser Thr Ser Ser Tyr
20                25                30

Glu Ala Lys Gln Val Ser Thr Gln Lys Lys Ser Ser Gly Ser Asp Ser
35                40                45

Lys Pro Gly Gly Gly Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu
50                55                60

```

Val Arg Lys Val Ile Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr
65 70 75 80

Leu Val Val Leu Gly Phe Leu Ile Val Leu Thr Ala Leu Val Ser Gly
85 90 95

Val Asp Phe Leu Ala Gly Leu Gly Val Glu Lys Ile Leu Thr Pro
100 105 110

<210> 55

<211> 1941

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1918)

<223> RXN02462

<400> 55

tccatcctca tcgacgaagc ccgcacccca ctgattatct ccgggaccag tagacggcac 60

atcgcagttc tacaacgtct tcgcacagat cgtcccacgc atg acc aag gac gtt 115
Met Thr Lys Asp Val
1 5

cac tac gaa gtc gac gaa cgt aaa aag acc gtc ggt gtg aaa gaa gaa 163
His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val Gly Val Lys Glu Glu
10 15 20

ggc gtc gaa tac gtc gaa gac caa ctc ggc atc gac aac ctc tac gca 211
Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile Asp Asn Leu Tyr Ala
25 30 35

cct gag cac tca cag ctg gtc agc tac ctg aac aac gcc atc aag gca 259
Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn Asn Ala Ile Lys Ala
40 45 50

cag gaa ctg ttc acc cgc gac aag gac tac atc gtc cgc aac ggc gaa 307
Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile Val Arg Asn Gly Glu
55 60 65

gtt atg atc gtc gac ggc ttc acc ggc cgt gtc ctt gcc ggc cgc cga 355
Val Met Ile Val Asp Gly Phe Thr Gly Arg Val Leu Ala Gly Arg Arg
70 75 80 85

tac aac gaa ggc atg cac cag gcg atc gaa gcc aaa gag cgc gta gag 403
Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala Lys Glu Arg Val Glu
90 95 100

atc aaa aac gag aac cag acc ctg gcg acc gtt acc ctc cag aac tac 451
Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val Thr Leu Gln Asn Tyr
105 110 115

ttc cgc ctc tac acc aaa ctc gcc ggc atg acc ggt acc gca gag acc 499
Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr
120 125 130

gaa gca gca gag ctc aac cag atc tac aag ctc gac gtc atc gcg atc 547
Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu Asp Val Ile Ala Ile

135	140	145	
cca acc aac cga cca aac cag cgc gaa gac ttg acc gac ttg gtg tac Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu Thr Asp Leu Val Tyr 150 155 160 165			595
aaa acc caa gag gct aag ttc gca gca gtc gtc gac gac atc gca gaa Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val Asp Asp Ile Ala Glu 170 175 180			643
cgc acc gaa aag ggc caa cca gtc ctc gtc ggt acc gtc tcc gtc gag Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly Thr Val Ser Val Glu 185 190 195			691
cgc tcc gaa tac ctc tcc cag ctg ttg acc aaa cga ggc atc aag cac Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys Arg Gly Ile Lys His 200 205 210			739
aac gtc ctc aat gcg aag cac cac gag cag gaa gca cag atc gtt gct Asn Val Leu Asn Ala Lys His His Glu Gln Glu Ala Gln Ile Val Ala 215 220 225			787
cag gca ggt ctt cca ggc gcc gtc acc gtt gcc acc aac atg gcg ggc Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala Thr Asn Met Ala Gly 230 235 240 245			835
cgt gga acc gac atc gtg ctc ggc gga aac cca gaa atc ctc ctc gac Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro Glu Ile Leu Leu Asp 250 255 260			883
atc aaa ctc cgc gaa cgt gga ctt gat cct ttc gaa gac gaa gaa agc Ile Lys Leu Arg Glu Arg Gly Leu Asp Pro Phe Glu Asp Glu Glu Ser 265 270 275			931
tac cag gaa gcc tgg gac gct gaa ctt cca gca atg aag cag cga tgc Tyr Gln Glu Ala Trp Asp Ala Glu Leu Pro Ala Met Lys Gln Arg Cys 280 285 290			979
gaa gaa cgt ggc gac aaa gtc cgc gaa gcc gga gga ctc tac gtc ctt Glu Glu Arg Gly Asp Lys Val Arg Glu Ala Gly Gly Leu Tyr Val Leu 295 300 305			1027
ggc acc gaa cgc cac gaa tcc cga cgc atc gac aac cag ctg cgc ggt Gly Thr Glu Arg His Glu Ser Arg Arg Ile Asp Asn Gln Leu Arg Gly 310 315 320 325			1075
cgt tct gca cgt cag ggc gac cca gga tcc acc cgc ttc tat ctc tct Arg Ser Ala Arg Gln Gly Asp Pro Gly Ser Thr Arg Phe Tyr Leu Ser 330 335 340			1123
atg cgc gac gac ctg atg gtt cgc ttc gtc ggc cca acc atg gaa aac Met Arg Asp Asp Leu Met Val Arg Phe Val Gly Pro Thr Met Glu Asn 345 350 355			1171
atg atg aac agg ctc aac gtc cca gac gat gtg ccc atc gaa tcc aaa Met Met Asn Arg Leu Asn Val Pro Asp Asp Val Pro Ile Glu Ser Lys 360 365 370			1219
acc gtc acc aac tcc atc aag ggc gcc caa gct cag gtg gag aac cag Thr Val Thr Asn Ser Ile Lys Gly Ala Gln Ala Gln Val Glu Asn Gln 375 380 385			1267

aac ttc gaa atg cgt aag aac gtt ctg aag tac gac gaa gtc atg aac	1315
Asn Phe Glu Met Arg Lys Asn Val Leu Lys Tyr Asp Glu Val Met Asn	
390 395 400 405	
gaa cag cgc aag gtt atc tac agc gag cga cgc gaa atc ctc gaa tcc	1363
Glu Gln Arg Lys Val Ile Tyr Ser Glu Arg Arg Glu Ile Leu Glu Ser	
410 415 420	
gca gac atc tcc cgc tac atc caa aac atg atc gaa gaa aca gtc agc	1411
Ala Asp Ile Ser Arg Tyr Ile Gln Asn Met Ile Glu Glu Thr Val Ser	
425 430 435	
gca tac gtc gac ggc gcc acc gcc aac ggc tac gtc gaa gac tgg gac	1459
Ala Tyr Val Asp Gly Ala Thr Ala Asn Gly Tyr Val Glu Asp Trp Asp	
440 445 450	
ctc gac aaa ctc tgg aac gcc ctc gaa gcc ctc tac gac cca tcg atc	1507
Leu Asp Lys Leu Trp Asn Ala Leu Glu Ala Leu Tyr Asp Pro Ser Ile	
455 460 465	
aac tgg acc gac ctc gtc gaa ggc agc gaa tac ggc aaa cca ggg gag	1555
Asn Trp Thr Asp Leu Val Glu Gly Ser Glu Tyr Gly Lys Pro Gly Glu	
470 475 480 485	
ctg tcc gcc gaa gat cta cgc acc gca ctc gtc aac gac gcc cac gcc	1603
Leu Ser Ala Glu Asp Leu Arg Thr Ala Leu Val Asn Asp Ala His Ala	
490 495 500	
gaa tac gca aaa ctc gaa gaa gcc gta tcc gca atc ggc ggc gaa gca	1651
Glu Tyr Ala Lys Leu Glu Glu Ala Val Ser Ala Ile Gly Gly Glu Ala	
505 510 515	
cag atc cgc aac atc gaa cga atg gtg ctc atg cca gtc atc gac acc	1699
Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met Pro Val Ile Asp Thr	
520 525 530	
aaa tgg cgc gaa cac ctc tac gaa atg gac tac ctg aaa gaa ggc atc	1747
Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr Leu Lys Glu Gly Ile	
535 540 545	
ggc ctg cgc gca atg gca cag cgc gac cca ctg gtc gaa tac caa aag	1795
Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu Val Glu Tyr Gln Lys	
550 555 560 565	
gaa ggc ggc gac atg ttc aac ggc atg aaa gac ggc atc aag gaa gaa	1843
Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp Gly Ile Lys Glu Glu	
570 575 580	
acc gtc cgc cag ctc ttc ctc tcc gca agc agt tca tca agc aag acg	1891
Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser Ser Ser Ser Lys Thr	
585 590 595	
cgg aag tcg ctg act aac tca gaa ccc tgaaattcag catccgccac	1938
Arg Lys Ser Leu Thr Asn Ser Glu Pro	
600 605	
atg	1941

<211> 606

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 56

```

Met Thr Lys Asp Val His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val
 1          5          10          15

Gly Val Lys Glu Glu Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile
          20          25          30

Asp Asn Leu Tyr Ala Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn
          35          40          45

Asn Ala Ile Lys Ala Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile
          50          55          60

Val Arg Asn Gly Glu Val Met Ile Val Asp Gly Phe Thr Gly Arg Val
          65          70          75          80

Leu Ala Gly Arg Arg Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala
          85          90          95

Lys Glu Arg Val Glu Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val
          100          105          110

Thr Leu Gln Asn Tyr Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr
          115          120          125

Gly Thr Ala Glu Thr Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu
          130          135          140

Asp Val Ile Ala Ile Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu
          145          150          155          160

Thr Asp Leu Val Tyr Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val
          165          170          175

Asp Asp Ile Ala Glu Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly
          180          185          190

Thr Val Ser Val Glu Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys
          195          200          205

Arg Gly Ile Lys His Asn Val Leu Asn Ala Lys His His Glu Gln Glu
          210          215          220

Ala Gln Ile Val Ala Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala
          225          230          235          240

Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro
          245          250          255

Glu Ile Leu Leu Asp Ile Lys Leu Arg Glu Arg Gly Leu Asp Pro Phe
          260          265          270

Glu Asp Glu Glu Ser Tyr Gln Glu Ala Trp Asp Ala Glu Leu Pro Ala
          275          280          285

Met Lys Gln Arg Cys Glu Glu Arg Gly Asp Lys Val Arg Glu Ala Gly
          290          295          300

```


Gly Leu Tyr Val Leu Gly Thr Glu Arg His Glu Ser Arg Arg Ile Asp
 305 310 315 320
 Asn Gln Leu Arg Gly Arg Ser Ala Arg Gln Gly Asp Pro Gly Ser Thr
 325 330 335
 Arg Phe Tyr Leu Ser Met Arg Asp Asp Leu Met Val Arg Phe Val Gly
 340 345 350
 Pro Thr Met Glu Asn Met Met Asn Arg Leu Asn Val Pro Asp Asp Val
 355 360 365
 Pro Ile Glu Ser Lys Thr Val Thr Asn Ser Ile Lys Gly Ala Gln Ala
 370 375 380
 Gln Val Glu Asn Gln Asn Phe Glu Met Arg Lys Asn Val Leu Lys Tyr
 385 390 395 400
 Asp Glu Val Met Asn Glu Gln Arg Lys Val Ile Tyr Ser Glu Arg Arg
 405 410 415
 Glu Ile Leu Glu Ser Ala Asp Ile Ser Arg Tyr Ile Gln Asn Met Ile
 420 425 430
 Glu Glu Thr Val Ser Ala Tyr Val Asp Gly Ala Thr Ala Asn Gly Tyr
 435 440 445
 Val Glu Asp Trp Asp Leu Asp Lys Leu Trp Asn Ala Leu Glu Ala Leu
 450 455 460
 Tyr Asp Pro Ser Ile Asn Trp Thr Asp Leu Val Glu Gly Ser Glu Tyr
 465 470 475 480
 Gly Lys Pro Gly Glu Leu Ser Ala Glu Asp Leu Arg Thr Ala Leu Val
 485 490 495
 Asn Asp Ala His Ala Glu Tyr Ala Lys Leu Glu Glu Ala Val Ser Ala
 500 505 510
 Ile Gly Gly Glu Ala Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met
 515 520 525
 Pro Val Ile Asp Thr Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr
 530 535 540
 Leu Lys Glu Gly Ile Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu
 545 550 555 560
 Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp
 565 570 575
 Gly Ile Lys Glu Glu Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser
 580 585 590
 Ser Ser Ser Lys Thr Arg Lys Ser Leu Thr Asn Ser Glu Pro
 595 600 605

<210> 57

<211> 1965

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1942)

<223> RXN01559

<400> 57

```

gtctggttga ttggaattga aggagacttt cttggctcgg caaaaaaaga gtgccgctag 60

cgctgggaa cgatggccaa aacgcgcaat agcgttggtt  gtg ctc atc gtc gtt 115
                                         Val Leu Ile Val Val
                                         1                               5

ggt gtt tat gcg ttg gtg ctg ttg aca ggc gat cgt tct gcc aca cca 163
Gly Val Tyr Ala Leu Val Leu Leu Thr Gly Asp Arg Ser Ala Thr Pro
                        10                        15                        20

aaa ttg ggt att gat ctg caa ggc gga acc cga gtg acc ctc gtg ccg 211
Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr Arg Val Thr Leu Val Pro
                        25                        30                        35

cag ggg cag gat cca act cag gac cag ctg aat cag gca cgc acc att 259
Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu Asn Gln Ala Arg Thr Ile
                        40                        45                        50

ctg gaa aac cgt gtg aac ggc atg ggc gtt tca ggt gca agc gtg gtc 307
Leu Glu Asn Arg Val Asn Gly Met Gly Val Ser Gly Ala Ser Val Val
                        55                        60                        65

gct gac ggt aac acg ctg gtg atc act gtt ccc ggg gaa aat acc gca 355
Ala Asp Gly Asn Thr Leu Val Ile Thr Val Pro Gly Glu Asn Thr Ala
                        70                        75                        80                        85

cag gcg caa tcc cta gga cag acc tcc cag ctg ctg ttc cgt ccc gtt 403
Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln Leu Leu Phe Arg Pro Val
                        90                        95                        100

ggt cag gca gga atg ccc gat atg acc acg ttg atg cca gag ctg gaa 451
Gly Gln Ala Gly Met Pro Asp Met Thr Thr Leu Met Pro Glu Leu Glu
                        105                        110                        115

gag atg gcc aac agg tgg gtt gaa tac ggc gtc atc acc gaa gag cag 499
Glu Met Ala Asn Arg Trp Val Glu Tyr Gly Val Ile Thr Glu Glu Gln
                        120                        125                        130

gca aat gcc tcc ttg gag gaa atg aac acc gct gtt gca tcg acc act 547
Ala Asn Ala Ser Leu Glu Glu Met Asn Thr Ala Val Ala Ser Thr Thr
                        135                        140                        145

gcg gtg gaa ggc gaa gaa gca act gag cca gaa ccc gtc acc gtg tcg 595
Ala Val Glu Gly Glu Glu Ala Thr Glu Pro Glu Pro Val Thr Val Ser
                        150                        155                        160                        165

gcg acc cct atg gat gag cca gcc aac tcc att gag gca aca cag cga 643
Ala Thr Pro Met Asp Glu Pro Ala Asn Ser Ile Glu Ala Thr Gln Arg
                        170                        175                        180

cgc cag gaa atc acg gac atg ctg cgc acc gac cgc cag tcc acc gat 691
Arg Gln Glu Ile Thr Asp Met Leu Arg Thr Asp Arg Gln Ser Thr Asp

```

			185				190				195							
ccc Pro	act Thr	gtc Val	cag Gln	atc Ile	gct Ala	gca Ala	agt Ser	tct Ser	ttg Leu	atg Met	cag Gln	tgc Cys	acc Thr	act Thr	gat Asp	739		
			200					205					210					
gag Glu	atg Met	gat Asp	cct Pro	ttg Leu	gcc Ala	ggc Gly	acc Thr	gat Asp	gat Asp	cca Pro	cgc Arg	ctg Leu	cca Pro	ttg Leu	gtg Val	787		
			215					220					225					
gca Ala	tgt Cys	gat Asp	cca Pro	gct Ala	gta Val	ggc Gly	ggc Gly	gtg Val	tat Tyr	gta Val	ctt Leu	gat Asp	cct Pro	gca Ala	cct Pro	835		
			230		235					240					245			
ttg Leu	ctc Leu	aac Asn	ggc Gly	gaa Glu	acc Thr	gat Asp	gag Glu	gaa Glu	aat Asn	ggt Gly	gcg Ala	cgc Arg	cta Leu	acc Thr	ggc Gly	883		
			250					255					260					
aat Asn	gag Glu	atc Ile	gat Asp	acc Thr	aac Asn	cgt Arg	ccc Pro	atc Ile	acc Thr	ggt Gly	gga Gly	ttc Phe	aac Asn	gcc Ala	cag Gln	931		
			265					270					275					
tcc Ser	ggc Gly	cag Gln	atg Met	gaa Glu	atc Ile	agc Ser	ttt Phe	gcc Ala	ttc Phe	aaa Lys	tcc Ser	ggc Gly	gat Asp	ggg Gly	gaa Glu	979		
			280					285					290					
gaa Glu	ggc Gly	tct Ser	gca Ala	act Thr	tgg Trp	tcc Ser	tct Ser	ctg Leu	acc Thr	agc Ser	cag Gln	tac Tyr	ctg Leu	cag Gln	cag Gln	1027		
			295					300					305					
cag Gln	atc Ile	gcc Ala	atc Ile	acc Thr	ctg Leu	gac Asp	tct Ser	cag Gln	gtg Val	att Ile	tct Ser	gca Ala	ccc Pro	gtg Val	att Ile	1075		
			310		315					320					325			
cag Gln	tca Ser	gca Ala	acc Thr	cct Pro	gtg Val	ggc Gly	tct Ser	gca Ala	aca Thr	tcc Ser	atc Ile	acc Thr	ggc Gly	gac Asp	ttc Phe	1123		
			330					335					340					
act Thr	caa Gln	act Thr	gaa Glu	gcc Ala	caa Gln	gat Asp	ctg Leu	gcg Ala	aac Asn	aac Asn	ctg Leu	cgc Arg	tac Tyr	ggc Gly	gca Ala	1171		
			345					350					355					
ttg Leu	ccc Pro	ctg Leu	agc Ser	ttc Phe	gca Ala	ggc Gly	gaa Glu	aac Asn	ggc Gly	gag Glu	cgc Arg	ggc Gly	gga Gly	act Thr	acc Thr	1219		
			360					365					370					
acc Thr	acc Thr	gtt Val	ccg Pro	cca Pro	tca Ser	cta Leu	ggc Gly	gca Ala	gca Ala	tcc Ser	ttg Leu	aag Lys	gcc Ala	gga Gly	ctg Leu	1267		
			375					380					385					
atc Ile	gca Ala	ggc Gly	atc Ile	gtc Val	ggc Gly	atc Ile	gcg Ala	ctg Leu	gtc Val	gcc Ala	atc Ile	ttc Phe	gtg Val	ttc Phe	gcc Ala	1315		
			390		395					400					405			
tac Tyr	tac Tyr	cgc Arg	gtc Val	ttc Phe	gga Gly	ttc Phe	gtt Val	tcc Ser	ctg Leu	ttc Phe	acc Thr	ctg Leu	ttt Phe	gcc Ala	gca Ala	1363		
			410					415					420					
ggc Gly	gtg Val	ttg Leu	gtc Val	tac Tyr	ggc Gly	ctt Leu	ctg Leu	gta Val	ctg Leu	ctg Leu	gga Gly	cgc Arg	tgg Trp	atc Ile	gga Gly	1411		
			425					430					435					

tat tcc cta gac ctt gct ggt atc gcc ggt ttg atc atc ggt atc ggt	1459
Tyr Ser Leu Asp Leu Ala Gly Ile Ala Gly Leu Ile Ile Gly Ile Gly	
440 445 450	
acc acc gcc gac tcc ttc gtg gtg ttc tat gag cgc atc aag gat gag	1507
Thr Thr Ala Asp Ser Phe Val Val Phe Tyr Glu Arg Ile Lys Asp Glu	
455 460 465	
atc cgt gaa gga aga tcc ttt aga tct gca gta cct cgt gca tgg gaa	1555
Ile Arg Glu Gly Arg Ser Phe Arg Ser Ala Val Pro Arg Ala Trp Glu	
470 475 480 485	
agc gcc aag cgc acc atc gtc aca ggc aac atg gtc act ttg ctc ggc	1603
Ser Ala Lys Arg Thr Ile Val Thr Gly Asn Met Val Thr Leu Leu Gly	
490 495 500	
gct atc gtg att tac ttg ctc gcg gtc ggc gaa gtc aag ggc ttt gcc	1651
Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu Val Lys Gly Phe Ala	
505 510 515	
ttc acc ctg ggt ctg acc acc gta ttc gat ctc gtt gtc acc ttc ctg	1699
Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu Val Val Thr Phe Leu	
520 525 530	
atc acg gca cca ctg gtt atc ctg gca tca cgc aac cca ttc ttt gcc	1747
Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg Asn Pro Phe Phe Ala	
535 540 545	
aag tca tcg gtc aac ggc atg gga cga gtg atg aag ctc gtt gaa gaa	1795
Lys Ser Ser Val Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu	
550 555 560 565	
cgc cgc gcc aac ggt gaa ttg gat gag cct gag tac ctg aaa aag atc	1843
Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile	
570 575 580	
cat gcc aag aat gcg gca gct gat aag gct tcc act gac aat tct tcc	1891
His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser	
585 590 595	
act gac aat tct gaa gca cct ggc acc gat acg aac caa gag gag gag	1939
Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr Asn Gln Glu Glu Glu	
600 605 610	
aag tagccatgac tgattcccag act	1965
Lys	

<210> 58

<211> 614

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 58

Val	Leu	Ile	Val	Val	Gly	Val	Tyr	Ala	Leu	Val	Leu	Leu	Thr	Gly	Asp
1				5					10					15	

Arg	Ser	Ala	Thr	Pro	Lys	Leu	Gly	Ile	Asp	Leu	Gln	Gly	Gly	Thr	Arg
			20					25					30		

Val Thr Leu Val Pro Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu Asn
 35 40 45
 Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val Ser
 50 55 60
 Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val Pro
 65 70 75 80
 Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln Leu
 85 90 95
 Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr Leu
 100 105 110
 Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly Val
 115 120 125
 Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr Ala
 130 135 140
 Val Ala Ser Thr Thr Ala Val Glu Gly Glu Glu Ala Thr Glu Pro Glu
 145 150 155 160
 Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser Ile
 165 170 175
 Glu Ala Thr Gln Arg Arg Gln Glu Ile Thr Asp Met Leu Arg Thr Asp
 180 185 190
 Arg Gln Ser Thr Asp Pro Thr Val Gln Ile Ala Ala Ser Ser Leu Met
 195 200 205
 Gln Cys Thr Thr Asp Glu Met Asp Pro Leu Ala Gly Thr Asp Asp Pro
 210 215 220
 Arg Leu Pro Leu Val Ala Cys Asp Pro Ala Val Gly Gly Val Tyr Val
 225 230 235 240
 Leu Asp Pro Ala Pro Leu Leu Asn Gly Glu Thr Asp Glu Glu Asn Gly
 245 250 255
 Ala Arg Leu Thr Gly Asn Glu Ile Asp Thr Asn Arg Pro Ile Thr Gly
 260 265 270
 Gly Phe Asn Ala Gln Ser Gly Gln Met Glu Ile Ser Phe Ala Phe Lys
 275 280 285
 Ser Gly Asp Gly Glu Glu Gly Ser Ala Thr Trp Ser Ser Leu Thr Ser
 290 295 300
 Gln Tyr Leu Gln Gln Gln Ile Ala Ile Thr Leu Asp Ser Gln Val Ile
 305 310 315 320
 Ser Ala Pro Val Ile Gln Ser Ala Thr Pro Val Gly Ser Ala Thr Ser
 325 330 335
 Ile Thr Gly Asp Phe Thr Gln Thr Glu Ala Gln Asp Leu Ala Asn Asn
 340 345 350

Leu Arg Tyr Gly Ala Leu Pro Leu Ser Phe Ala Gly Glu Asn Gly Glu
 355 360 365
 Arg Gly Gly Thr Thr Thr Thr Val Pro Pro Ser Leu Gly Ala Ala Ser
 370 375 380
 Leu Lys Ala Gly Leu Ile Ala Gly Ile Val Gly Ile Ala Leu Val Ala
 385 390 395 400
 Ile Phe Val Phe Ala Tyr Tyr Arg Val Phe Gly Phe Val Ser Leu Phe
 405 410 415
 Thr Leu Phe Ala Ala Gly Val Leu Val Tyr Gly Leu Leu Val Leu Leu
 420 425 430
 Gly Arg Trp Ile Gly Tyr Ser Leu Asp Leu Ala Gly Ile Ala Gly Leu
 435 440 445
 Ile Ile Gly Ile Gly Thr Thr Ala Asp Ser Phe Val Val Phe Tyr Glu
 450 455 460
 Arg Ile Lys Asp Glu Ile Arg Glu Gly Arg Ser Phe Arg Ser Ala Val
 465 470 475 480
 Pro Arg Ala Trp Glu Ser Ala Lys Arg Thr Ile Val Thr Gly Asn Met
 485 490 495
 Val Thr Leu Leu Gly Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu
 500 505 510
 Val Lys Gly Phe Ala Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu
 515 520 525
 Val Val Thr Phe Leu Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg
 530 535 540
 Asn Pro Phe Phe Ala Lys Ser Ser Val Asn Gly Met Gly Arg Val Met
 545 550 555 560
 Lys Leu Val Glu Glu Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu
 565 570 575
 Tyr Leu Lys Lys Ile His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser
 580 585 590
 Thr Asp Asn Ser Ser Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr
 595 600 605
 Asn Gln Glu Glu Glu Lys
 610

<210> 59

<211> 819

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(796)

<223> RXN00046

<400> 59

```

tggtgcccac gcagccgtca tcgcagcagc aaaatatgcc cgcgataacg ccttttaagc 60

acctaaaacg ctgtttctcaa cacaggagtt tccttaaata atg gac tta aat act 115
              Met Asp Leu Asn Thr
              1              5

caa cgc tca aag ctc tac gca cag ctt caa ggc cag ctc att gtt tcc 163
Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly Gln Leu Ile Val Ser
              10              15              20

gtg caa gct ccc gac ggc cat gcc atg cga gat acc cat acg ctc acc 211
Val Gln Ala Pro Asp Gly His Ala Met Arg Asp Thr His Thr Leu Thr
              25              30              35

cat gtg gcc gca gcc tgt gtc gat ggc ggt gct cct gcc att cgc tgt 259
His Val Ala Ala Ala Cys Val Asp Gly Gly Ala Pro Ala Ile Arg Cys
              40              45              50

ggc ggt tac ggc ggt ttg gaa gat atc cgt tca atc tcc aac cgt gtc 307
Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser Ile Ser Asn Arg Val
              55              60              65

gac gtt ccc gtt ttc gga ctc acc aaa gaa ggc tcc gaa gga gtt tac 355
Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly Ser Glu Gly Val Tyr
              70              75              80              85

atc acc cca acc agg gat tcc gtt cga gca gtg gca gaa tcc ggc gcc 403
Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val Ala Glu Ser Gly Ala
              90              95              100

act gta gtc tgc gcg gat gca act ttc cga cct agg cct gac ggc tcc 451
Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro Arg Pro Asp Gly Ser
              105              110              115

acc ttt gca gag ctg gtc act gtt gcc cac gat tcc gga att ctc atc 499
Thr Phe Ala Glu Leu Val Thr Val Ala His Asp Ser Gly Ile Leu Ile
              120              125              130

atg gcg gac tgc gca act ccc gaa gaa gtt ctc agt gcg cat aag gct 547
Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu Ser Ala His Lys Ala
              135              140              145

ggc gcg gat ttt gtg tcc acc acg ctt gct gga tac acc gaa cac cgc 595
Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly Tyr Thr Glu His Arg
              150              155              160              165

gag aaa aca gtc ggt cca gat ttc gat tgc ctc cgc gaa gca cgt gag 643
Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu Arg Glu Ala Arg Glu
              170              175              180

tta gtt ccc gat gcg ttc ctc att ggc gaa ggt cgc ttc tcc aac cct 691
Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly Arg Phe Ser Asn Pro
              185              190              195

gcg gat gtg gcg cac ggt cgt ctc att ggt gcc aac gcg atc atc gtg 739
Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala Asn Ala Ile Ile Val
              200              205              210

ggc acc gca atc act gac cct ggt ttc atc act gga cag ttc gcg tca 787

```

Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr Gly Gln Phe Ala Ser
 215 220 225

ctg ttg cac tagcacttag tccagcgctg cac

819

Leu Leu His

230

<210> 60

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

Met Asp Leu Asn Thr Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly
 1 5 10 15

Gln Leu Ile Val Ser Val Gln Ala Pro Asp Gly His Ala Met Arg Asp
 20 25 30

Thr His Thr Leu Thr His Val Ala Ala Ala Cys Val Asp Gly Gly Ala
 35 40 45

Pro Ala Ile Arg Cys Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser
 50 55 60

Ile Ser Asn Arg Val Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly
 65 70 75 80

Ser Glu Gly Val Tyr Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val
 85 90 95

Ala Glu Ser Gly Ala Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro
 100 105 110

Arg Pro Asp Gly Ser Thr Phe Ala Glu Leu Val Thr Val Ala His Asp
 115 120 125

Ser Gly Ile Leu Ile Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu
 130 135 140

Ser Ala His Lys Ala Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly
 145 150 155 160

Tyr Thr Glu His Arg Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu
 165 170 175

Arg Glu Ala Arg Glu Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly
 180 185 190

Arg Phe Ser Asn Pro Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala
 195 200 205

Asn Ala Ile Ile Val Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr
 210 215 220

Gly Gln Phe Ala Ser Leu Leu His
 225 230

<210> 61

<211> 1219

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (48) .. (1196)

<223> RXN01863

<400> 61

```

ggtatcatatc cgatatgaac caaatagaaa gaaggaagtt taagacg atg aat agc 56
                                     Met Asn Ser
                                     1

gtc aaa ttg aag caa cct gtt agc att tac aat gat cca tgg gaa tca 104
Val Lys Leu Lys Gln Pro Val Ser Ile Tyr Asn Asp Pro Trp Glu Ser
      5                      10                      15

tat aac gat gtt aaa gaa cat ggc caa tta act tta agt aac atc gaa 152
Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser Asn Ile Glu
  20                      25                      30                      35

ttt aca act aca aat ctt tgt aat atg cgt tgt agc cac tgt gca gtt 200
Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His Cys Ala Val
                      40                      45                      50

ggg tat act tta caa act gtc gac ccc gag cct tta gat atg gac tta 248
Gly Tyr Thr Leu Gln Thr Val Asp Pro Glu Pro Leu Asp Met Asp Leu
                      55                      60                      65

att tat cgt aga ctt gat gaa att cca aat ctg cga acg atg tca att 296
Ile Tyr Arg Arg Leu Asp Glu Ile Pro Asn Leu Arg Thr Met Ser Ile
                      70                      75                      80

aca ggt ggc gaa cca atg ttt tct aaa aag tct att aga aat gtt gtt 344
Thr Gly Gly Glu Pro Met Phe Ser Lys Lys Ser Ile Arg Asn Val Val
      85                      90                      95

aaa cct cta tta aag tat gca cat cat cga ggt ata tat aca caa atg 392
Lys Pro Leu Leu Lys Tyr Ala His His Arg Gly Ile Tyr Thr Gln Met
100                      105                      110                      115

aat tca aac cta aca ttg cct caa gat cgt tat tta gat att gct gaa 440
Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp Ile Ala Glu
                      120                      125                      130

tat atc gat gtt atg cat atc tca cat aac tgg gga aca act gat gaa 488
Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr Thr Asp Glu
                      135                      140                      145

ttc gca aat gtt ggc ttt ggc gca atg aag aag caa cca ccg tta aaa 536
Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro Pro Leu Lys
                      150                      155                      160

gct aag tta aaa tta tat gaa caa atg att tcg aat gca cgt aca tta 584
Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala Arg Thr Leu
                      165                      170                      175

tca gaa caa gga atg ttt gta tct gcg gaa aca atg ctc aat caa agt 632
Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu Asn Gln Ser
180                      185                      190                      195

```

acg cta cca cat tta cga aaa ata cat caa gaa gtc gtt cat gat atg 680
 Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val His Asp Met
 200 205 210

aaa tgt agc aga cac gag att cac cct atg tat cca gct gac ttt gca 728
 Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala Asp Phe Ala
 215 220 225

agt caa tta aat gtg tta act cta gcg gaa atg aaa aag aca att cat 776
 Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys Thr Ile His
 230 235 240

gat ata ttg gat ttc aga gat gaa gat att tgg atg tta ttt ggt act 824
 Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu Phe Gly Thr
 245 250 255

ttg cct gtg ttt cca tgc tta aag gat gat gaa gat caa aag tta cta 872
 Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln Lys Leu Leu
 260 265 270 275

tca cgt tta aga aat gct aac aat gta acg act aga aat gac ccg gat 920
 Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn Asp Pro Asp
 280 285 290

ggc cgt agt cgt tta aat gtc aat gta ttt aca ggt aat gta atc gta 968
 Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn Val Ile Val
 295 300 305

act gat ttc gga gat gaa aca ggt aca att tcg aat ata caa aaa gat 1016
 Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile Gln Lys Asp
 310 315 320

aaa tta aca gat gta ttt gat aaa tgg tta tcc tct gat ctt gct aaa 1064
 Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp Leu Ala Lys
 325 330 335

tca tta aat tgt cat tgt tcc gag ttt agt tgt tta gga cca aat gtt 1112
 Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly Pro Asn Val
 340 345 350 355

ctt gtt aaa aat atg tac tat ccg aat atg gat ttt aaa gat aat gag 1160
 Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys Asp Asn Glu
 360 365 370

cgt cat atg cac aaa caa cca caa att ata caa ttt taaaaactct 1206
 Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe
 375 380

taattatgcg gag 1219

<210> 62

<211> 383

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 62

Met Asn Ser Val Lys Leu Lys Gln Pro Val Ser Ile Tyr Asn Asp Pro
 1 5 10 15

Trp	Glu	Ser	Tyr	Asn	Asp	Val	Lys	Glu	His	Gly	Gln	Leu	Thr	Leu	Ser		
			20					25					30				
Asn	Ile	Glu	Phe	Thr	Thr	Thr	Asn	Leu	Cys	Asn	Met	Arg	Cys	Ser	His		
		35					40					45					
Cys	Ala	Val	Gly	Tyr	Thr	Leu	Gln	Thr	Val	Asp	Pro	Glu	Pro	Leu	Asp		
	50					55					60						
Met	Asp	Leu	Ile	Tyr	Arg	Arg	Leu	Asp	Glu	Ile	Pro	Asn	Leu	Arg	Thr		
	65				70					75					80		
Met	Ser	Ile	Thr	Gly	Gly	Glu	Pro	Met	Phe	Ser	Lys	Lys	Ser	Ile	Arg		
				85					90					95			
Asn	Val	Val	Lys	Pro	Leu	Leu	Lys	Tyr	Ala	His	His	Arg	Gly	Ile	Tyr		
			100					105					110				
Thr	Gln	Met	Asn	Ser	Asn	Leu	Thr	Leu	Pro	Gln	Asp	Arg	Tyr	Leu	Asp		
		115					120					125					
Ile	Ala	Glu	Tyr	Ile	Asp	Val	Met	His	Ile	Ser	His	Asn	Trp	Gly	Thr		
	130					135					140						
Thr	Asp	Glu	Phe	Ala	Asn	Val	Gly	Phe	Gly	Ala	Met	Lys	Lys	Gln	Pro		
145					150					155					160		
Pro	Leu	Lys	Ala	Lys	Leu	Lys	Leu	Tyr	Glu	Gln	Met	Ile	Ser	Asn	Ala		
				165					170					175			
Arg	Thr	Leu	Ser	Glu	Gln	Gly	Met	Phe	Val	Ser	Ala	Glu	Thr	Met	Leu		
			180					185					190				
Asn	Gln	Ser	Thr	Leu	Pro	His	Leu	Arg	Lys	Ile	His	Gln	Glu	Val	Val		
		195					200					205					
His	Asp	Met	Lys	Cys	Ser	Arg	His	Glu	Ile	His	Pro	Met	Tyr	Pro	Ala		
	210					215					220						
Asp	Phe	Ala	Ser	Gln	Leu	Asn	Val	Leu	Thr	Leu	Ala	Glu	Met	Lys	Lys		
225					230					235					240		
Thr	Ile	His	Asp	Ile	Leu	Asp	Phe	Arg	Asp	Glu	Asp	Ile	Trp	Met	Leu		
				245					250					255			
Phe	Gly	Thr	Leu	Pro	Val	Phe	Pro	Cys	Leu	Lys	Asp	Asp	Glu	Asp	Gln		
			260					265					270				
Lys	Leu	Leu	Ser	Arg	Leu	Arg	Asn	Ala	Asn	Asn	Val	Thr	Thr	Arg	Asn		
			275				280					285					
Asp	Pro	Asp	Gly	Arg	Ser	Arg	Leu	Asn	Val	Asn	Val	Phe	Thr	Gly	Asn		
	290					295					300						
Val	Ile	Val	Thr	Asp	Phe	Gly	Asp	Glu	Thr	Gly	Thr	Ile	Ser	Asn	Ile		
305					310					315					320		
Gln	Lys	Asp	Lys	Leu	Thr	Asp	Val	Phe	Asp	Lys	Trp	Leu	Ser	Ser	Asp		
				325					330					335			
Leu	Ala	Lys	Ser	Leu	Asn	Cys	His	Cys	Ser	Glu	Phe	Ser	Cys	Leu	Gly		

340	345	350	
Pro Asn Val Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys			
355	360	365	
Asp Asn Glu Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe			
370	375	380	
 <210> 63			
<211> 618			
<212> DNA			
<213> Corynebacterium glutamicum			
 <220>			
<221> CDS			
<222> (101)..(595)			
<223> RXN00833			
 <400> 63			
agctttttgc atgtgtcata tcgtaccggt tgcataaggcc tgttcgcgct tgggtgaacct 60			
tttctagcac caaaacaaaa ctctccctag tatgggggtcc atg gct aaa aca cat 115			
		Met Ala Lys Thr His	5
		1	
ttt caa ggc aac gaa act gct acc tcc ggc gaa ctg cca cag gtc ggc 163			
Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu Leu Pro Gln Val Gly			
	10	15	20
gac aac ctc gca gag ttc aac ctc gtc aac acc gaa ctg ggc gag gtc 211			
Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr Glu Leu Gly Glu Val			
	25	30	35
tcc tca aag gac ttc cag ggc cgc aag ctt gtc ctg aac atc ttc cca 259			
Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val Leu Asn Ile Phe Pro			
	40	45	50
tcc gtt gac acc ggc gtt tgt gca aca tca gtc cgc aag ttc aac gag 307			
Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val Arg Lys Phe Asn Glu			
	55	60	65
gca gca gca agc ctg gaa aac acc acc gtg ctg tgc atc tcc aag gat 355			
Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu Cys Ile Ser Lys Asp			
	70	75	80
ctt cca ttc gca ctg ggc cgt ttc tgc tcc gca gaa ggc atc gag aac 403			
Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala Glu Gly Ile Glu Asn			
	90	95	100
gtc acc cca gta tcc gca ttc cgt tcc acc ttc ggt gaa gac aac ggc 451			
Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe Gly Glu Asp Asn Gly			
	105	110	115
atc gtg ctc gaa ggc tca cca ctt aag ggt ctt ctt gca cgc agc gtc 499			
Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu Leu Ala Arg Ser Val			
	120	125	130
atc gtc gtc gat gaa aac ggc aag gtt gct tac acc cag ttg gtt gat 547			
Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr Thr Gln Leu Val Asp			
	135	140	145

gag atc ttc act gaa cct gat tac gac gct gca ctt gct ggg ctg aac 595
 Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala Leu Ala Gly Leu Asn
 150 155 160 165

taatttactt cgctcagggg aat 618

<210> 64
 <211> 165
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 64
 Met Ala Lys Thr His Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu
 1 5 10 15
 Leu Pro Gln Val Gly Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr
 20 25 30
 Glu Leu Gly Glu Val Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val
 35 40 45
 Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val
 50 55 60
 Arg Lys Phe Asn Glu Ala Ala Ser Leu Glu Asn Thr Thr Val Leu
 65 70 75 80
 Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala
 85 90 95
 Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe
 100 105 110
 Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu
 115 120 125
 Leu Ala Arg Ser Val Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr
 130 135 140
 Thr Gln Leu Val Asp Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala
 145 150 155 160
 Leu Ala Gly Leu Asn
 165

<210> 65
 <211> 879
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(856)
 <223> RXN01676

<400> 65
 agttatagct tttctcggtg gcacactcgc gctacttagc ccttggtgccg cactcctttt 60

accagcattt	tttgcatacct	cagtgggtgc	tggcccgcgc	atg	atc	ctt	cac	ggt	115							
				Met	Ile	Leu	His	Gly								
				1				5								
gtt	gtg	ttc	tac	gca	gga	ctt	cta	gta	ctt	ctc	gtg	cca	ctt	ggc	ctt	163
Val	Val	Phe	Tyr	Ala	Gly	Leu	Leu	Val	Leu	Leu	Val	Pro	Leu	Gly	Leu	
				10				15						20		
ggt	gcg	gga	atc	ctc	ggc	gag	ctg	ttt	atc	acc	caa	cgc	cag	acc	atc	211
Gly	Ala	Gly	Ile	Leu	Gly	Glu	Leu	Phe	Ile	Thr	Gln	Arg	Gln	Thr	Ile	
			25				30						35			
atc	gtg	gtt	tca	tcg	atc	gtg	ctg	att	atc	cta	ggt	ttt	gtc	cag	atc	259
Ile	Val	Val	Ser	Ser	Ile	Val	Leu	Ile	Ile	Leu	Gly	Phe	Val	Gln	Ile	
		40					45						50			
ttc	ggc	ggc	gga	ttc	gac	ttc	gga	aaa	gca	ctc	cca	gga	tta	gat	cgt	307
Phe	Gly	Gly	Gly	Phe	Asp	Phe	Gly	Lys	Ala	Leu	Pro	Gly	Leu	Asp	Arg	
	55					60					65					
ctg	caa	tct	aag	gcc	act	gtg	acc	tca	ggt	cta	gga	aag	agc	ttt	tta	355
Leu	Gln	Ser	Lys	Ala	Thr	Val	Thr	Ser	Gly	Leu	Gly	Lys	Ser	Phe	Leu	
70					75					80					85	
cta	gga	atg	acc	agt	agt	att	gcc	ggt	ttt	tgt	tcc	gga	cca	atc	ctc	403
Leu	Gly	Met	Thr	Ser	Ser	Ile	Ala	Gly	Phe	Cys	Ser	Gly	Pro	Ile	Leu	
				90					95					100		
ggc	gcc	gtt	ctt	act	ttg	gct	gcc	acc	agt	gga	aac	tcc	atc	acc	tca	451
Gly	Ala	Val	Leu	Thr	Leu	Ala	Ala	Thr	Ser	Gly	Asn	Ser	Ile	Thr	Ser	
		105						110					115			
gca	ctc	att	ttg	agt	gct	tat	ggt	gcg	gga	atg	gtg	ctg	ccc	ctg	atg	499
Ala	Leu	Ile	Leu	Ser	Ala	Tyr	Gly	Ala	Gly	Met	Val	Leu	Pro	Leu	Met	
		120					125					130				
gct	att	gca	gcg	ctc	tgg	gcc	aaa	ctc	gga	cag	cgt	gga	cag	cag	atg	547
Ala	Ile	Ala	Ala	Leu	Trp	Ala	Lys	Leu	Gly	Gln	Arg	Gly	Gln	Gln	Met	
	135					140					145					
ctc	cgc	ggc	cgg	gaa	ttc	acc	ttc	ttg	ggc	agg	cag	tgg	cac	att	gtt	595
Leu	Arg	Gly	Arg	Glu	Phe	Thr	Phe	Leu	Gly	Arg	Gln	Trp	His	Ile	Val	
150					155					160					165	
tct	gtc	att	agc	ggt	gcc	ctg	atc	atc	gct	gtc	gga	atc	ctc	ttt	tgg	643
Ser	Val	Ile	Ser	Gly	Ala	Leu	Ile	Ile	Ala	Val	Gly	Ile	Leu	Phe	Trp	
				170					175					180		
tcc	acg	aac	ggc	ctt	gtc	agc	atg	ccg	gag	ctc	gtt	cca	atg	gac	acc	691
Ser	Thr	Asn	Gly	Leu	Val	Ser	Met	Pro	Glu	Leu	Val	Pro	Met	Asp	Thr	
			185					190					195			
cag	atc	tgg	cta	cag	gaa	gcc	aca	ttc	tca	ctc	ggg	tca	cca	ctc	ttt	739
Gln	Ile	Trp	Leu	Gln	Glu	Ala	Thr	Phe	Ser	Leu	Gly	Ser	Pro	Leu	Phe	
		200					205					210				
gac	atc	gca	ttg	atc	att	gtc	gcc	gct	ggc	ttg	ttc	ttg	tac	ttc	tgg	787
Asp	Ile	Ala	Leu	Ile	Ile	Val	Ala	Ala	Gly	Leu	Phe	Leu	Tyr	Phe	Trp	
	215					220					225					
aac	aaa	cga	caa	aag	cga	aaa	gaa	gaa	gct	cag	cga	ccc	aaa	gaa	agt	835

Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln Arg Pro Lys Glu Ser
 230 235 240 245

gga tgg gtt att aac cct cgc taattattag ttttggagcg agg
 Gly Trp Val Ile Asn Pro Arg
 250

879

<210> 66

<211> 252

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

Met Ile Leu His Gly Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu
 1 5 10 15

Val Pro Leu Gly Leu Gly Ala Gly Ile Leu Gly Glu Leu Phe Ile Thr
 20 25 30

Gln Arg Gln Thr Ile Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu
 35 40 45

Gly Phe Val Gln Ile Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu
 50 55 60

Pro Gly Leu Asp Arg Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu
 65 70 75 80

Gly Lys Ser Phe Leu Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys
 85 90 95

Ser Gly Pro Ile Leu Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly
 100 105 110

Asn Ser Ile Thr Ser Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met
 115 120 125

Val Leu Pro Leu Met Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln
 130 135 140

Arg Gly Gln Gln Met Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg
 145 150 155 160

Gln Trp His Ile Val Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val
 165 170 175

Gly Ile Leu Phe Trp Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu
 180 185 190

Val Pro Met Asp Thr Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu
 195 200 205

Gly Ser Pro Leu Phe Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu
 210 215 220

Phe Leu Tyr Phe Trp Asn Lys Arg Gln Lys Arg Lys Glu Glu Ala Gln
 225 230 235 240

Arg Pro Lys Glu Ser Gly Trp Val Ile Asn Pro Arg
 245 250

<400> 67																	60
caggcaatgc gacctcgct cagtgacatc cttgggtgttc caagacgatc aaattgtcgg																	
cgtgcattac aacgaaccag ctcaggagat ttgatcactc																	115
Val Arg Leu Thr Lys																	5
cta gca gca aca atc ggc tgc gtg aca ctc agc gga ctt gcg cta gta																	163
Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser Gly Leu Ala Leu Val																	20
gcc tgc agc agt gac agt acc gct ggt act gac gct gtt gct gtc ggc																	211
Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp Ala Val Ala Val Gly																	35
gga acc ttc caa ttc cac tcc ccg gat gga aag atg gaa att ttc tac																	259
Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys Met Glu Ile Phe Tyr																	50
gac gag gct gac cgt caa caa ctc ccc gac att ggt gga gat tcc ctc																	307
Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile Gly Gly Asp Ser Leu																	65
atg gaa gag ggc aca cag atc aac ctg tct gat ttc gaa aac caa gtt																	355
Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp Phe Glu Asn Gln Val																	85
gtc atc ctc aat gcg tgg ggg cag tgg tgt gca ccg tgc cgc tcc gaa																	403
Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala Pro Cys Arg Ser Glu																	100
tcc gat gat ctc cag att atc cat gag gaa ctc caa gct gcc gga aac																	451
Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu Gln Ala Ala Gly Asn																	115
ggc gac acc cct ggt ggc acc gtg ttg ggt atc aat gtg cgt gat tac																	499
Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile Asn Val Arg Asp Tyr																	130
tcc cgc gac atc gcc caa gac ttt gtc acc gac aac ggc ctt gat tac																	547
Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp Asn Gly Leu Asp Tyr																	145
cca agc att tac gat cca cca ttt atg aca gca gca tcc ctc ggt ggt																	595
Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala Ala Ser Leu Gly Gly																	165
gtt ctc gca tcg gtg atc cca acc acc atc gtg ctg gat aaa cag cac																	643
Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val Leu Asp Lys Gln His																	

	170		175		180	
cgc ccc gca gca gtg ttc ttg cgc gaa gtc acc tcc aaa gat gtg ttg						691
Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr Ser Lys Asp Val Leu						
	185		190		195	
gat gtt gcg ttg cca ttg gta gat gag gcc taaatgtctg agattgtggt						741
Asp Val Ala Leu Pro Leu Val Asp Glu Ala						
	200		205			
agc						744

<210> 68
 <211> 207
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 68
 Val Arg Leu Thr Lys Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser
 1 5 10 15
 Gly Leu Ala Leu Val Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp
 20 25 30
 Ala Val Ala Val Gly Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys
 35 40 45
 Met Glu Ile Phe Tyr Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile
 50 55 60
 Gly Gly Asp Ser Leu Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp
 65 70 75 80
 Phe Glu Asn Gln Val Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala
 85 90 95
 Pro Cys Arg Ser Glu Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu
 100 105 110
 Gln Ala Ala Gly Asn Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile
 115 120 125
 Asn Val Arg Asp Tyr Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp
 130 135 140
 Asn Gly Leu Asp Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala
 145 150 155 160
 Ala Ser Leu Gly Gly Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val
 165 170 175
 Leu Asp Lys Gln His Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr
 180 185 190
 Ser Lys Asp Val Leu Asp Val Ala Leu Pro Leu Val Asp Glu Ala
 195 200 205

<210> 69
 <211> 495

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(472)

<223> RXN00937

<400> 69

```

agctgccggt caatgaagaa aatccttggc cggaataaac tacagtcgcg tgaaagttgg 60

tctatatata gaccttacaa atcttgaacg gagattctta atg gca acc atc gat 115
                                         Met Ala Thr Ile Asp
                                         1 5

gta acc gaa gaa aca ttt gag agc aca gtt acc ggc gac gga att gtc 163
Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr Gly Asp Gly Ile Val
                        10 15 20

ctc gta gac gca tgg gca tcc tgg tgc gga cct tgc cgc cag ttc gcc 211
Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro Cys Arg Gln Phe Ala
                        25 30 35

cca acc tac gag aag gtt tcc gaa acc cac acc gac gca acc ttc gcc 259
Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr Asp Ala Thr Phe Ala
                        40 45 50

aag ctt gat acc gaa gca aac cag ggc ctg gct gca gca ctg cag atc 307
Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala Ala Ala Leu Gln Ile
                        55 60 65

cag tcc atc cca act ctg atg gtt ttc cgc gac ggc atc atg gtc tac 355
Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp Gly Ile Met Val Tyr
                        70 75 80 85

cgc gaa gcc ggc acc atg cca gct cct gca ctg gat gat ctg gtc aac 403
Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu Asp Asp Leu Val Asn
                        90 95 100

cag gtt aag gca ctc gac atg gat gac gtt cgt cgc cag gtc gca gag 451
Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg Arg Gln Val Ala Glu
                        105 110 115

cag cag ggt tct gca gag gca taagcttcca attgtgtttt ggt 495
Gln Gln Gly Ser Ala Glu Ala
                        120

```

<210> 70

<211> 124

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 70

```

Met Ala Thr Ile Asp Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr
  1 5 10 15

Gly Asp Gly Ile Val Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro
  20 25 30

Cys Arg Gln Phe Ala Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr

```

35	40	45
Asp Ala Thr Phe Ala Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala		
50	55	60
Ala Ala Leu Gln Ile Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp		
65	70	75
Gly Ile Met Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu		
	85	90
Asp Asp Leu Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg		
	100	105
		110
Arg Gln Val Ala Glu Gln Gln Gly Ser Ala Glu Ala		
115	120	

<210> 71
 <211> 990
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(967)
 <223> RXN02325

<400> 71
 cagagatttg aagatggaga ccaaggctca aagggaatcc atgccgtctt ggtttaatac 60
 tgcacccgtc taatgaaaat cattactatt aggtgtcatg atg gac cat gca cac 115
 Met Asp His Ala His
 1 5
 gat tcc tgc tca cca act ctg cgc cgt gat ttg gag gtc act ggc cag 163
 Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp Leu Glu Val Thr Gly Gln
 10 15 20
 ctc caa cct gag aaa gct gtc gat tta gca gcg ccg cac gaa ggg aag 211
 Leu Gln Pro Glu Lys Ala Val Asp Leu Ala Ala Pro His Glu Gly Lys
 25 30 35
 gtt gcc aat ata acg aag gtg acc tcc tca aat atg gag cac acc atc 259
 Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn Met Glu His Thr Ile
 40 45 50
 acg cag gcc tca aaa gct aag gag gtg gtg gtg ctc att ggt cac tcc 307
 Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val Leu Ile Gly His Ser
 55 60 65
 ctg ctg ccc aca ttt cag gat ttg gaa aaa gac att ctg cac ttt cag 355
 Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp Ile Leu His Phe Gln
 70 75 80 85
 gca ggt aat aaa ggg cga ttt tct gta gcg att gtt gat cct gat cgc 403
 Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile Val Asp Pro Asp Arg
 90 95 100
 agt gca gat gtg gtt gcc aga ttt agg cca aaa cag att ccg gtg gca 451
 Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys Gln Ile Pro Val Ala

105	110	115	
tac gtg gtg aaa gat ggc gcc agc att gcg gag ttc aac tcg ctc aac			499
Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu Phe Asn Ser Leu Asn			
120	125	130	
aag gag ccg gtt gca caa tgg ctt gat cat ttt gtg tcg cgg gaa acg			547
Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe Val Ser Arg Glu Thr			
135	140	145	
atc ccc aat gaa aaa gag ggg gac gtc gat aag caa ata gac ccg cgc			595
Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys Gln Ile Asp Pro Arg			
150	155	160	165
ctg tgg ccg gca gcg gaa ttg gtg aac gcc ggt gat ttt cgc gcg gcg			643
Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly Asp Phe Arg Ala Ala			
170	175	180	
ttg gcg ttg tat gag cag ttg ccg cag gat gcg acg gtg aag cgg gcg			691
Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala Thr Val Lys Arg Ala			
185	190	195	
cac gcg gcg gtg tcg gta ttg gcg ccg atg tct gtg gcg gat ccg gga			739
His Ala Ala Val Ser Val Leu Ala Arg Met Ser Val Ala Asp Arg Gly			
200	205	210	
gag gat ccg atc gag aag tcg cgc ccg gat cca gac gat gtg aac aag			787
Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro Asp Asp Val Asn Lys			
215	220	225	
gcg ctg gcg gcg gcg gat atg tat gtg ttg atg aat cag ccg gac aca			835
Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met Asn Gln Pro Asp Thr			
230	235	240	245
gcg ctc gcg cac ctt gca gca cta ttg cca aaa ccg gag gct gcc ccg			883
Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys Pro Glu Ala Ala Arg			
250	255	260	
ccg atc gtg gag ttg ctg aac ttg ttt gat ccg ctg gac ctg gtc gca			931
Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro Leu Asp Leu Val Ala			
265	270	275	
ttg gaa atc agg gcg cag gtg ggg aat gca atg agc taagaaaaca			977
Leu Glu Ile Arg Ala Gln Val Gly Asn Ala Met Ser			
280	285		
ctttaaatat tct			990
<210> 72			
<211> 289			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 72			
Met Asp His Ala His Asp Ser Cys Ser Pro Thr Leu Arg Arg Asp Leu			
1	5	10	15
Glu Val Thr Gly Gln Leu Gln Pro Glu Lys Ala Val Asp Leu Ala Ala			
20	25	30	

Pro His Glu Gly Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn
 35 40 45
 Met Glu His Thr Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val
 50 55 60
 Leu Ile Gly His Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp
 65 70 75 80
 Ile Leu His Phe Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile
 85 90 95
 Val Asp Pro Asp Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys
 100 105 110
 Gln Ile Pro Val Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu
 115 120 125
 Phe Asn Ser Leu Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe
 130 135 140
 Val Ser Arg Glu Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys
 145 150 155 160
 Gln Ile Asp Pro Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly
 165 170 175
 Asp Phe Arg Ala Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala
 180 185 190
 Thr Val Lys Arg Ala His Ala Ala Val Ser Val Leu Ala Arg Met Ser
 195 200 205
 Val Ala Asp Arg Gly Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro
 210 215 220
 Asp Asp Val Asn Lys Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met
 225 230 235 240
 Asn Gln Pro Asp Thr Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys
 245 250 255
 Pro Glu Ala Ala Arg Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro
 260 265 270
 Leu Asp Leu Val Ala Leu Glu Ile Arg Ala Gln Val Gly Asn Ala Met
 275 280 285

Ser

<210> 73
 <211> 900
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(877)
 <223> RXN01837

<400> 73

```

cccccatcat tccctcaagg tgtgaagata cggtaggat agaaaagaat ttttttgacg 60

ttggacattc tcaaaatcaa gtagcaaggg atcaaactct gtg agt act aat aag 115
                               Val Ser Thr Asn Lys
                               1                               5

gaa cga cgc caa cag gcg ctt tcc cag ctg gag aaa gaa atc aaa agc 163
Glu Arg Arg Gln Gln Ala Leu Ser Gln Leu Glu Lys Glu Ile Lys Ser
                               10                               15                               20

cgg gac cgc aaa gaa aag acc aag cca cta acc gtg gtc ttt gct tcc 211
Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr Val Val Phe Ala Ser
                               25                               30                               35

ctg gct gtc atc ctg gtt gtc gtt ggc ggt atc tgg tac gca gct acc 259
Leu Ala Val Ile Leu Val Val Val Gly Gly Ile Trp Tyr Ala Ala Thr
                               40                               45                               50

cgc agc acc gaa gac gaa gtc atc acc gct gat gaa aca tcc acc acc 307
Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp Glu Thr Ser Thr Thr
                               55                               60                               65

gca gag acc cct gac tac cag cca ctg gcg ctg acc cgc acc acc gcg 355
Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu Thr Arg Thr Thr Ala
                               70                               75                               80                               85

ctc ggc gac tcc gtg acc tgt gag tac cca gat gct ggc gag gct tcc 403
Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp Ala Gly Glu Ala Ser
                               90                               95                               100

aag gat gtc tcc aag cct gct act gaa aac gtg cca gca acc ggc acc 451
Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val Pro Ala Thr Gly Thr
                               105                               110                               115

gtg acc gtc aac ctg acc acc gcc cag ggc aac atc ggc atg gaa ctt 499
Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn Ile Gly Met Glu Leu
                               120                               125                               130

gat cgc tcc gta tcc cct tgt acc gtc aac gct gtt gag cac atg gct 547
Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala Val Glu His Met Ala
                               135                               140                               145

tcc gag ggc tac tac aac gat act gtc tgc cac cgc atc acc acc tct 595
Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His Arg Ile Thr Thr Ser
                               150                               155                               160                               165

ggc att tac gtt ctc cag tgc ggc gat cca agc agc acc ggc gca ggc 643
Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser Ser Thr Gly Ala Gly
                               170                               175                               180

ggc cca ggg ttc agc ttc gcc aac gaa tac cca acc gac gaa gca act 691
Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro Thr Asp Glu Ala Thr
                               185                               190                               195

gac cta acc acc cca gtc atc tac gag cgc ggc acc atc gcc atg gcc 739
Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly Thr Ile Ala Met Ala
                               200                               205                               210

aac gct ggc gct gac acc aac ggg ctc cca gtt ctt cct caa cta cga 787

```

Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val Leu Pro Gln Leu Arg
 215 220 225
 gga ttc ccc act ggc acc gaa cta cac cta ctt cgg cca gat cac cga 835
 Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu Arg Pro Asp His Arg
 230 235 240 245
 aga agg cct tgc aac cct cga cgc cat cgc aga agt tgg cac 877
 Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg Ser Trp His
 250 255
 tgaaggtgga accggcgacg gag 900

<210> 74
 <211> 259
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 74
 Val Ser Thr Asn Lys Glu Arg Arg Gln Gln Ala Leu Ser Gln Leu Glu
 1 5 10 15
 Lys Glu Ile Lys Ser Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr
 20 25 30
 Val Val Phe Ala Ser Leu Ala Val Ile Leu Val Val Val Gly Gly Ile
 35 40 45
 Trp Tyr Ala Ala Thr Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp
 50 55 60
 Glu Thr Ser Thr Thr Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu
 65 70 75 80
 Thr Arg Thr Thr Ala Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp
 85 90 95
 Ala Gly Glu Ala Ser Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val
 100 105 110
 Pro Ala Thr Gly Thr Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn
 115 120 125
 Ile Gly Met Glu Leu Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala
 130 135 140
 Val Glu His Met Ala Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His
 145 150 155 160
 Arg Ile Thr Thr Ser Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser
 165 170 175
 Ser Thr Gly Ala Gly Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro
 180 185 190
 Thr Asp Glu Ala Thr Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly
 195 200 205
 Thr Ile Ala Met Ala Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val
 210 215 220

Leu Pro Gln Leu Arg Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu
 225 230 235 240

Arg Pro Asp His Arg Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg
 245 250 255

Ser Trp His

<210> 75
 <211> 741
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(741)
 <223> RXN01926

<400> 75
 ctg cga agc ttc tac acc cca gaa caa gcc atc gaa cgc gaa ggc gac 48
 Leu Arg Ser Phe Tyr Thr Pro Glu Gln Ala Ile Glu Arg Glu Gly Asp
 1 5 10 15

gtc tgg aaa gcc gcc acc gaa gaa gca gaa ctc ctc gca gct gac ggc 96
 Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
 20 25 30

gcc gtc cac gac cag gaa ctc ttc ctc aac tgc acc acc tcc cca ctg 144
 Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
 35 40 45

atc ttc gcc tcc gcg atg ctc aac ttc ggc gtc cac caa atc ctg gac 192
 Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
 50 55 60

acc ctc tgc caa ctc gca cca tcc ccc gcc ggc cgc gac gca gac ccc 240
 Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro
 65 70 75 80

aaa gcc ctc gaa gcc gcc acc tcc gca atg gac gac cac cgc gac acc 288
 Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr
 85 90 95

acc gac gac ttc tcc ggc gtc gtc ttc aaa gtc caa gcc ggc atg gac 336
 Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp
 100 105 110

aaa aac cac cgc gat acc ctc gcc ttc atg cgc gtc gtc tcc ggc gaa 384
 Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu
 115 120 125

ttc gac cgc ggc atg caa gtc acc cac tcc caa tcc ggc cgc agc ttc 432
 Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe
 130 135 140

tcc acc aaa tac gcc ctc acc gtc ttc ggc cgc acc cgc tct acc gtc 480
 Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val
 145 150 155 160

gaa acc gcc ttc ccc ggc gac atc gtc ggc ctc gtc aac gcc ggc gcc 528
 Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala
 165 170 175
 ctc gca cca ggc gac acc atc ttc gaa ggc cga aaa atc caa tac cca 576
 Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro
 180 185 190
 cca atg cca aaa ttc gcg cca gaa cac ttc cgc atc ctg cgc gcc aaa 624
 Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys
 195 200 205
 tca ctc ggc aaa tac aaa cag ttc cgc aaa gcc ctc gag cag ctg gac 672
 Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
 210 215 220
 tcc gaa ggt gtc gtc cag atc ctc aag aac gac ctg cgt ggc gac gcc 720
 Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala
 225 230 235 240
 aac cca ggt cat ggc cgg tgt 741
 Asn Pro Gly His Gly Arg Cys
 245

<210> 76
 <211> 247
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 76
 Leu Arg Ser Phe Tyr Thr Pro Glu Gln Ala Ile Glu Arg Glu Gly Asp
 1 5 10 15
 Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
 20 25 30
 Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
 35 40 45
 Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
 50 55 60
 Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro
 65 70 75 80
 Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr
 85 90 95
 Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp
 100 105 110
 Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu
 115 120 125
 Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe
 130 135 140
 Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val
 145 150 155 160

Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala
 165 170 175
 Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro
 180 185 190
 Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys
 195 200 205
 Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
 210 215 220
 Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala
 225 230 235 240
 Asn Pro Gly His Gly Arg Cys
 245

<210> 77
 <211> 478
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(478)
 <223> RXN02002

<400> 77
 aagtggcaaa aaacgtttca agcaggcaac gccggcgctac aacttcgctg agctggggcg 60
 attatggccc agcgcccaca acccgctatt cttaataccc atg agc aac gcc aat 115
 Met Ser Asn Ala Asn
 1 5
 tcc gac acc acc gcc gcc gag gca cat cgc cgc aga aca ttc gcc gta 163
 Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg Thr Phe Ala Val
 10 15 20
 atc gca cac ccc gac gcc ggt aaa tcc acc ctc acc gag gca ttg gcg 211
 Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu Thr Glu Ala Leu Ala
 25 30 35
 ctg cat gca cac atc atc tcc gaa gcc ggc gcc acc cac ggc aaa gca 259
 Leu His Ala His Ile Ile Ser Glu Ala Gly Ala Thr His Gly Lys Ala
 40 45 50
 ggc cgc aaa gcc acc gtt tcc gac tgg atg gaa atg gaa aaa gac cgc 307
 Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu Met Glu Lys Asp Arg
 55 60 65
 ggc atc tcc atc gcc tcc tcc gca ctc caa ttc gag tac gca cca gaa 355
 Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe Glu Tyr Ala Pro Glu
 70 75 80 85
 ggc cac gca ggc gag ccc ttc atg atc aac ctc gtg gac acc cca ggc 403
 Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu Val Asp Thr Pro Gly
 90 95 100

cac gcc gac ttc tcc gaa gac acc tac cgc gtc ctc atg gcc gtc gac 451
 His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val Leu Met Ala Val Asp
 105 110 115

gca gca gtc atg ctt atg cac tcc gtc 478
 Ala Ala Val Met Leu Met His Ser Val
 120 125

<210> 78

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 78

Met Ser Asn Ala Asn Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg
 1 5 10 15

Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu
 20 25 30

Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser Glu Ala Gly Ala
 35 40 45

Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu
 50 55 60

Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe
 65 70 75 80

Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu
 85 90 95

Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val
 100 105 110

Leu Met Ala Val Asp Ala Ala Val Met Leu Met His Ser Val
 115 120 125

<210> 79

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1057)

<223> RXN02736

<400> 79

cagaggatta cccagcgggt acgtgggggtc caaagagcgc tgatgaaatg ctttcccgca 60

acggtcacac ctggcgcagg ccataattta ggggcaaaaa atg atc ttt gaa ctt 115
 Met Ile Phe Glu Leu
 1 5

ccg gat acc acc acc cag caa att tcc aag acc cta act cga ctg cgt 163
 Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr Leu Thr Arg Leu Arg
 10 15 20

gaa tgc ggc acc cag gtc acc acc ggc cga gtg ctc acc ctc atc gtg	211
Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val Leu Thr Leu Ile Val	
25 30 35	
gtc act gac tcc gaa agc gat gtc gct gca gtt acc gag tcc acc aat	259
Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val Thr Glu Ser Thr Asn	
40 45 50	
gaa gcc tcg cgc gag cac cca tct cgc gtg atc att ttg gtg gtt ggc	307
Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile Ile Leu Val Val Gly	
55 60 65	
gat aaa act gca gaa aac aaa gtt gac gca gaa gtc cgt atc ggt ggc	355
Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu Val Arg Ile Gly Gly	
70 75 80 85	
gac gct ggt gct tcc gag atg atc atc atg cat ctc aac gga cct gtc	403
Asp Ala Gly Ala Ser Glu Met Ile Ile Met His Leu Asn Gly Pro Val	
90 95 100	
gct gac aag ctc cag tat gtc gtc aca cca ctg ttg ctt cct gac acc	451
Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu Leu Leu Pro Asp Thr	
105 110 115	
ccc atc gtt gct tgg tgg cca ggt gaa tca cca aag aat cct tcc cag	499
Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro Lys Asn Pro Ser Gln	
120 125 130	
gac cca att gga cgc atc gca caa cga cgc atc act gat gct ttg tac	547
Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile Thr Asp Ala Leu Tyr	
135 140 145	
gac cgt gat gac gca cta gaa gat cgt gtt gag aac tat cac cca ggt	595
Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu Asn Tyr His Pro Gly	
150 155 160 165	
gat acc gac atg acg tgg gcg cgc ctt acc cag tgg cgg gga ctt gtt	643
Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln Trp Arg Gly Leu Val	
170 175 180	
gcc tcc tca ttg gat cac cca cca cac agc gaa atc act tcc gtg agg	691
Ala Ser Ser Leu Asp His Pro Pro His Ser Glu Ile Thr Ser Val Arg	
185 190 195	
ctg acc ggt gca agc ggc agt acc tcg gtg gat ttg gct gca ggc tgg	739
Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp Leu Ala Ala Gly Trp	
200 205 210	
ttg gcg cgg agg ctg aaa gtg cct gtg atc cgc gag gtg aca gat gct	787
Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg Glu Val Thr Asp Ala	
215 220 225	
ccc acc gtg cca acc gat gag ttt ggt act cca ctg ctg gct atc cag	835
Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro Leu Leu Ala Ile Gln	
230 235 240 245	
cgc ctg gag atc gtt cgc acc acc ggc tcg atc atc atc acc atc tat	883
Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile Ile Ile Thr Ile Tyr	
250 255 260	
gac gct cat acc ctt cag gta gag atg ccg gaa tcc ggc aat gcc cca	931

Asp Ala His Thr Leu Gln Val Glu Met Pro Glu Ser Gly Asn Ala Pro
 265 270 275
 tcg ctg gtg gct att ggt cgt cga agt gag tcc gac tgc ttg tct gag 979
 Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser Asp Cys Leu Ser Glu
 280 285 290
 gag ctt cgc cac atg gat cca gat ttg ggc tac cag cac gca cta tcc 1027
 Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr Gln His Ala Leu Ser
 295 300 305
 ggc ttg tcc agc gtc aag ctg gaa acc gtc taaggagaaa tacaacacta 1077
 Gly Leu Ser Ser Val Lys Leu Glu Thr Val
 310 315
 tgg 1080

 <210> 80
 <211> 319
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 80
 Met Ile Phe Glu Leu Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr
 1 5 10 15
 Leu Thr Arg Leu Arg Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val
 20 25 30
 Leu Thr Leu Ile Val Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val
 35 40 45
 Thr Glu Ser Thr Asn Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile
 50 55 60
 Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu
 65 70 75 80
 Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His
 85 90 95
 Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu
 100 105 110
 Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro
 115 120 125
 Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile
 130 135 140
 Thr Asp Ala Leu Tyr Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu
 145 150 155 160
 Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln
 165 170 175
 Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu
 180 185 190
 Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp

195					200					205					
Leu	Ala	Ala	Gly	Trp	Leu	Ala	Arg	Arg	Leu	Lys	Val	Pro	Val	Ile	Arg
210					215					220					
Glu	Val	Thr	Asp	Ala	Pro	Thr	Val	Pro	Thr	Asp	Glu	Phe	Gly	Thr	Pro
225					230					235					240
Leu	Leu	Ala	Ile	Gln	Arg	Leu	Glu	Ile	Val	Arg	Thr	Thr	Gly	Ser	Ile
				245					250					255	
Ile	Ile	Thr	Ile	Tyr	Asp	Ala	His	Thr	Leu	Gln	Val	Glu	Met	Pro	Glu
			260					265					270		
Ser	Gly	Asn	Ala	Pro	Ser	Leu	Val	Ala	Ile	Gly	Arg	Arg	Ser	Glu	Ser
		275					280					285			
Asp	Cys	Leu	Ser	Glu	Glu	Leu	Arg	His	Met	Asp	Pro	Asp	Leu	Gly	Tyr
	290					295					300				
Gln	His	Ala	Leu	Ser	Gly	Leu	Ser	Ser	Val	Lys	Leu	Glu	Thr	Val	
305					310					315					
<210> 81															
<211> 331															
<212> DNA															
<213> Corynebacterium glutamicum															
<220>															
<221> CDS															
<222> (101)..(301)															
<223> RXS03217															
<400> 81															
tctgtgaagg tagatgggtt gacgaggagt tccaacgact cggacgctgg tgaatcatgc 60															
tggcgaacgt agcatcacct gattaggaaa aggtacaaat atg gca cag ggt act 115															
Met Ala Gln Gly Thr 5															
1															
gtg aaa tgg ttc aac ggc gaa aag gga ttt ggt ttc atc gct ccc aac 163															
Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly Phe Ile Ala Pro Asn 20															
10															
15															
gat ggc tcc gca gat ctc ttc gtc cac tac tct gag att cag ggc tcc 211															
Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser Glu Ile Gln Gly Ser 35															
25															
30															
ggt ttc cgt aat ctt gag gaa aac cag cca gtt gaa ttt gag gtc ggc 259															
Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val Glu Phe Glu Val Gly 50															
40															
45															
gag ggc gcc aag ggc cca cag gct cag cag gtt cgt gct ctc 301															
Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val Arg Ala Leu 65															
55															
60															
taagctctaa ctgctagcta aaaattccgc 331															
<210> 82															

<211> 67

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 82

Met Ala Gln Gly Thr Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly
 1 5 10 15

Phe Ile Ala Pro Asn Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser
 20 25 30

Glu Ile Gln Gly Ser Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val
 35 40 45

Glu Phe Glu Val Gly Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val
 50 55 60

Arg Ala Leu
 65

<210> 83

<211> 324

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(301)

<223> FRXA01917

<400> 83

tctgtgaagg tagatgggtt gacgaggagt tccaacgact cggacgctgg tgaatcatgc 60

tggcgaacgt agcatcacct gattaggaaa aggtacaaat atg gca cag ggt act 115
 Met Ala Gln Gly Thr
 1 5

gtg aaa tgg ttc aac ggc gaa aag gga ttt ggt ttc atc gct ccc aac 163
 Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly Phe Ile Ala Pro Asn
 10 15 20

gat ggc tcc gca gat ctc ttc gtc cac tac tct gag att cag ggc tcc 211
 Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser Glu Ile Gln Gly Ser
 25 30 35

ggt ttc cgt aat ctt gag gaa aac cag cca gtt gaa ttt gag gtc ggc 259
 Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val Glu Phe Glu Val Gly
 40 45 50

gag ggc gcc aag ggc cca cag gct cag cag gtt cgt gct ctc 301
 Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val Arg Ala Leu
 55 60 65

taagctctaa ctgctagcta aaa 324

<210> 84

<211> 67

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 84

Met Ala Gln Gly Thr Val Lys Trp Phe Asn Gly Glu Lys Gly Phe Gly
 1 5 10 15
 Phe Ile Ala Pro Asn Asp Gly Ser Ala Asp Leu Phe Val His Tyr Ser
 20 25 30
 Glu Ile Gln Gly Ser Gly Phe Arg Asn Leu Glu Glu Asn Gln Pro Val
 35 40 45
 Glu Phe Glu Val Gly Glu Gly Ala Lys Gly Pro Gln Ala Gln Gln Val
 50 55 60
 Arg Ala Leu
 65

<210> 85

<211> 504

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(481)

<223> RXA02184

<400> 85

tttaccgcga tgcttgccggt gtataataat ttcttctggt caaaaatagt tgatcaattt 60
 gaatcagcat atgaattagg aatgaaagtg gtgaggacaa gtg cct gtc gga aca 115
 Val Pro Val Gly Thr
 1 5
 gtg aag tgg tac gac gcg gag cgt ggt ttc ggc ttt gtc tcc aat cca 163
 Val Lys Trp Tyr Asp Ala Glu Arg Gly Phe Gly Phe Val Ser Asn Pro
 10 15 20
 ggt ggt gaa gat tgc ttc gta ggt aag caa gta ctt ccc aag gga gtc 211
 Gly Gly Glu Asp Cys Phe Val Gly Lys Gln Val Leu Pro Lys Gly Val
 25 30 35
 acc gaa ttg cac aag gga cag cga atc gat ttt gac ttc gcc gca ggc 259
 Thr Glu Leu His Lys Gly Gln Arg Ile Asp Phe Asp Phe Ala Ala Gly
 40 45 50
 cgt aag ggc cct caa gca ctt cga ata aag att ctt gaa act cca cgc 307
 Arg Lys Gly Pro Gln Ala Leu Arg Ile Lys Ile Leu Glu Thr Pro Arg
 55 60 65
 agg cgt cca cag cac aaa tac aag cca gaa gag ctc aac gga atg atc 355
 Arg Arg Pro Gln His Lys Tyr Lys Pro Glu Glu Leu Asn Gly Met Ile
 70 75 80 85
 tct gac ctc atc acg ctt cta gaa agt gga gtg caa cca ggc ctt gcc 403
 Ser Asp Leu Ile Thr Leu Leu Glu Ser Gly Val Gln Pro Gly Leu Ala
 90 95 100
 aaa ggg caa tac ccg gag cac aaa gct gga gcg cag gta gca gaa att 451
 Lys Gly Gln Tyr Pro Glu His Lys Ala Gly Ala Gln Val Ala Glu Ile

105	110	115	
ctt cgc gtt gtt gcg aag gag ctt gag tct taaaacaata aggagaggat			501
Leu Arg Val Val Ala Lys Glu Leu Glu Ser			
120	125		

ccg	504
-----	-----

<210> 86
 <211> 127
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 86	
Val Pro Val Gly Thr Val Lys Trp Tyr Asp Ala Glu Arg Gly Phe Gly	
1 5 10 15	
Phe Val Ser Asn Pro Gly Gly Glu Asp Cys Phe Val Gly Lys Gln Val	
20 25 30	
Leu Pro Lys Gly Val Thr Glu Leu His Lys Gly Gln Arg Ile Asp Phe	
35 40 45	
Asp Phe Ala Ala Gly Arg Lys Gly Pro Gln Ala Leu Arg Ile Lys Ile	
50 55 60	
Leu Glu Thr Pro Arg Arg Arg Pro Gln His Lys Tyr Lys Pro Glu Glu	
65 70 75 80	
Leu Asn Gly Met Ile Ser Asp Leu Ile Thr Leu Leu Glu Ser Gly Val	
85 90 95	
Gln Pro Gly Leu Ala Lys Gly Gln Tyr Pro Glu His Lys Ala Gly Ala	
100 105 110	
Gln Val Ala Glu Ile Leu Arg Val Val Ala Lys Glu Leu Glu Ser	
115 120 125	

<210> 87
 <211> 324
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(301)
 <223> RXA00810

<400> 87	
tcggcggttcg ttcaagaaac ggccagatgt tgctgttcga gctcatgcaa gagtgggaaca	60
tcgaaccggt tagtaattcc aatcagtaaa ggtaagacaa atg gca cag ggc act	115
Met Ala Gln Gly Thr	
1 5	
gtt aag tgg ttc aac cca gag aag ggc ttc ggc ttc atc gct cct tcc	163
Val Lys Trp Phe Asn Pro Glu Lys Gly Phe Gly Phe Ile Ala Pro Ser	
10 15 20	

<400> 89																
cggcgctcgat	tccagaaggt	ttgtagacat	gcttcaaggt	tgcgctaatt	gaaaagaacg											60
cggtagacgg	tactttcata	tccacccata	taatgttgat	atg	gat	aat	ggg	tgg								115
				Met	Asp	Asn	Gly	Trp								
				1				5								
ccg	aac	ctg	caa	act	ctc	gca	ctc	ttt	gtg	gcg	att	gtg	gaa	gag	ggg	163
Pro	Asn	Leu	Gln	Thr	Leu	Ala	Leu	Phe	Val	Ala	Ile	Val	Glu	Glu	Gly	
				10					15					20		
agc	ctc	ggg	gcc	ggg	gct	cga	aaa	gtc	gga	atg	gcc	caa	cct	aat	gcc	211
Ser	Leu	Gly	Ala	Gly	Ala	Arg	Lys	Val	Gly	Met	Ala	Gln	Pro	Asn	Ala	
			25					30					35			

agt cgg gct atc gca gag ctt gag gca gac atg aaa gcc gaa ttg ttg	259
Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met Lys Ala Glu Leu Leu	
40 45 50	
gta cgt cat cct cga gga tca cat cca aca gct gct gga ctt gcg ctt	307
Val Arg His Pro Arg Gly Ser His Pro Thr Ala Ala Gly Leu Ala Leu	
55 60 65	
gtt gag cat tcg cgc gat ctg ctt caa tct gta caa gaa ttt act gaa	355
Val Glu His Ser Arg Asp Leu Leu Gln Ser Val Gln Glu Phe Thr Glu	
70 75 80 85	
tgg gtg aca gag gga cga act gag cag ccg ctg aaa ttg cat gtt ggg	403
Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu Lys Leu His Val Gly	
90 95 100	
gcc agt atg acc att gcc gag gct cta ctt cca gct tgg gtt gcg gac	451
Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro Ala Trp Val Ala Asp	
105 110 115	
atg cgc acg cgt ttt cct gcc tgc cgt gtc gac gtc tct gtg atg aat	499
Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp Val Ser Val Met Asn	
120 125 130	
tct tct caa gta att gaa gcc gtc cag aaa ggg cac ttg caa cta ggt	547
Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly His Leu Gln Leu Gly	
135 140 145	
ttt att gaa aca ccg cat gtt ccc gta cgg ctt cat gct cgt gtg gtg	595
Phe Ile Glu Thr Pro His Val Pro Val Arg Leu His Ala Arg Val Val	
150 155 160 165	
caa gag gac aag ctg att gtg gtg att tct cct aat cat gag tgg gct	643
Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro Asn His Glu Trp Ala	
170 175 180	
aat cgc acg ggt agg atc agt ctt cgg gag ttg tcg gaa act ccg ctg	691
Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu Ser Glu Thr Pro Leu	
185 190 195	
ata gtg agg gaa gtc ggc tca ggt acc cga gaa gca tta caa gaa tta	739
Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu Ala Leu Gln Glu Leu	
200 205 210	
ctt gcg gat tat gac atg gct gag ccg att caa gtg tta aac agc aat	787
Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln Val Leu Asn Ser Asn	
215 220 225	
gct gcg gta cgt gtt gtt gtt gaa gca ggg gca ggt cct gca gta ctt	835
Ala Ala Val Arg Val Val Val Glu Ala Gly Ala Gly Pro Ala Val Leu	
230 235 240 245	
ggt gaa tta gcc ttg cgt gat cat ctt gcg ctc ggc agg ctg ttg agt	883
Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu Gly Arg Leu Leu Ser	
250 255 260	
gtg cca ttt gaa ggc agt gga gtt act cgt cct ctt aca gct gtg tgg	931
Val Pro Phe Glu Gly Ser Gly Val Thr Arg Pro Leu Thr Ala Val Trp	
265 270 275	

agt gga ccc cgc aga ttg ccg att cta gcg gga gaa tta gtg tcc atc 979
 Ser Gly Pro Arg Arg Leu Pro Ile Leu Ala Gly Glu Leu Val Ser Ile
 280 285 290

gca tcg aac cac atc tgattttgag ccctggctaa cgg 1017
 Ala Ser Asn His Ile
 295

<210> 90

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

Met Asp Asn Gly Trp Pro Asn Leu Gln Thr Leu Ala Leu Phe Val Ala
 1 5 10 15

Ile Val Glu Glu Gly Ser Leu Gly Ala Gly Ala Arg Lys Val Gly Met
 20 25 30

Ala Gln Pro Asn Ala Ser Arg Ala Ile Ala Glu Leu Glu Ala Asp Met
 35 40 45

Lys Ala Glu Leu Leu Val Arg His Pro Arg Gly Ser His Pro Thr Ala
 50 55 60

Ala Gly Leu Ala Leu Val Glu His Ser Arg Asp Leu Leu Gln Ser Val
 65 70 75 80

Gln Glu Phe Thr Glu Trp Val Thr Glu Gly Arg Thr Glu Gln Pro Leu
 85 90 95

Lys Leu His Val Gly Ala Ser Met Thr Ile Ala Glu Ala Leu Leu Pro
 100 105 110

Ala Trp Val Ala Asp Met Arg Thr Arg Phe Pro Ala Cys Arg Val Asp
 115 120 125

Val Ser Val Met Asn Ser Ser Gln Val Ile Glu Ala Val Gln Lys Gly
 130 135 140

His Leu Gln Leu Gly Phe Ile Glu Thr Pro His Val Pro Val Arg Leu
 145 150 155 160

His Ala Arg Val Val Gln Glu Asp Lys Leu Ile Val Val Ile Ser Pro
 165 170 175

Asn His Glu Trp Ala Asn Arg Thr Gly Arg Ile Ser Leu Arg Glu Leu
 180 185 190

Ser Glu Thr Pro Leu Ile Val Arg Glu Val Gly Ser Gly Thr Arg Glu
 195 200 205

Ala Leu Gln Glu Leu Leu Ala Asp Tyr Asp Met Ala Glu Pro Ile Gln
 210 215 220

Val Leu Asn Ser Asn Ala Ala Val Arg Val Val Val Glu Ala Gly Ala
 225 230 235 240

Gly Pro Ala Val Leu Gly Glu Leu Ala Leu Arg Asp His Leu Ala Leu

245										250					255				
Gly	Arg	Leu	Leu	Ser	Val	Pro	Phe	Glu	Gly	Ser	Gly	Val	Thr	Arg	Pro				
		260						265					270						
Leu	Thr	Ala	Val	Trp	Ser	Gly	Pro	Arg	Arg	Leu	Pro	Ile	Leu	Ala	Gly				
		275					280					285							
Glu	Leu	Val	Ser	Ile	Ala	Ser	Asn	His	Ile										
	290					295													
<210> 91																			
<211> 1214																			
<212> DNA																			
<213> Corynebacterium glutamicum																			
<220>																			
<221> CDS																			
<222> (1)..(1191)																			
<223> RXA02431																			
<400> 91																			
gtg	gtg	gtg	aca	ccc	cgt	cat	atc	gtt	tac	tcc	gca	gcc	tcg	cgc	cgg		48		
Val	Val	Val	Thr	Pro	Arg	His	Ile	Val	Tyr	Ser	Ala	Ala	Ser	Arg	Arg				
1				5				10					15						
gtg	ttc	caa	atc	gtg	gaa	aaa	cgc	gcc	gga	att	gtc	gaa	cgc	ctc	agc		96		
Val	Phe	Gln	Ile	Val	Glu	Lys	Arg	Ala	Gly	Ile	Val	Glu	Arg	Leu	Ser				
		20						25					30						
atc	gat	gaa	ggc	ttc	atg	gaa	cca	gag	gct	ctc	gtt	gga	gcc	acc	cca		144		
Ile	Asp	Glu	Gly	Phe	Met	Glu	Pro	Glu	Ala	Leu	Val	Gly	Ala	Thr	Pro				
		35					40					45							
gaa	gag	gtg	aaa	cag	tgg	gcg	gaa	gaa	tta	cgc	gcg	gaa	att	aaa	gaa		192		
Glu	Glu	Val	Lys	Gln	Trp	Ala	Glu	Glu	Leu	Arg	Ala	Glu	Ile	Lys	Glu				
		50				55					60								
gtt	act	ggc	tta	ccc	tcc	tcg	gtt	ggg	gct	ggc	tcc	ggg	aag	cag	atc		240		
Val	Thr	Gly	Leu	Pro	Ser	Ser	Val	Gly	Ala	Gly	Ser	Gly	Lys	Gln	Ile				
65					70			75						80					
gcc	aaa	att	ggg	tca	ggc	gaa	gca	aag	cca	gat	ggg	gtg	ttt	gtc	gtg		288		
Ala	Lys	Ile	Gly	Ser	Gly	Glu	Ala	Lys	Pro	Asp	Gly	Val	Phe	Val	Val				
				85				90						95					
cca	gta	gac	aag	caa	cat	gac	ttg	ctt	gat	cca	ctt	cct	gtg	ggc	gca		336		
Pro	Val	Asp	Lys	Gln	His	Asp	Leu	Leu	Asp	Pro	Leu	Pro	Val	Gly	Ala				
			100				105						110						
ctt	tgg	gga	gtg	ggg	cct	gtg	aca	ggc	tcc	aag	ctt	gcc	tca	atg	ggg		384		
Leu	Trp	Gly	Val	Gly	Pro	Val	Thr	Gly	Ser	Lys	Leu	Ala	Ser	Met	Gly				
		115					120					125							
gtg	gaa	aca	att	ggg	gat	cta	gca	gcg	cta	acc	caa	aaa	gaa	gta	gaa		432		
Val	Glu	Thr	Ile	Gly	Asp	Leu	Ala	Ala	Leu	Thr	Gln	Lys	Glu	Val	Glu				
		130				135					140								
atc	agc	ctc	ggg	gca	acc	atc	gga	ata	tca	ctg	tgg	aac	ctt	gcc	cga		480		
Ile	Ser	Leu	Gly	Ala	Thr	Ile	Gly	Ile	Ser	Leu	Trp	Asn	Leu	Ala	Arg				

145	150	155	160	
gga atc gac gac cgc cct gtg gaa ccc cgc gcc gaa gca aaa cag atc				528
Gly Ile Asp Asp Arg Pro Val Glu Pro Arg Ala Glu Ala Lys Gln Ile	165	170	175	
tcc caa gag cac acc tat gaa aaa gac ctc ctc acc agg caa caa gta				576
Ser Gln Glu His Thr Tyr Glu Lys Asp Leu Leu Thr Arg Gln Gln Val	180	185	190	
gat gct gcc atc att cga tca gcc gaa ggc gca cac cga cgg ctc ctc				624
Asp Ala Ala Ile Ile Arg Ser Ala Glu Gly Ala His Arg Arg Leu Leu	195	200	205	
aaa gac gga cgc ggt gcc aga act gtc agc gtg aaa ctg cgg atg gcc				672
Lys Asp Gly Arg Gly Ala Arg Thr Val Ser Val Lys Leu Arg Met Ala	210	215	220	
gac ttt cgt att gag tct cgt tcc tac acc ttg tcc tat gcc acc gat				720
Asp Phe Arg Ile Glu Ser Arg Ser Tyr Thr Leu Ser Tyr Ala Thr Asp	225	230	235	240
gat tac gca act ctt gag gca aca gca ttc cga ctt gcc cgc tac ccc				768
Asp Tyr Ala Thr Leu Glu Ala Thr Ala Phe Arg Leu Ala Arg Tyr Pro	245	250	255	
gga gaa gta ggc ccc atc cgc ctt gtc gga gta agt ttt tct ggt ttg				816
Gly Glu Val Gly Pro Ile Arg Leu Val Gly Val Ser Phe Ser Gly Leu	260	265	270	
gaa gaa tcc cgc caa gac atc ctc ttc ccg gaa ctt gac caa caa atc				864
Glu Glu Ser Arg Gln Asp Ile Leu Phe Pro Glu Leu Asp Gln Gln Ile	275	280	285	
atc gta cca cca gca ccc gac acc gat tat gag gta ggc gtg caa tcc				912
Ile Val Pro Pro Ala Pro Asp Thr Asp Tyr Glu Val Gly Val Gln Ser	290	295	300	
tct tct agt tcc gaa agt act caa gtt gaa gcg ccg caa gat gtc gcg				960
Ser Ser Ser Ser Glu Ser Thr Gln Val Glu Ala Pro Gln Asp Val Ala	305	310	315	320
ttg agt atg tgg tgc gca acg caa gat gtc tac cac cca gaa tat ggc				1008
Leu Ser Met Trp Cys Ala Thr Gln Asp Val Tyr His Pro Glu Tyr Gly	325	330	335	
cac ggt tgg gta caa ggt gcc ggt cac ggt gtt gta tca gta cgt ttt				1056
His Gly Trp Val Gln Gly Ala Gly His Gly Val Val Ser Val Arg Phe	340	345	350	
gaa acc cgc agc acc aca aaa ggg cga act aaa agt ttt tcc atg gat				1104
Glu Thr Arg Ser Thr Thr Lys Gly Arg Thr Lys Ser Phe Ser Met Asp	355	360	365	
gac ccg gac ctc acc ccg gca gac cct cta gat agt ttg gat tgg gct				1152
Asp Pro Asp Leu Thr Pro Ala Asp Pro Leu Asp Ser Leu Asp Trp Ala	370	375	380	
gac tgg ttt gct gaa aat ggt gaa acg ggg gat gac gaa tagggtttca				1201
Asp Trp Phe Ala Glu Asn Gly Glu Thr Gly Asp Asp Glu	385	390	395	

tcggggtttcg ggg

1214

<210> 92

<211> 397

<212> PRT

<213> Corynebacterium glutamicum

<400> 92

Val	Val	Val	Thr	Pro	Arg	His	Ile	Val	Tyr	Ser	Ala	Ala	Ser	Arg	Arg
1				5					10					15	

Val	Phe	Gln	Ile	Val	Glu	Lys	Arg	Ala	Gly	Ile	Val	Glu	Arg	Leu	Ser
			20					25					30		

Ile	Asp	Glu	Gly	Phe	Met	Glu	Pro	Glu	Ala	Leu	Val	Gly	Ala	Thr	Pro
		35					40					45			

Glu	Glu	Val	Lys	Gln	Trp	Ala	Glu	Glu	Leu	Arg	Ala	Glu	Ile	Lys	Glu
	50					55					60				

Val	Thr	Gly	Leu	Pro	Ser	Ser	Val	Gly	Ala	Gly	Ser	Gly	Lys	Gln	Ile
65					70					75					80

Ala	Lys	Ile	Gly	Ser	Gly	Glu	Ala	Lys	Pro	Asp	Gly	Val	Phe	Val	Val
				85					90					95	

Pro	Val	Asp	Lys	Gln	His	Asp	Leu	Leu	Asp	Pro	Leu	Pro	Val	Gly	Ala
			100					105					110		

Leu	Trp	Gly	Val	Gly	Pro	Val	Thr	Gly	Ser	Lys	Leu	Ala	Ser	Met	Gly
		115					120						125		

Val	Glu	Thr	Ile	Gly	Asp	Leu	Ala	Ala	Leu	Thr	Gln	Lys	Glu	Val	Glu
	130					135					140				

Ile	Ser	Leu	Gly	Ala	Thr	Ile	Gly	Ile	Ser	Leu	Trp	Asn	Leu	Ala	Arg
145					150					155					160

Gly	Ile	Asp	Asp	Arg	Pro	Val	Glu	Pro	Arg	Ala	Glu	Ala	Lys	Gln	Ile
				165					170					175	

Ser	Gln	Glu	His	Thr	Tyr	Glu	Lys	Asp	Leu	Leu	Thr	Arg	Gln	Gln	Val
			180					185					190		

Asp	Ala	Ala	Ile	Ile	Arg	Ser	Ala	Glu	Gly	Ala	His	Arg	Arg	Leu	Leu
		195					200					205			

Lys	Asp	Gly	Arg	Gly	Ala	Arg	Thr	Val	Ser	Val	Lys	Leu	Arg	Met	Ala
	210					215					220				

Asp	Phe	Arg	Ile	Glu	Ser	Arg	Ser	Tyr	Thr	Leu	Ser	Tyr	Ala	Thr	Asp
225					230					235					240

Asp	Tyr	Ala	Thr	Leu	Glu	Ala	Thr	Ala	Phe	Arg	Leu	Ala	Arg	Tyr	Pro
			245						250					255	

Gly	Glu	Val	Gly	Pro	Ile	Arg	Leu	Val	Gly	Val	Ser	Phe	Ser	Gly	Leu
			260					265					270		

Glu Glu Ser Arg Gln Asp Ile Leu Phe Pro Glu Leu Asp Gln Gln Ile
 275 280 285
 Ile Val Pro Pro Ala Pro Asp Thr Asp Tyr Glu Val Gly Val Gln Ser
 290 295 300
 Ser Ser Ser Ser Glu Ser Thr Gln Val Glu Ala Pro Gln Asp Val Ala
 305 310 315 320
 Leu Ser Met Trp Cys Ala Thr Gln Asp Val Tyr His Pro Glu Tyr Gly
 325 330 335
 His Gly Trp Val Gln Gly Ala Gly His Gly Val Val Ser Val Arg Phe
 340 345 350
 Glu Thr Arg Ser Thr Thr Lys Gly Arg Thr Lys Ser Phe Ser Met Asp
 355 360 365
 Asp Pro Asp Leu Thr Pro Ala Asp Pro Leu Asp Ser Leu Asp Trp Ala
 370 375 380
 Asp Trp Phe Ala Glu Asn Gly Glu Thr Gly Asp Asp Glu
 385 390 395

<210> 93
 <211> 558
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(535)
 <223> RXA02446

<400> 93
 caggaaatct tgctgtctaa tgcacaacgg aaaactgctc acggacgaac tagttgtagc 60
 gagcgtattc tttgtgttct ctcacgacag gaataactgct atg gcg atc gag tcc 115
 Met Ala Ile Glu Ser
 1 5
 atc gcg tac acc agt gaa gca ctc tca acc ggc agt ggc cgg ctg ggg 163
 Ile Ala Tyr Thr Ser Glu Ala Leu Ser Thr Gly Ser Gly Arg Leu Gly
 10 15 20
 cat gtg cgc tcc aca gat ggt gcg ctc gaa ttt gaa atg aca cgg cca 211
 His Val Arg Ser Thr Asp Gly Ala Leu Glu Phe Glu Met Thr Pro Pro
 25 30 35
 aag gct ttg ggc gga tcc ggt gaa ggc acc aat cca gaa cag ctg ttc 259
 Lys Ala Leu Gly Gly Ser Gly Glu Gly Thr Asn Pro Glu Gln Leu Phe
 40 45 50
 gcg gta ggt tac gca gcc tgt ttc cac tct gcc atg cac tct gtc gca 307
 Ala Val Gly Tyr Ala Ala Cys Phe His Ser Ala Met His Ser Val Ala
 55 60 65
 cgc agc cgc aag atc act ctt gaa gac aca gcg gtt ggt gcc cga gtt 355
 Arg Ser Arg Lys Ile Thr Leu Glu Asp Thr Ala Val Gly Ala Arg Val
 70 75 80 85

agc atc ggg cca aac ggc gct ggt gga ttt gag att gcc gta gaa ctc 403
 Ser Ile Gly Pro Asn Gly Ala Gly Gly Phe Glu Ile Ala Val Glu Leu
 90 95 100

gaa gta tcg att cct caa ttg cca caa gca gaa gcc cag gaa ctt gct 451
 Glu Val Ser Ile Pro Gln Leu Pro Gln Ala Glu Ala Gln Glu Leu Ala
 105 110 115

gat gcc gcg cac cag gtg tgc ccg tat tcc aac gcc aca cga ggc aat 499
 Asp Ala Ala His Gln Val Cys Pro Tyr Ser Asn Ala Thr Arg Gly Asn
 120 125 130

atc tcg gta act gtg tca gtc atc gac gaa gag gct taaaaccaca 545
 Ile Ser Val Thr Val Ser Val Ile Asp Glu Glu Ala
 135 140 145

ggattaacaa aac 558

<210> 94
 <211> 145
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 94
 Met Ala Ile Glu Ser Ile Ala Tyr Thr Ser Glu Ala Leu Ser Thr Gly
 1 5 10 15

Ser Gly Arg Leu Gly His Val Arg Ser Thr Asp Gly Ala Leu Glu Phe
 20 25 30

Glu Met Thr Pro Pro Lys Ala Leu Gly Gly Ser Gly Glu Gly Thr Asn
 35 40 45

Pro Glu Gln Leu Phe Ala Val Gly Tyr Ala Ala Cys Phe His Ser Ala
 50 55 60

Met His Ser Val Ala Arg Ser Arg Lys Ile Thr Leu Glu Asp Thr Ala
 65 70 75 80

Val Gly Ala Arg Val Ser Ile Gly Pro Asn Gly Ala Gly Gly Phe Glu
 85 90 95

Ile Ala Val Glu Leu Glu Val Ser Ile Pro Gln Leu Pro Gln Ala Glu
 100 105 110

Ala Gln Glu Leu Ala Asp Ala Ala His Gln Val Cys Pro Tyr Ser Asn
 115 120 125

Ala Thr Arg Gly Asn Ile Ser Val Thr Val Ser Val Ile Asp Glu Glu
 130 135 140

Ala
 145

<210> 95
 <211> 1206
 <212> DNA
 <213> Corynebacterium glutamicum

<223> RXA02861

ggt atc acg gcg ctc ggt gct tcc gga cta acc aaa aac ctg ctg gac 691
Gly Ile Thr Ala Leu Gly Ala Ser Gly Leu Thr Lys Asn Leu Leu Asp
185 190 195

ttt gtg ggc ctg ggg gag att ccg ggc att agc tac atc acc tgg gtg 739
 Phe Val Gly Leu Gly Glu Ile Pro Gly Ile Ser Tyr Ile Thr Trp Val
 200 205 210

gtc gca gca ctt gtt ggt gtc ttg gct aac ttc ctg gtg ttc atg tgg 787
 Val Ala Ala Leu Val Gly Val Leu Ala Asn Phe Leu Val Phe Met Trp
 215 220 225

ctg att ttc tcc ctg cca cgt acc aaa gtt ccc atg aaa ccg ggt ctt 835
 Leu Ile Phe Ser Leu Pro Arg Thr Lys Val Pro Met Lys Pro Gly Leu
 230 235 240 245

cag gca gca ctg ctt ggc gca atc ggt ttt gag gtg gtc aag cag gtt 883
 Gln Ala Ala Leu Leu Gly Ala Ile Gly Phe Glu Val Val Lys Gln Val
 250 255 260

gga tgc ctg ttg gct tca aat gca ttg agt aac ccc gcg ggt gca gca 931
 Gly Ser Leu Leu Ala Ser Asn Ala Leu Ser Asn Pro Ala Gly Ala Ala
 265 270 275

ttc ggt ccg atc atc ggc atc atg gtt gtg ctg tat ttg atc tgg cgc 979
 Phe Gly Pro Ile Ile Gly Ile Met Val Val Leu Tyr Leu Ile Trp Arg
 280 285 290

atc ctc atg tat tgc tct gcg tgg gct gcc acc agt gaa gaa gcg ttg 1027
 Ile Leu Met Tyr Cys Ser Ala Trp Ala Ala Thr Ser Glu Glu Ala Leu
 295 300 305

cgt ctt gcg act gtt cca gca cca gag cct gcg atc att cgg gtt cgc 1075
 Arg Leu Ala Thr Val Pro Ala Pro Glu Pro Ala Ile Ile Arg Val Arg
 310 315 320 325

cat gaa att gat cca ggt gaa gaa gtc tcc caa tct gct cga aaa gtg 1123
 His Glu Ile Asp Pro Gly Glu Glu Val Ser Gln Ser Ala Arg Lys Val
 330 335 340

ggc att gga gtg gcc gtg ggt gcc gcg act gcg ggt gct ttt gcg ctg 1171
 Gly Ile Gly Val Ala Val Gly Ala Ala Thr Ala Gly Ala Phe Ala Leu
 345 350 355

ttg cgt aaa aaa tagtttttat taagggcatt ccc 1206
 Leu Arg Lys Lys
 360

<210> 96

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 96

Met Ser Thr Arg Thr Thr Pro Gln Asp Arg Tyr Thr Asp Glu Tyr Gly
 1 5 10 15

Ile Glu Arg Val Asn Lys Asp Glu Pro Gly Leu Val Asp Lys Leu Arg
 20 25 30

Asp Lys His Asp Trp Phe Asp His Leu Met Arg Met Asn Glu Arg Phe
 35 40 45

Gly Ala Lys Gly Gly Asn Gln Leu Ser Ala Gly Ile Thr Tyr Phe Ser

50					55					60					
Val	Leu	Ser	Ile	Phe	Pro	Ile	Ala	Met	Leu	Val	Phe	Gly	Ile	Ala	Gly
65					70					75					80
Val	Ile	Leu	Ala	Gly	Asn	Pro	Glu	Val	Leu	Thr	Asp	Ile	Gln	Asn	Arg
				85					90					95	
Ile	Asn	Asp	Ala	Leu	Glu	Gly	Glu	Ile	Gly	Asn	Thr	Val	Asn	Gly	Ile
			100					105					110		
Ile	Asp	Ser	Ala	Ile	Ala	Gln	Arg	Gly	Ala	Val	Leu	Gly	Ile	Gly	Gly
		115					120					125			
Val	Thr	Ala	Leu	Trp	Ser	Gly	Leu	Gly	Trp	Met	Ala	Asn	Leu	Arg	Phe
	130					135					140				
Gly	Val	Ser	Arg	Met	Trp	Ala	Ile	Asp	Pro	Thr	Glu	Gly	Asn	Phe	Ile
145						150					155				160
Gln	Lys	Lys	Leu	Thr	Asp	Leu	Val	Ala	Leu	Ile	Val	Leu	Leu	Leu	Ala
			165						170						175
Met	Gly	Val	Ala	Phe	Gly	Ile	Thr	Ala	Leu	Gly	Ala	Ser	Gly	Leu	Thr
			180					185					190		
Lys	Asn	Leu	Leu	Asp	Phe	Val	Gly	Leu	Gly	Glu	Ile	Pro	Gly	Ile	Ser
		195					200					205			
Tyr	Ile	Thr	Trp	Val	Val	Ala	Ala	Leu	Val	Gly	Val	Leu	Ala	Asn	Phe
	210					215					220				
Leu	Val	Phe	Met	Trp	Leu	Ile	Phe	Ser	Leu	Pro	Arg	Thr	Lys	Val	Pro
225						230					235				240
Met	Lys	Pro	Gly	Leu	Gln	Ala	Ala	Leu	Leu	Gly	Ala	Ile	Gly	Phe	Glu
			245						250					255	
Val	Val	Lys	Gln	Val	Gly	Ser	Leu	Leu	Ala	Ser	Asn	Ala	Leu	Ser	Asn
			260					265					270		
Pro	Ala	Gly	Ala	Ala	Phe	Gly	Pro	Ile	Ile	Gly	Ile	Met	Val	Val	Leu
		275					280					285			
Tyr	Leu	Ile	Trp	Arg	Ile	Leu	Met	Tyr	Cys	Ser	Ala	Trp	Ala	Ala	Thr
	290					295					300				
Ser	Glu	Glu	Ala	Leu	Arg	Leu	Ala	Thr	Val	Pro	Ala	Pro	Glu	Pro	Ala
305						310					315				320
Ile	Ile	Arg	Val	Arg	His	Glu	Ile	Asp	Pro	Gly	Glu	Glu	Val	Ser	Gln
			325						330					335	
Ser	Ala	Arg	Lys	Val	Gly	Ile	Gly	Val	Ala	Val	Gly	Ala	Ala	Thr	Ala
			340					345					350		
Gly	Ala	Phe	Ala	Leu	Leu	Arg	Lys	Lys							
		355					360								

<400> 97															60	
aaccaatggc	tggtgactga	tgtggtgatc	agtgcccagt	ttcttctttc	tactagtgtc											
ggatagaagt	acccccagtc	cagaatgaag	gtcaccacca	atg	tca	gag	aat	ttg								115
				Met	Ser	Glu	Asn	Leu								5
				1												
cca	gcg	ccc	gag	aat	ctc	ctg	gac	gcc	gag	aga	att	cag	atg	atc	aag	163
Pro	Ala	Pro	Glu	Asn	Leu	Leu	Asp	Ala	Glu	Arg	Ile	Gln	Met	Ile	Lys	
				10					15					20		
aac	ttc	cgc	aac	gaa	tta	acg	ggg	ttc	atg	ctc	aac	tac	caa	ttt	ggc	211
Asn	Phe	Arg	Asn	Glu	Leu	Thr	Gly	Phe	Met	Leu	Asn	Tyr	Gln	Phe	Gly	
			25					30					35			
att	gat	gag	atc	ctg	acc	aag	atc	aac	atc	ctg	aaa	act	gaa	ttc	agc	259
Ile	Asp	Glu	Ile	Leu	Thr	Lys	Ile	Asn	Ile	Leu	Lys	Thr	Glu	Phe	Ser	
		40					45					50				
cag	ctg	cac	gaa	tac	gca	cct	atc	gag	cac	gta	tct	tca	cga	ttg	aag	307
Gln	Leu	His	Glu	Tyr	Ala	Pro	Ile	Glu	His	Val	Ser	Ser	Arg	Leu	Lys	
	55					60					65					
aca	cca	gaa	agc	atc	gtc	aaa	aag	gtc	atc	cga	aaa	gga	gac	gag	ctc	355
Thr	Pro	Glu	Ser	Ile	Val	Lys	Lys	Val	Ile	Arg	Lys	Gly	Asp	Glu	Leu	
70					75					80					85	
tcc	ctc	gca	gct	atc	aaa	gac	aca	gtg	ttt	gat	atc	gca	ggc	att	cga	403
Ser	Leu	Ala	Ala	Ile	Lys	Asp	Thr	Val	Phe	Asp	Ile	Ala	Gly	Ile	Arg	
				90					95					100		
atc	gtc	tgc	agt	ttc	ctc	aaa	gat	gcc	tac	gca	atc	gcc	gat	atg	ctg	451
Ile	Val	Cys	Ser	Phe	Leu	Lys	Asp	Ala	Tyr	Ala	Ile	Ala	Asp	Met	Leu	
			105					110					115			
acc	aac	caa	aaa	gac	gtc	acg	gtc	atc	gag	gcc	aaa	gac	tac	atc	gct	499
Thr	Asn	Gln	Lys	Asp	Val	Thr	Val	Ile	Glu	Ala	Lys	Asp	Tyr	Ile	Ala	
		120					125					130				
aac	cca	aag	ccg	aac	ggc	tac	aag	agt	ttg	cac	ctt	atc	ctc	caa	gtg	547
Asn	Pro	Lys	Pro	Asn	Gly	Tyr	Lys	Ser	Leu	His	Leu	Ile	Leu	Gln	Val	
135						140					145					
cct	gtc	ttc	ctg	tct	aac	tcc	gtg	gaa	aag	gtc	aat	gtt	gaa	gtc	cag	595
Pro	Val	Phe	Leu	Ser	Asn	Ser	Val	Glu	Lys	Val	Asn	Val	Glu	Val	Gln	
150					155					160					165	
atc	cgc	acc	att	gcc												

Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser Ile Leu Asp Glu Leu
 185 190 195
 agt gaa gat gga aag aat cca cgg gga agt gaa gtc act taaacctcca 740
 Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu Val Thr
 200 205 210

gttgaaacca ctg 753

<210> 98
 <211> 210
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 98
 Met Ser Glu Asn Leu Pro Ala Pro Glu Asn Leu Leu Asp Ala Glu Arg
 1 5 10 15
 Ile Gln Met Ile Lys Asn Phe Arg Asn Glu Leu Thr Gly Phe Met Leu
 20 25 30
 Asn Tyr Gln Phe Gly Ile Asp Glu Ile Leu Thr Lys Ile Asn Ile Leu
 35 40 45
 Lys Thr Glu Phe Ser Gln Leu His Glu Tyr Ala Pro Ile Glu His Val
 50 55 60
 Ser Ser Arg Leu Lys Thr Pro Glu Ser Ile Val Lys Lys Val Ile Arg
 65 70 75 80
 Lys Gly Asp Glu Leu Ser Leu Ala Ala Ile Lys Asp Thr Val Phe Asp
 85 90 95
 Ile Ala Gly Ile Arg Ile Val Cys Ser Phe Leu Lys Asp Ala Tyr Ala
 100 105 110
 Ile Ala Asp Met Leu Thr Asn Gln Lys Asp Val Thr Val Ile Glu Ala
 115 120 125
 Lys Asp Tyr Ile Ala Asn Pro Lys Pro Asn Gly Tyr Lys Ser Leu His
 130 135 140
 Leu Ile Leu Gln Val Pro Val Phe Leu Ser Asn Ser Val Glu Lys Val
 145 150 155 160
 Asn Val Glu Val Gln Ile Arg Thr Ile Ala Met Asp Phe Trp Ala Ser
 165 170 175
 Leu Glu His Lys Ile Tyr Tyr Lys Phe Glu Gln Glu Val Pro Gln Ser
 180 185 190
 Ile Leu Asp Glu Leu Ser Glu Asp Gly Lys Asn Pro Arg Gly Ser Glu
 195 200 205
 Val Thr
 210

<210> 99
 <211> 1098

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1075)

<223> RXN00786

<400> 99

```

tccttcttcc accagctaaa agtgaattac cccgcctttg tcgggggtggt tgcattccca 60

gtctaggtgt ttagcctcaa cggttgatac gctgggaggc atg agc tca cct gtt 115
                                         Met Ser Ser Pro Val
                                         1                               5

atc agc ccc gaa acc aaa acc gga aag aag atc ctg ctt gca gcc cct 163
Ile Ser Pro Glu Thr Lys Thr Gly Lys Lys Ile Leu Leu Ala Ala Pro
                        10                               15                        20

cgc gga tac tgt gcc ggc gta gac cgt gca gtg gaa acc gtc gag cgc 211
Arg Gly Tyr Cys Ala Gly Val Asp Arg Ala Val Glu Thr Val Glu Arg
                        25                               30                        35

gcg ctc gag gaa tac ggc gcc cca att tat gtc cgt aaa gaa atc gtg 259
Ala Leu Glu Glu Tyr Gly Ala Pro Ile Tyr Val Arg Lys Glu Ile Val
                        40                               45                        50

cac aac cgt tac gtt gtg gac acc ctg gca gaa aag ggc gcg att ttt 307
His Asn Arg Tyr Val Val Asp Thr Leu Ala Glu Lys Gly Ala Ile Phe
                        55                               60                        65

gtc aac gaa gca tct gaa gca cca gaa ggt gcc aac atg gtg ttc tct 355
Val Asn Glu Ala Ser Glu Ala Pro Glu Gly Ala Asn Met Val Phe Ser
                        70                               75                        80                        85

gca cac ggc gtg agc cca atg gtc cac gaa gaa gct gca gct aaa aac 403
Ala His Gly Val Ser Pro Met Val His Glu Glu Ala Ala Ala Lys Asn
                        90                               95                        100

atc aag gct att gac gcg gcc tgc ccg ctg gtc acc aaa gtg cac aag 451
Ile Lys Ala Ile Asp Ala Ala Cys Pro Leu Val Thr Lys Val His Lys
                        105                               110                        115

gaa gtc cag cgc ttt gat aag cag gga ttc cac att ctc ttc atc ggt 499
Glu Val Gln Arg Phe Asp Lys Gln Gly Phe His Ile Leu Phe Ile Gly
                        120                               125                        130

cac gaa ggc cat gaa gaa gta gag ggc acc atg ggt cat tcc gtt gag 547
His Glu Gly His Glu Glu Val Glu Gly Thr Met Gly His Ser Val Glu
                        135                               140                        145

aaa acc cac ctg gtt gac ggc gtt gct ggc att gcc acc ctg cct gaa 595
Lys Thr His Leu Val Asp Gly Val Ala Gly Ile Ala Thr Leu Pro Glu
                        150                               155                        160                        165

ttc tta aac gat gaa cca aac ctg atc tgg ctg tct cag acc acg ctt 643
Phe Leu Asn Asp Glu Pro Asn Leu Ile Trp Leu Ser Gln Thr Thr Leu
                        170                               175                        180

tct gtg gac gag acc atg gag atc gtc cgc gag ctg aag gtg aag ttc 691
Ser Val Asp Glu Thr Met Glu Ile Val Arg Glu Leu Lys Val Lys Phe

```

185										190										195																			
cct	cag	ctg	cag	gat	cca	ccg	tca	gat	gat	att	tgc	tac	gcc	acg	cag	739																							
Pro	Gln	Leu	Gln	Asp	Pro	Pro	Ser	Asp	Asp	Ile	Cys	Tyr	Ala	Thr	Gln																								
200										205										210																			
aac	cgc	cag	gtt	gcc	gtc	aag	gct	atc	gct	gag	cgc	tgc	gag	ctg	atg	787																							
Asn	Arg	Gln	Val	Ala	Val	Lys	Ala	Ile	Ala	Glu	Arg	Cys	Glu	Leu	Met																								
215										220										225																			
att	gtg	gtc	ggg	tcc	cgc	aac	tcc	tcc	aac	tcg	gtt	cgt	ctg	gtt	gag	835																							
Ile	Val	Val	Gly	Ser	Arg	Asn	Ser	Ser	Asn	Ser	Val	Arg	Leu	Val	Glu																								
230										235										240										245									
gtc	gct	aag	caa	aac	ggg	gcc	gat	aac	gcc	tac	ctg	gtg	gat	tac	gcc	883																							
Val	Ala	Lys	Gln	Asn	Gly	Ala	Asp	Asn	Ala	Tyr	Leu	Val	Asp	Tyr	Ala																								
250										255										260																			
cgc	gaa	atc	gac	cca	gca	tgg	ttc	gaa	ggc	gta	gag	acc	atc	ggg	atc	931																							
Arg	Glu	Ile	Asp	Pro	Ala	Trp	Phe	Glu	Gly	Val	Glu	Thr	Ile	Gly	Ile																								
265										270										275																			
tcc	tcc	ggc	gct	tcc	gtg	cct	gag	atc	ctc	gtc	cag	ggc	gtc	att	gag	979																							
Ser	Ser	Gly	Ala	Ser	Val	Pro	Glu	Ile	Leu	Val	Gln	Gly	Val	Ile	Glu																								
280										285										290																			
cgc	ctg	gct	gag	ttc	ggc	tac	gac	gac	gtc	gag	gaa	gtc	acc	tcc	gcc	1027																							
Arg	Leu	Ala	Glu	Phe	Gly	Tyr	Asp	Asp	Val	Glu	Glu	Val	Thr	Ser	Ala																								
295										300										305																			
gct	gag	aag	att	gtt	ttc	gcg	ctg	cct	cgc	gtg	ctg	cgc	cac	aag	aat	1075																							
Ala	Glu	Lys	Ile	Val	Phe	Ala	Leu	Pro	Arg	Val	Leu	Arg	His	Lys	Asn																								
310										315										320										325									
taattgcaag aatgaaaaat ccc																1098																							

<210> 100

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 100

Met	Ser	Ser	Pro	Val	Ile	Ser	Pro	Glu	Thr	Lys	Thr	Gly	Lys	Lys	Ile
1				5					10					15	

Leu	Leu	Ala	Ala	Pro	Arg	Gly	Tyr	Cys	Ala	Gly	Val	Asp	Arg	Ala	Val
		20						25					30		

Glu	Thr	Val	Glu	Arg	Ala	Leu	Glu	Glu	Tyr	Gly	Ala	Pro	Ile	Tyr	Val
		35					40					45			

Arg	Lys	Glu	Ile	Val	His	Asn	Arg	Tyr	Val	Val	Asp	Thr	Leu	Ala	Glu
	50					55					60				

Lys	Gly	Ala	Ile	Phe	Val	Asn	Glu	Ala	Ser	Glu	Ala	Pro	Glu	Gly	Ala
	65					70				75					80

Asn	Met	Val	Phe	Ser	Ala	His	Gly	Val	Ser	Pro	Met	Val	His	Glu	Glu
				85					90					95	

Ala Ala Ala Lys Asn Ile Lys Ala Ile Asp Ala Ala Cys Pro Leu Val
 100 105 110
 Thr Lys Val His Lys Glu Val Gln Arg Phe Asp Lys Gln Gly Phe His
 115 120 125
 Ile Leu Phe Ile Gly His Glu Gly His Glu Glu Val Glu Gly Thr Met
 130 135 140
 Gly His Ser Val Glu Lys Thr His Leu Val Asp Gly Val Ala Gly Ile
 145 150 155 160
 Ala Thr Leu Pro Glu Phe Leu Asn Asp Glu Pro Asn Leu Ile Trp Leu
 165 170 175
 Ser Gln Thr Thr Leu Ser Val Asp Glu Thr Met Glu Ile Val Arg Glu
 180 185 190
 Leu Lys Val Lys Phe Pro Gln Leu Gln Asp Pro Pro Ser Asp Asp Ile
 195 200 205
 Cys Tyr Ala Thr Gln Asn Arg Gln Val Ala Val Lys Ala Ile Ala Glu
 210 215 220
 Arg Cys Glu Leu Met Ile Val Val Gly Ser Arg Asn Ser Ser Asn Ser
 225 230 235 240
 Val Arg Leu Val Glu Val Ala Lys Gln Asn Gly Ala Asp Asn Ala Tyr
 245 250 255
 Leu Val Asp Tyr Ala Arg Glu Ile Asp Pro Ala Trp Phe Glu Gly Val
 260 265 270
 Glu Thr Ile Gly Ile Ser Ser Gly Ala Ser Val Pro Glu Ile Leu Val
 275 280 285
 Gln Gly Val Ile Glu Arg Leu Ala Glu Phe Gly Tyr Asp Asp Val Glu
 290 295 300
 Glu Val Thr Ser Ala Ala Glu Lys Ile Val Phe Ala Leu Pro Arg Val
 305 310 315 320
 Leu Arg His Lys Asn
 325

<210> 101

<211> 1131

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1108)

<223> RXS01027

<400> 101

aatagatgga agtagttttt cattcactta tgtg'gcggtt tttaatctgg tttctaccaa 60

 gaactgtgtg caccacaacg cggaaggtga atcgcaccca atg gca aat aag aac 115
 Met Ala Asn Lys Asn

												1					5	
aat	aag	cct	cat	gag	gtg	gac	aaa	gac	caa	gat	tca	gcc	atg	ctg	atc	163		
Asn	Lys	Pro	His	Glu	Val	Asp	Lys	Asp	Gln	Asp	Ser	Ala	Met	Leu	Ile			
				10					15					20				
aac	ggg	cgc	ctg	caa	cag	atc	ccg	gcg	cgt	ccc	act	gag	gaa	ttc	acc	211		
Asn	Gly	Arg	Leu	Gln	Gln	Ile	Pro	Ala	Arg	Pro	Thr	Glu	Glu	Phe	Thr			
				25					30					35				
cgc	cca	act	ctt	gca	gca	ggg	gca	gta	ctg	tgg	cgc	ggc	gac	atc	acc	259		
Arg	Pro	Thr	Leu	Ala	Ala	Gly	Ala	Val	Leu	Trp	Arg	Gly	Asp	Ile	Thr			
				40					45					50				
aac	ccg	gac	agc	atc	gag	gtc	gct	gtc	atc	cac	cgc	ccg	cac	tat	gat	307		
Asn	Pro	Asp	Ser	Ile	Glu	Val	Ala	Val	Ile	His	Arg	Pro	His	Tyr	Asp			
				55					60					65				
gac	tgg	tcc	ctg	gcc	aag	ggc	aaa	gtc	gat	ccc	ggc	gag	tct	att	ccg	355		
Asp	Trp	Ser	Leu	Ala	Lys	Gly	Lys	Val	Asp	Pro	Gly	Glu	Ser	Ile	Pro			
				70					75					80	85			
aca	acc	gcg	gcc	cgt	gaa	atc	ctt	gaa	gaa	act	ggc	tac	gac	atc	cgt	403		
Thr	Thr	Ala	Ala	Arg	Glu	Ile	Leu	Glu	Glu	Thr	Gly	Tyr	Asp	Ile	Arg			
				90					95					100				
ctg	ggc	aag	ctg	atc	ggc	aag	gtt	act	tac	cct	gtg	ctc	gac	cga	acc	451		
Leu	Gly	Lys	Leu	Ile	Gly	Lys	Val	Thr	Tyr	Pro	Val	Leu	Asp	Arg	Thr			
				105					110					115				
aaa	gtg	gtc	tac	tac	tgg	act	gcc	cag	gtt	ctt	ggg	gga	gag	ttt	gtc	499		
Lys	Val	Val	Tyr	Tyr	Trp	Thr	Ala	Gln	Val	Leu	Gly	Gly	Glu	Phe	Val			
				120					125					130				
ccc	aac	gat	gaa	gtt	gat	gaa	atc	cgt	tgg	ctg	tct	gtt	gat	gaa	gca	547		
Pro	Asn	Asp	Glu	Val	Asp	Glu	Ile	Arg	Trp	Leu	Ser	Val	Asp	Glu	Ala			
				135					140					145				
tgc	gag	ttg	ctc	agc	tac	caa	gta	gat	acc	gaa	gtt	ctg	gcc	aag	gca	595		
Cys	Glu	Leu	Leu	Ser	Tyr	Gln	Val	Asp	Thr	Glu	Val	Leu	Ala	Lys	Ala			
				150					155					160	165			
gca	aag	cgt	ttc	cgc	act	cct	tcc	acc	act	cgg	gtg	ctg	tat	gtt	cgc	643		
Ala	Lys	Arg	Phe	Arg	Thr	Pro	Ser	Thr	Thr	Arg	Val	Leu	Tyr	Val	Arg			
				170					175					180				
cat	gct	cat	gca	cat	ggg	cgc	caa	acc	tgg	ggg	ggc	gac	gac	aat	aag	691		
His	Ala	His	Ala	His	Gly	Arg	Gln	Thr	Trp	Gly	Gly	Asp	Asp	Asn	Lys			
				185					190					195				
cgc	cca	ttg	gac	aaa	aag	ggg	cgt	cga	caa	gca	gaa	atg	ctc	gta	ccc	739		
Arg	Pro	Leu	Asp	Lys	Lys	Gly	Arg	Arg	Gln	Ala	Glu	Met	Leu	Val	Pro			
				200					205					210				
atg	ttg	ttg	ccc	ttc	aaa	ccc	acc	gca	att	tac	tgc	gcg	gtg	ccc	gat	787		

gtg tcc gtc aac cga ctg ttc ggc gac gac gcc tgg gaa acc gat ccc 883
Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala Trp Glu Thr Asp Pro
250 255 260

gag gcc tgc aag aag cgc ttc acc gac gtg gtc gcg caa ggt ggc gtg 931
Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val Ala Gln Gly Gly Val
265 270 275

ccg atg atc gtt ggg cag ggc gac atc att ccg gaa atg atc aaa tgg 979
Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro Glu Met Ile Lys Trp
280 285 290

ttc tcc gag aac ggc acc ctc cct atc gat gag aag atc aag gcg aaa 1027
Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu Lys Ile Lys Ala Lys
295 300 305

aag ggc agc gtg tgg gtg ttg agc ttt cac gac ggt gtg ttc acc ggc 1075
Lys Gly Ser Val Trp Val Leu Ser Phe His Asp Gly Val Phe Thr Gly
310 315 320 325

gct gat tac ctg gcg agt tcc ctg ccg gtt aaa taggagcgcg tttaaggcct 1128
Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
330 335

cca 1131

<210> 102

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

Met Ala Asn Lys Asn Asn Lys Pro His Glu Val Asp Lys Asp Gln Asp
1 5 10 15

Ser Ala Met Leu Ile Asn Gly Arg Leu Gln Gln Ile Pro Ala Arg Pro
20 25 30

Thr Glu Glu Phe Thr Arg Pro Thr Leu Ala Ala Gly Ala Val Leu Trp
35 40 45

Arg Gly Asp Ile Thr Asn Pro Asp Ser Ile Glu Val Ala Val Ile His
50 55 60

Arg Pro His Tyr Asp Asp Trp Ser Leu Ala Lys Gly Lys Val Asp Pro
65 70 75 80

Gly Glu Ser Ile Pro Thr Thr Ala Ala Arg Glu Ile Leu Glu Glu Thr
85 90 95

Gly Tyr Asp Ile Arg Leu Gly Lys Leu Ile Gly Lys Val Thr Tyr Pro
100 105 110

Val Leu Asp Arg Thr Lys Val Val Tyr Tyr Trp Thr Ala Gln Val Leu
115 120 125

Gly Gly Glu Phe Val Pro Asn Asp Glu Val Asp Glu Ile Arg Trp Leu
130 135 140

Ser Val Asp Glu Ala Cys Glu Leu Leu Ser Tyr Gln Val Asp Thr Glu
 145 150 155 160
 Val Leu Ala Lys Ala Ala Lys Arg Phe Arg Thr Pro Ser Thr Thr Arg
 165 170 175
 Val Leu Tyr Val Arg His Ala His Ala His Gly Arg Gln Thr Trp Gly
 180 185 190
 Gly Asp Asp Asn Lys Arg Pro Leu Asp Lys Lys Gly Arg Arg Gln Ala
 195 200 205
 Glu Met Leu Val Pro Met Leu Leu Pro Phe Lys Pro Thr Ala Ile Tyr
 210 215 220
 Ser Ala Val Pro Asp Arg Cys Gln Ala Thr Ala Leu Pro Leu Ala Asp
 225 230 235 240
 Glu Leu Gly Leu Asp Val Ser Val Asn Arg Leu Phe Gly Asp Asp Ala
 245 250 255
 Trp Glu Thr Asp Pro Glu Ala Cys Lys Lys Arg Phe Thr Asp Val Val
 260 265 270
 Ala Gln Gly Gly Val Pro Met Ile Val Gly Gln Gly Asp Ile Ile Pro
 275 280 285
 Glu Met Ile Lys Trp Phe Ser Glu Asn Gly Thr Leu Pro Ile Asp Glu
 290 295 300
 Lys Ile Lys Ala Lys Lys Gly Ser Val Trp Val Leu Ser Phe His Asp
 305 310 315 320
 Gly Val Phe Thr Gly Ala Asp Tyr Leu Ala Ser Ser Leu Pro Val Lys
 325 330 335

<210> 103

<211> 651

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(628)

<223> RXS01528

<400> 103

caccctaaacc caaacctctc agtcgaataa gcagaagtct caggacaacc gcaggggtaa 60

gggtcgtagg tctccaacca ggaggcggtc caacacgagg gtg aat cag gcg tgg 115
 Val Asn Gln Ala Trp
 1 5

cag cag tcc cgt ttg gtt act tct gat gag act tcc gca ggt ggt ctc 163
 Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr Ser Ala Gly Gly Leu
 10 15 20

gtg gtg tca ggt ttg gct gag gcg gtc aac gct aac aat gag gtt gat 211
 Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala Asn Asn Glu Val Asp
 25 30 35

```

ctg tcg aag att tat gtt gcg ttg att ggt cgc ctt gat cgt cgt ggt 259
Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg Leu Asp Arg Arg Gly
      40                      45                      50

cgt ttg ttg tgg tcg atg ccg aag ggc cat gtt gag cct ggt gag gat 307
Arg Leu Leu Trp Ser Met Pro Lys Gly His Val Glu Pro Gly Glu Asp
      55                      60                      65

aag gct gcg act gct gag cgt gag gtg tgg gag gag acc ggc atc cac 355
Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu Glu Thr Gly Ile His
      70                      75                      80                      85

ggt gag gtg ttc act gag ttg ggt gtg att gat tat tgg ttc gtt tcg 403
Gly Glu Val Phe Thr Glu Leu Gly Val Ile Asp Tyr Trp Phe Val Ser
      90                      95                      100

gaa ggg aag cgg atc cat aag acg gtg cat cat cat ttg ttg cgt tat 451
Glu Gly Lys Arg Ile His Lys Thr Val His His His Leu Leu Arg Tyr
      105                      110                      115

gtt gat ggc gat ttg aat gat gag gat cca gaa gtc act gag gtg gcg 499
Val Asp Gly Asp Leu Asn Asp Glu Asp Pro Glu Val Thr Glu Val Ala
      120                      125                      130

tgg att ccg gcg aat cag ttg att gag cat ttg gct ttt gcg gat gag 547
Trp Ile Pro Ala Asn Gln Leu Ile Glu His Leu Ala Phe Ala Asp Glu
      135                      140                      145

cgg aag ttg gct agg cag gcg cat gat ttg ttg cct gag ttt gct ttg 595
Arg Lys Leu Ala Arg Gln Ala His Asp Leu Leu Pro Glu Phe Ala Leu
      150                      155                      160                      165

aag gaa aag gcg gag gga agg tcc acc cca agg tgattccgaa ccccaaccg 648
Lys Glu Lys Ala Glu Gly Arg Ser Thr Pro Arg
      170                      175

aac 651

```

<210> 104

<211> 176

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 104

```

Val Asn Gln Ala Trp Gln Gln Ser Arg Leu Val Thr Ser Asp Glu Thr
  1                      5                      10                      15

```

```

Ser Ala Gly Gly Leu Val Val Ser Gly Leu Ala Glu Ala Val Asn Ala
      20                      25                      30

```

```

Asn Asn Glu Val Asp Leu Ser Lys Ile Tyr Val Ala Leu Ile Gly Arg
      35                      40                      45

```

```

Leu Asp Arg Arg Gly Arg Leu Leu Trp Ser Met Pro Lys Gly His Val
      50                      55                      60

```

```

Glu Pro Gly Glu Asp Lys Ala Ala Thr Ala Glu Arg Glu Val Trp Glu
      65                      70                      75                      80

```

```
<210> 105
<211> 509
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(486)
<223> RXS01716
```

<400> 105																
gaa	gtc	act	cct	gag	gga	ttc	aaa	gag	atc	acc	cgt	gaa	aac	acc	atc	48
Glu	Val	Thr	Pro	Glu	Gly	Phe	Lys	Glu	Ile	Thr	Arg	Glu	Asn	Thr	Ile	
1				5				10				15				
gtt	cgc	ctg	ggc	aaa	ggc	gtc	gac	gcc	acc	ggg	cag	cta	gac	ccc	gag	96
Val	Arg	Leu	Gly	Lys	Gly	Val	Asp	Ala	Thr	Gly	Gln	Leu	Asp	Pro	Glu	
20				25				30								
gca	atc	gag	cgc	act	cgt	gtc	gct	ttg	gaa	aac	tac	gtt	gaa	ctc	atg	144
Ala	Ile	Glu	Arg	Thr	Arg	Val	Ala	Leu	Glu	Asn	Tyr	Val	Glu	Leu	Met	
35				40				45								
gaa	acc	cat	ggg	gta	gag	gcc	gta	cga	atg	gtt	gcc	acc	tcc	gca	acc	192
Glu	Thr	His	Gly	Val	Glu	Ala	Val	Arg	Met	Val	Ala	Thr	Ser	Ala	Thr	
50				55				60								
cgc	gat	gcg	tcc	aac	cgc	gat	gaa	ttc	ttt	tcg	atg	acc	cgc	cag	ctt	240
Arg	Asp	Ala	Ser	Asn	Arg	Asp	Glu	Phe	Phe	Ser	Met	Thr	Arg	Gln	Leu	
65				70				75				80				
ctg	tcc	aag	atc	cgt	cct	gga	tac	caa	gct	gaa	gta	att	tcc	ggc	gaa	288
Leu	Ser	Lys	Ile	Arg	Pro	Gly	Tyr	Gln	Ala	Glu	Val	Ile	Ser	Gly	Glu	
85				90				95								
gag	gaa	gct	ctg	ctg	tcc	ttc	cga	ggg	gca	atc	gtt	gac	ctg	cct	gaa	336
Glu	Glu	Ala	Leu	Leu	Ser	Phe	Arg	Gly	Ala	Ile	Val	Asp	Leu	Pro	Glu	
100				105				110								
gac	caa	ggg	cct	ttc	tgt	gtt	atc	gac	ctt	ggc	ggg	gga	tcc	act	gag	384
Asp	Gln	Gly	Pro	Phe	Cys	Val	Ile	Asp	Leu	Gly	Gly	Gly	Ser	Thr	Glu	
115				120				125								

ttc atc gtt ggc acc tac gac ggt gaa atc cta ggc tcc cac tca acc 432
 Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr
 130 135 140

 caa atg gga tgc gtg cgc ctg acc gaa cga atc atg cgc agc gac cca 480
 Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro
 145 150 155 160

 ccc gac tgaaaccgaa gtggaaatcg ccc 509
 Pro Asp

<210> 106
 <211> 162
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 106
 Glu Val Thr Pro Glu Gly Phe Lys Glu Ile Thr Arg Glu Asn Thr Ile
 1 5 10 15

 Val Arg Leu Gly Lys Gly Val Asp Ala Thr Gly Gln Leu Asp Pro Glu
 20 25 30

 Ala Ile Glu Arg Thr Arg Val Ala Leu Glu Asn Tyr Val Glu Leu Met
 35 40 45

 Glu Thr His Gly Val Glu Ala Val Arg Met Val Ala Thr Ser Ala Thr
 50 55 60

 Arg Asp Ala Ser Asn Arg Asp Glu Phe Phe Ser Met Thr Arg Gln Leu
 65 70 75 80

 Leu Ser Lys Ile Arg Pro Gly Tyr Gln Ala Glu Val Ile Ser Gly Glu
 85 90 95

 Glu Glu Ala Leu Leu Ser Phe Arg Gly Ala Ile Val Asp Leu Pro Glu
 100 105 110

 Asp Gln Gly Pro Phe Cys Val Ile Asp Leu Gly Gly Gly Ser Thr Glu
 115 120 125

 Phe Ile Val Gly Thr Tyr Asp Gly Glu Ile Leu Gly Ser His Ser Thr
 130 135 140

 Gln Met Gly Cys Val Arg Leu Thr Glu Arg Ile Met Arg Ser Asp Pro
 145 150 155 160

 Pro Asp

<210> 107
 <211> 654
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<222> (101)..(631)

<223> RXS01835

<400> 107

```

tcaacatcta ttctctctgc gatttgcacg ggatatatat taaaaattct agccgaaagt 60

ttctctgcgtg aatacacttt ccccgcgccct tcgcaaagct atg aat act gcc gcg 115
               Met Asn Thr Ala Ala
               1               5

tgg gca cac cgc cac cac gta cgc aaa ggc ggt gga att ccg tat gtc 163
Trp Ala His Arg His His Val Arg Lys Gly Gly Gly Ile Pro Tyr Val
               10               15               20

agc cat ctt tat tca gtg atg tac ttg ctg gcc agc gtc act aat gat 211
Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala Ser Val Thr Asn Asp
               25               30               35

gaa gat gtg ctc atc gcc ggg ctg ctc cac gac acc ctc gaa gac gta 259
Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp Thr Leu Glu Asp Val
               40               45               50

ccc gag gaa tac aat tct gcc caa ctt gaa gct gat ttt ggt ccg cgg 307
Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala Asp Phe Gly Pro Arg
               55               60               65

gtg cgc gag ttg gtg gaa gag ctc acc aaa cag ccc tta aaa agc tgg 355
Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln Pro Leu Lys Ser Trp
               70               75               80               85

aaa gcg cgt gcc gac gct tac ctc ctg cac ctc agc gca ggt gcc agc 403
Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu Ser Ala Gly Ala Ser
               90               95               100

tta gag gct gtc tta atc tcc acc gca gat aaa ctg cat aat ctc atg 451
Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys Leu His Asn Leu Met
               105               110               115

tcc atc ttg gat gac ctt gaa ata cac ggt gaa gat tta tgg caa cgc 499
Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu Asp Leu Trp Gln Arg
               120               125               130

ttt aac gct ggc aaa gag cag caa atc tgg tgg tat agc gag gtt tat 547
Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp Tyr Ser Glu Val Tyr
               135               140               145

cag ata tct ctc cag cgc tta ggg ttc aat gag ttg aat aaa caa ctg 595
Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu Leu Asn Lys Gln Leu
               150               155               160               165

ggg ttg tgc gtc gaa aag ctc tta aag caa agc gcc taggcgctcg 641
Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser Ala
               170               175

gcggcgctcga taa 654

```

<210> 108

<211> 177

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 108

Met Asn Thr Ala Ala Trp Ala His Arg His His Val Arg Lys Gly Gly
 1 5 10 15

Gly Ile Pro Tyr Val Ser His Leu Tyr Ser Val Met Tyr Leu Leu Ala
 20 25 30

Ser Val Thr Asn Asp Glu Asp Val Leu Ile Ala Gly Leu Leu His Asp
 35 40 45

Thr Leu Glu Asp Val Pro Glu Glu Tyr Asn Ser Ala Gln Leu Glu Ala
 50 55 60

Asp Phe Gly Pro Arg Val Arg Glu Leu Val Glu Glu Leu Thr Lys Gln
 65 70 75 80

Pro Leu Lys Ser Trp Lys Ala Arg Ala Asp Ala Tyr Leu Leu His Leu
 85 90 95

Ser Ala Gly Ala Ser Leu Glu Ala Val Leu Ile Ser Thr Ala Asp Lys
 100 105 110

Leu His Asn Leu Met Ser Ile Leu Asp Asp Leu Glu Ile His Gly Glu
 115 120 125

Asp Leu Trp Gln Arg Phe Asn Ala Gly Lys Glu Gln Gln Ile Trp Trp
 130 135 140

Tyr Ser Glu Val Tyr Gln Ile Ser Leu Gln Arg Leu Gly Phe Asn Glu
 145 150 155 160

Leu Asn Lys Gln Leu Gly Leu Cys Val Glu Lys Leu Leu Lys Gln Ser
 165 170 175

Ala

<210> 109

<211> 1050

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1027)

<223> RXS02497

<400> 109

tcgatgccgc cgctggcgaa gactcgggga aacctaaaaa taccgaagaa gaatttgacc 60

gattcacact ttgccaccct agaccgtcta accttttaggt gtg aga tta ggt gta 115
 Val Arg Leu Gly Val
 1 5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163
 Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg
 10 15 20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211

Pro	Gly	Gly	His	Pro	Thr	Pro	Met	Ser	Asn	Trp	Arg	Thr	Pro	Leu	Arg	
			25					30					35			
ctt	gtt	gag	ctt	ctt	gat	gac	tcc	ggg	gcg	atc	tcc	gaa	aag	ggc	atc	259
Leu	Val	Glu	Leu	Leu	Asp	Asp	Ser	Gly	Ala	Ile	Ser	Glu	Lys	Gly	Ile	
		40					45					50				
aac	aaa	ctc	acc	tca	gca	gtc	ggg	gaa	gca	gca	gac	cta	gcg	aaa	acg	307
Asn	Lys	Leu	Thr	Ser	Ala	Val	Gly	Glu	Ala	Ala	Asp	Leu	Ala	Lys	Thr	
	55					60					65					
ctc	ggc	tgc	gct	gaa	ctg	atg	cca	ttt	gct	aca	tcg	gca	gtc	cgc	tcc	355
Leu	Gly	Cys	Ala	Glu	Leu	Met	Pro	Phe	Ala	Thr	Ser	Ala	Val	Arg	Ser	
70					75					80					85	
gcc	acc	aac	agc	gag	gca	gtg	ctc	gac	cac	gtg	gag	aag	gaa	acc	ggc	403
Ala	Thr	Asn	Ser	Glu	Ala	Val	Leu	Asp	His	Val	Glu	Lys	Glu	Thr	Gly	
				90					95					100		
gtc	cgc	ctg	tcc	atc	ctt	tcc	ggg	gaa	gac	gaa	gca	cgc	caa	act	ttc	451
Val	Arg	Leu	Ser	Ile	Leu	Ser	Gly	Glu	Asp	Glu	Ala	Arg	Gln	Thr	Phe	
			105					110					115			
ctc	gca	gtt	cga	cgt	tgg	tat	gga	tgg	tcc	gca	ggg	cgc	ata	act	aac	499
Leu	Ala	Val	Arg	Arg	Trp	Tyr	Gly	Trp	Ser	Ala	Gly	Arg	Ile	Thr	Asn	
		120					125					130				
ctc	gac	atc	ggg	ggc	ggc	tcc	ctg	gaa	cta	tcc	tcc	gga	acc	gac	gaa	547
Leu	Asp	Ile	Gly	Gly	Gly	Ser	Leu	Glu	Leu	Ser	Ser	Gly	Thr	Asp	Glu	
	135					140					145					
tcc	cca	gac	ctc	gcg	ttc	tca	ctg	gat	ctg	ggg	gcg	ggc	cgc	ttg	acc	595
Ser	Pro	Asp	Leu	Ala	Phe	Ser	Leu	Asp	Leu	Gly	Ala	Gly	Arg	Leu	Thr	
150					155					160					165	
cac	aac	tgg	ttc	gac	acc	gat	cca	ccg	gca	cgt	aag	aaa	atc	aac	ctc	643
His	Asn	Trp	Phe	Asp	Thr	Asp	Pro	Pro	Ala	Arg	Lys	Lys	Ile	Asn	Leu	
				170					175					180		
ctg	cgc	gat	tat	atc	gat	gcg	gaa	ctt	gca	gaa	ccc	gcc	cgc	cag	atg	691
Leu	Arg	Asp	Tyr	Ile	Asp	Ala	Glu	Leu	Ala	Glu	Pro	Ala	Arg	Gln	Met	
			185					190					195			
cgc	acc	cta	ggg	ccc	gcg	cgc	ctg	gca	gtg	gga	aca	tcc	aaa	act	ttc	739
Arg	Thr	Leu	Gly	Pro	Ala	Arg	Leu	Ala	Val	Gly	Thr	Ser	Lys	Thr	Phe	
		200					205					210				
cgc	acc	ctg	gca	cga	ctg	act	ggg	gct	gcg	ccc	tca	tcc	gca	gga	cca	787
Arg	Thr	Leu	Ala	Arg	Leu	Thr	Gly	Ala	Ala	Pro	Ser	Ser	Ala	Gly	Pro	
	215					220					225					
cac	gtc	acc	cga	acc	ctc	acc	gcg	ccg	ggg	ctg	cgc	cag	ctg	atc	gca	835
His	Val	Thr	Arg	Thr	Leu	Thr	Ala	Pro	Gly	Leu	Arg	Gln	Leu	Ile	Ala	
230					235					240					245	
ttt	atc	tca	cga	atg	act	gcg	gcg	gac	cgc	gct	gag	ctg	gaa	ggg	atc	883
Phe	Ile	Ser	Arg	Met	Thr	Ala	Ala	Asp	Arg	Ala	Glu	Leu	Glu	Gly	Ile	
				250					255					260		
agc	tcg	gat	cgg	tca	cat	cag	atc	gtg	gca	ggg	gcg	cta	gtt	gcg	gaa	931
Ser	Ser	Asp	Arg	Ser	His	Gln	Ile	Val	Ala	Gly	Ala	Leu	Val	Ala	Glu	

265	270	275	
gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg			979
Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp			
280	285	290	
gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag			1027
Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu			
295	300	305	
taacattttac ccggaaagga gtt			1050

<210> 110
 <211> 309
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 110
 Val Arg Leu Gly Val Leu Asp Val Gly Ser Asn Thr Val His Leu Val
 1 5 10 15
 Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp
 20 25 30
 Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
 35 40 45
 Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
 50 55 60
 Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
 65 70 75 80
 Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
 85 90 95
 Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
 100 105 110
 Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
 115 120 125
 Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
 130 135 140
 Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
 145 150 155 160
 Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
 165 170 175
 Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
 180 185 190
 Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
 195 200 205
 Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
 210 215 220

Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
 225 230 235 240

Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
 245 250 255

Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
 260 265 270

Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
 275 280 285

Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile
 290 295 300

Asp Lys Gly Leu Glu
 305

<210> 111
 <211> 534
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(511)
 <223> RXS02972

<400> 111
 acctacgacg gtgaaatcct aggctccac tcaacccaaa tgggatgcgt ggcctgacc 60

gaacgaatca tgcgcagcga cccacccgac tgaaaccgaa gtg gaa atc gcc cgc 115
 Val Glu Ile Ala Arg
 1 5

gac tac gtt gca gaa cgc atc cag gaa gta aaa gcc atc gtc cca att 163
 Asp Tyr Val Ala Glu Arg Ile Gln Glu Val Lys Ala Ile Val Pro Ile
 10 15 20

tca aag gca aaa acc ttt gtg gga tgc gca ggc acc ttc acc aca atc 211
 Ser Lys Ala Lys Thr Phe Val Gly Cys Ala Gly Thr Phe Thr Thr Ile
 25 30 35

tcc gcc tgg gtg caa ggc cta gaa agc tac gac cgc gac gcg atc cac 259
 Ser Ala Trp Val Gln Gly Leu Glu Ser Tyr Asp Arg Asp Ala Ile His
 40 45 50

ctc tct gca ctc aac ttc gat gca ctg cga gtt gtc acc gat gag atc 307
 Leu Ser Ala Leu Asn Phe Asp Ala Leu Arg Val Val Thr Asp Glu Ile
 55 60 65

att tca gaa tca tca tca cag cgc gcc agc aac cca gtt gtt gat cca 355
 Ile Ser Glu Ser Ser Ser Gln Arg Ala Ser Asn Pro Val Val Asp Pro
 70 75 80 85

ggg cgc gcc gac gtc atc ggt ggc gga tcc gtt gtt gtc caa gca gcg 403
 Gly Arg Ala Asp Val Ile Gly Gly Gly Ser Val Val Val Gln Ala Ala
 90 95 100

atc gac tta gcc tcc aaa gaa gcc ggt gta gac tac atc att att tcc 451

```

<400> 113
tgatggacca gcgtccaaag ttttcgatga agcagaaaac cgcctccacg ctcagaaagc 60

actgctgggtg tggctgctgg ccaaccagcc gaggtaagac atg tcc ctt ggc tca 115
               Met Ser Leu Gly Ser

```

	1	5	
acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc			163
Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg Thr Ala Arg			
	10	20	
caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc acc agc cag			211
Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val Thr Ser Gln			
	25	35	
gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag			259
Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp Ile Thr Gln			
	40	50	
gcc acc ttg tcc cga gat ctc gat gaa ctc ggt gca cgc aag gtt cgc			307
Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg Lys Val Arg			
	55	65	
ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc			355
Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Pro Val Asp Ser Ile			
	70	80	85
gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc cgc atg ctt			403
Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg Arg Met Leu			
	90	95	100
gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg			451
Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile Ala Met Leu			
	105	110	115
cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc atc gat agg			499
Arg Thr Pro Pro Gly Ala Ala Tyr Leu Ala Ser Phe Ile Asp Arg			
	120	125	130
gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt			547
Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp Asp Thr Val			
	135	140	145
ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta			595
Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu Gly Glu Leu			
	150	155	160
ctc agc ggg cgc acc act taaagcgccc ctagttcaag gct			636
Leu Ser Gly Arg Thr Thr			
	170		

<210> 114

<211> 171

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 114

Met	Ser	Leu	Gly	Ser	Thr	Pro	Ser	Thr	Pro	Glu	Asn	Leu	Asn	Pro	Val
1				5					10					15	

Thr	Arg	Thr	Ala	Arg	Gln	Ala	Leu	Ile	Leu	Gln	Ile	Leu	Asp	Lys	Gln
			20					25					30		

Lys	Val	Thr	Ser	Gln	Val	Gln	Leu	Ser	Glu	Leu	Leu	Leu	Asp	Glu	Gly
			35				40					45			

Ile Asp Ile Thr Gln Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly
 50 55 60
 Ala Arg Lys Val Arg Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly
 65 70 75 80
 Pro Val Asp Ser Ile Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys
 85 90 95
 Leu Arg Arg Met Leu Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly
 100 105 110
 Asn Ile Ala Met Leu Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala
 115 120 125
 Ser Phe Ile Asp Arg Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala
 130 135 140
 Gly Asp Asp Thr Val Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys
 145 150 155 160
 Glu Leu Gly Glu Leu Leu Ser Gly Arg Thr Thr
 165 170

<210> 115
 <211> 486
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(463)
 <223> RXA02201

<400> 115
 tctaccagcc aaatcatcaa ctcatagcga aggaatcaac ttcatgaata atcaaccatc 60
 agtacttttgc gtttgcgtcg gcaatggtgg aaaatctcaa atg gcc gca gcg cta 115
 Met Ala Ala Ala Leu 5
 gcc aaa aaa cat gcc ggg gac gct ctc aaa gtt tat tca gct ggc aca 163
 Ala Lys Lys His Ala Gly Asp Ala Leu Lys Val Tyr Ser Ala Gly Thr 20
 10 15
 aag cca ggt acg aaa tta aat caa cag tcc ctt gat tcc att gct gaa 211
 Lys Pro Gly Thr Lys Leu Asn Gln Gln Ser Leu Asp Ser Ile Ala Glu 35
 25 30
 gtt ggc gca gat atg tct caa ggg ttt cca aag ggc att gac cag gag 259
 Val Gly Ala Asp Met Ser Gln Gly Phe Pro Lys Gly Ile Asp Gln Glu 50
 40 45
 tta att aag cga gta gac cgc gtg gtc att ctt ggt gcc gaa gct caa 307
 Leu Ile Lys Arg Val Asp Arg Val Val Ile Leu Gly Ala Glu Ala Gln 65
 55 60
 cta gaa atg cct atc gat gca aac ggc ata cta cag cgc tgg gta act 355
 Leu Glu Met Pro Ile Asp Ala Asn Gly Ile Leu Gln Arg Trp Val Thr

```

70              75              80              85
gac gaa ccc tct gaa cgt gga att gaa ggt atg gaa cgc atg cgc ctg 403
Asp Glu Pro Ser Glu Arg Gly Ile Glu Gly Met Glu Arg Met Arg Leu
              90              95              100

gtc cga gat gat att gac gcc cga gtc caa aac ctc gtc gct gaa cta 451
Val Arg Asp Asp Ile Asp Ala Arg Val Gln Asn Leu Val Ala Glu Leu
              105              110              115

acc caa aac gca tagcagtttt ctaatctcac aca 486
Thr Gln Asn Ala
              120

```

<210> 116
 <211> 121
 <212> PRT
 <213> Corynebacterium glutamicum

```

<400> 116
Met Ala Ala Ala Leu Ala Lys Lys His Ala Gly Asp Ala Leu Lys Val
  1              5              10              15

Tyr Ser Ala Gly Thr Lys Pro Gly Thr Lys Leu Asn Gln Gln Ser Leu
              20              25              30

Asp Ser Ile Ala Glu Val Gly Ala Asp Met Ser Gln Gly Phe Pro Lys
              35              40              45

Gly Ile Asp Gln Glu Leu Ile Lys Arg Val Asp Arg Val Val Ile Leu
              50              55              60

Gly Ala Glu Ala Gln Leu Glu Met Pro Ile Asp Ala Asn Gly Ile Leu
              65              70              75              80

Gln Arg Trp Val Thr Asp Glu Pro Ser Glu Arg Gly Ile Glu Gly Met
              85              90              95

Glu Arg Met Arg Leu Val Arg Asp Asp Ile Asp Ala Arg Val Gln Asn
              100              105              110

Leu Val Ala Glu Leu Thr Gln Asn Ala
              115              120

```

<210> 117
 <211> 510
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(487)
 <223> RXA00599

```

<400> 117
gaacgatcgg ccctttgatt gaagtcccag tattagtcgg attggtttat gtcattgtgt 60

ggcttggacc aaaaatcttt aaaaaggaga atgcaggatc atg aaa tca gtt ttg 115
              Met Lys Ser Val Leu

```


	1	5	
ttt gtg tgc gtc ggt aat ggc gga aaa tca cag atg gcg gcg gcg ctg			163
Phe Val Cys Val Gly Asn Gly Gly Lys Ser Gln Met Ala Ala Ala Leu	10	15	20
gca cag aag tat gca tca gat tca gta gag atc cat tct gct gga acc			211
Ala Gln Lys Tyr Ala Ser Asp Ser Val Glu Ile His Ser Ala Gly Thr	25	30	35
aag cct gca cag ggg cta aac caa ttg tct gtg gaa tcc atc gct gag			259
Lys Pro Ala Gln Gly Leu Asn Gln Leu Ser Val Glu Ser Ile Ala Glu	40	45	50
gtg ggc gct gat atg tcg caa gga att ccc aaa gcg atc gat ccg gag			307
Val Gly Ala Asp Met Ser Gln Gly Ile Pro Lys Ala Ile Asp Pro Glu	55	60	65
ctg ctg cgc act gtc gat cgt gtg gtt att ttg ggc gat gac gca cag			355
Leu Leu Arg Thr Val Asp Arg Val Val Ile Leu Gly Asp Asp Ala Gln	70	75	80
gta gat atg cct gaa tct gca cag ggc gct ctt gag cgt tgg tca att			403
Val Asp Met Pro Glu Ser Ala Gln Gly Ala Leu Glu Arg Trp Ser Ile	90	95	100
gag gaa ccg gat gct caa ggt atg gaa cgt atg cgt att gtg cgg gat			451
Glu Glu Pro Asp Ala Gln Gly Met Glu Arg Met Arg Ile Val Arg Asp	105	110	115
cag atc gat aac cga gtc caa gct ttg cta gcg gga taagcgccga			497
Gln Ile Asp Asn Arg Val Gln Ala Leu Leu Ala Gly	120	125	
aaaaggggca tgt			510

<210> 118

<211> 129

<212> PRT

<213> Corynebacterium glutamicum

<400> 118

Met Lys Ser Val Leu Phe Val Cys Val Gly Asn Gly Gly Lys Ser Gln	1	5	10	15
Met Ala Ala Ala Leu Ala Gln Lys Tyr Ala Ser Asp Ser Val Glu Ile	20	25	30	
His Ser Ala Gly Thr Lys Pro Ala Gln Gly Leu Asn Gln Leu Ser Val	35	40	45	
Glu Ser Ile Ala Glu Val Gly Ala Asp Met Ser Gln Gly Ile Pro Lys	50	55	60	
Ala Ile Asp Pro Glu Leu Leu Arg Thr Val Asp Arg Val Val Ile Leu	65	70	75	80
Gly Asp Asp Ala Gln Val Asp Met Pro Glu Ser Ala Gln Gly Ala Leu	85	90	95	

Glu Arg Trp Ser Ile Glu Glu Pro Asp Ala Gln Gly Met Glu Arg Met
 100 105 110

Arg Ile Val Arg Asp Gln Ile Asp Asn Arg Val Gln Ala Leu Leu Ala
 115 120 125

Gly

<210> 119

<211> 1221

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1198)

<223> RXA00600

<400> 119

cggagttaat gagcggtagg tggatgggtg cggatcatgtc cgtcattata tattgacgca 60
 catcgatatt gaaggtatatt ttatatcggc aaacatcaat atg att gaa ggc tgg 115
 Met Ile Glu Gly Trp
 1 5

ctc atg acc ctt act aaa gag cat tcg aca cct cga gcg gct ggc tca 163
 Leu Met Thr Leu Thr Lys Glu His Ser Thr Pro Arg Ala Ala Gly Ser
 10 15 20

atg tcg ttt ctt gac cgc tgg tta gct gcc tgg att ttc ttg gct atg 211
 Met Ser Phe Leu Asp Arg Trp Leu Ala Ala Trp Ile Phe Leu Ala Met
 25 30 35

gct gct ggg ttg tta atc ggc aag gtc ttt cca gga att ggg gcg ctt 259
 Ala Ala Gly Leu Leu Ile Gly Lys Val Phe Pro Gly Ile Gly Ala Leu
 40 45 50

ttg agc gcg gtg gaa att ggt gga att tcc att cca att gct atc ggt 307
 Leu Ser Ala Val Glu Ile Gly Gly Ile Ser Ile Pro Ile Ala Ile Gly
 55 60 65

ttg atc gtc atg atg tat cca cct ttg gcc aag gtg cgc tac gac aaa 355
 Leu Ile Val Met Met Tyr Pro Pro Leu Ala Lys Val Arg Tyr Asp Lys
 70 75 80 85

act aaa gaa atc agc aca gac cgc gct ctc atg gtg gtg tcg att atg 403
 Thr Lys Glu Ile Ser Thr Asp Arg Ala Leu Met Val Val Ser Ile Met
 90 95 100

ttg aac tgg atc gtt gga cca gca ctt atg ttt agc ctg gcg tgg ctg 451
 Leu Asn Trp Ile Val Gly Pro Ala Leu Met Phe Ser Leu Ala Trp Leu
 105 110 115

ttt ctt cca gat caa cca gag ctt cgc act ggg cta att atc gtg ggc 499
 Phe Leu Pro Asp Gln Pro Glu Leu Arg Thr Gly Leu Ile Ile Val Gly
 120 125 130

ctt gcg cgc tgt atc gcg atg gtt ttg gta tgg agt gat ctc gct tgt 547
 Leu Ala Arg Cys Ile Ala Met Val Leu Val Trp Ser Asp Leu Ala Cys

135	140	145	
ggt gac cgg gaa gca act gct gtg ctg gtt gca atc aac tcg gtg ttc Gly Asp Arg Glu Ala Thr Ala Val Leu Val Ala Ile Asn Ser Val Phe 150 155 160 165			595
cag atc ctt atg ttc ggt gtg ctt ggt tgg ttt tac ctg cag att ctt Gln Ile Leu Met Phe Gly Val Leu Gly Trp Phe Tyr Leu Gln Ile Leu 170 175 180			643
ccc tcg tgg ctg gga tta gac acc acg tcg gtg act ttc tct gtg gta Pro Ser Trp Leu Gly Leu Asp Thr Thr Ser Val Thr Phe Ser Val Val 185 190 195			691
tca atc gtg act tcc gtt ctc gtg ttc ttg ggc ata cca ctt gta gct Ser Ile Val Thr Ser Val Leu Val Phe Leu Gly Ile Pro Leu Val Ala 200 205 210			739
gga gtt tta tct cgc gtc att ggt gaa aaa aca aag gga cgg cgc tgg Gly Val Leu Ser Arg Val Ile Gly Glu Lys Thr Lys Gly Arg Arg Trp 215 220 225			787
tac gag gac acg ttc ctg cct aag att tca ccc ttg gcg ctg att ggc Tyr Glu Asp Thr Phe Leu Pro Lys Ile Ser Pro Leu Ala Leu Ile Gly 230 235 240 245			835
ttg cta tac aca att gtt ctg ctg ttt tcg ttg cag ggg gat gaa atc Leu Leu Tyr Thr Ile Val Leu Leu Phe Ser Leu Gln Gly Asp Glu Ile 250 255 260			883
aca gcg cag cct tgg aca gta gct cgt ctt gca ttg ccg ctg ctg atg Thr Ala Gln Pro Trp Thr Val Ala Arg Leu Ala Leu Pro Leu Leu Met 265 270 275			931
tac ttt gtg ggc atg ttt ttc att tcc ctg gtg gta tcc aaa ctg tcc Tyr Phe Val Gly Met Phe Phe Ile Ser Leu Val Val Ser Lys Leu Ser 280 285 290			979
ggg tta act tat gag cga gct gct tcc gtg tct ttt act gca gca gga Gly Leu Thr Tyr Glu Arg Ala Ala Ser Val Ser Phe Thr Ala Ala Gly 295 300 305			1027
aac aac ttt gaa tta gcg att gcg gta tcg atc gga acc ttt ggt gcg Asn Asn Phe Glu Leu Ala Ile Ala Val Ser Ile Gly Thr Phe Gly Ala 310 315 320 325			1075
aca tca ccg cag gca tta gct gga acg atc ggc cct ttg att gaa gtc Thr Ser Pro Gln Ala Leu Ala Gly Thr Ile Gly Pro Leu Ile Glu Val 330 335 340			1123
cca gta tta gtc gga ttg gtt tat gtc atg ttg tgg ctt gga cca aaa Pro Val Leu Val Gly Leu Val Tyr Val Met Leu Trp Leu Gly Pro Lys 345 350 355			1171
atc ttt aaa aag gag aat gca gga tca tgaaatcagt tttgtttgtg Ile Phe Lys Lys Glu Asn Ala Gly Ser 360 365			1218
tgc			1221

<210> 120

<211> 366

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 120

```

Met Ile Glu Gly Trp Leu Met Thr Leu Thr Lys Glu His Ser Thr Pro
  1           5           10           15

Arg Ala Ala Gly Ser Met Ser Phe Leu Asp Arg Trp Leu Ala Ala Trp
          20           25           30

Ile Phe Leu Ala Met Ala Ala Gly Leu Leu Ile Gly Lys Val Phe Pro
          35           40           45

Gly Ile Gly Ala Leu Leu Ser Ala Val Glu Ile Gly Gly Ile Ser Ile
          50           55           60

Pro Ile Ala Ile Gly Leu Ile Val Met Met Tyr Pro Pro Leu Ala Lys
          65           70           75           80

Val Arg Tyr Asp Lys Thr Lys Glu Ile Ser Thr Asp Arg Ala Leu Met
          85           90           95

Val Val Ser Ile Met Leu Asn Trp Ile Val Gly Pro Ala Leu Met Phe
          100          105          110

Ser Leu Ala Trp Leu Phe Leu Pro Asp Gln Pro Glu Leu Arg Thr Gly
          115          120          125

Leu Ile Ile Val Gly Leu Ala Arg Cys Ile Ala Met Val Leu Val Trp
          130          135          140

Ser Asp Leu Ala Cys Gly Asp Arg Glu Ala Thr Ala Val Leu Val Ala
          145          150          155          160

Ile Asn Ser Val Phe Gln Ile Leu Met Phe Gly Val Leu Gly Trp Phe
          165          170          175

Tyr Leu Gln Ile Leu Pro Ser Trp Leu Gly Leu Asp Thr Thr Ser Val
          180          185          190

Thr Phe Ser Val Val Ser Ile Val Thr Ser Val Leu Val Phe Leu Gly
          195          200          205

Ile Pro Leu Val Ala Gly Val Leu Ser Arg Val Ile Gly Glu Lys Thr
          210          215          220

Lys Gly Arg Arg Trp Tyr Glu Asp Thr Phe Leu Pro Lys Ile Ser Pro
          225          230          235          240

Leu Ala Leu Ile Gly Leu Leu Tyr Thr Ile Val Leu Leu Phe Ser Leu
          245          250          255

Gln Gly Asp Glu Ile Thr Ala Gln Pro Trp Thr Val Ala Arg Leu Ala
          260          265          270

Leu Pro Leu Leu Met Tyr Phe Val Gly Met Phe Phe Ile Ser Leu Val
          275          280          285

Val Ser Lys Leu Ser Gly Leu Thr Tyr Glu Arg Ala Ala Ser Val Ser

```

290	295	300
Phe Thr Ala Ala Gly	Asn Asn Phe Glu Leu	Ala Ile Ala Val Ser Ile
305	310	315 320
Gly Thr Phe Gly Ala Thr Ser Pro Gln	Ala Leu Ala Gly Thr Ile Gly	
	325 330	335
Pro Leu Ile Glu Val Pro Val Leu Val Gly Leu Val Tyr Val Met Leu		
	340 345	350
Trp Leu Gly Pro Lys Ile Phe Lys Lys Glu Asn Ala Gly Ser		
	355 360	365

<210> 121
 <211> 1233
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1210)
 <223> RXA02200

<400> 121
 attgtgtgga gagtgggtcat aaatccacta tatattgacg aatgtcgata ttgaaagtat 60

tttgaatatc gacaggtatc aatataccga aagggtgtcgc atg aca aac tca act 115
 Met Thr Asn Ser Thr
 1 5

cag acg cgg gcc aag cca gcc cga atc tca ttt ctt gat aaa tac att 163
 Gln Thr Arg Ala Lys Pro Ala Arg Ile Ser Phe Leu Asp Lys Tyr Ile
 10 15 20

cca ctt tgg att att ttg gcg atg gcg ttt ggg cta ttt tta ggc cgg 211
 Pro Leu Trp Ile Ile Leu Ala Met Ala Phe Gly Leu Phe Leu Gly Arg
 25 30 35

agc gtt tgc gga ctc tca ggc ttt cta ggc gca atg gaa gtc gga ggg 259
 Ser Val Ser Gly Leu Ser Gly Phe Leu Gly Ala Met Glu Val Gly Gly
 40 45 50

atc tcc ttg cca atc gct tta ggc ctc ctt gta atg atg tac cca ccg 307
 Ile Ser Leu Pro Ile Ala Leu Gly Leu Leu Val Met Met Tyr Pro Pro
 55 60 65

ttg gcc aaa gtt cgg tat gac aaa act aaa caa att gcc act gat aag 355
 Leu Ala Lys Val Arg Tyr Asp Lys Thr Lys Gln Ile Ala Thr Asp Lys
 70 75 80 85

cat ttg atg ggc gtg tca ctc att ctc aat tgg gtg gtg ggt cct gcc 403
 His Leu Met Gly Val Ser Leu Ile Leu Asn Trp Val Val Gly Pro Ala
 90 95 100

tta atg ttc gcg cta gct tgg ttg ttc ctc cca gac caa ccg gaa tta 451
 Leu Met Phe Ala Leu Ala Trp Leu Phe Leu Pro Asp Gln Pro Glu Leu
 105 110 115

cga acc ggc ctg att att gta gga ctc gca cga tgt att gcg atg gtc 499

Arg	Thr	Gly	Leu	Ile	Ile	Val	Gly	Leu	Ala	Arg	Cys	Ile	Ala	Met	Val	
		120					125					130				
ttg	gtt	tgg	tct	gat	atg	tcc	tgt	gga	gac	cgc	gag	gct	aca	gca	gtt	547
Leu	Val	Trp	Ser	Asp	Met	Ser	Cys	Gly	Asp	Arg	Glu	Ala	Thr	Ala	Val	
	135					140					145					
ctc	gta	gcc	att	aat	tca	gtt	ttt	caa	gtc	gca	atg	ttt	ggt	gca	ctt	595
Leu	Val	Ala	Ile	Asn	Ser	Val	Phe	Gln	Val	Ala	Met	Phe	Gly	Ala	Leu	
150					155					160					165	
ggc	tgg	ttc	tat	ctg	caa	gtt	tta	cca	tcc	tgg	cta	gga	tta	cca	act	643
Gly	Trp	Phe	Tyr	Leu	Gln	Val	Leu	Pro	Ser	Trp	Leu	Gly	Leu	Pro	Thr	
				170					175					180		
acc	acc	gct	caa	ttc	tct	ttc	tgg	tca	att	gtg	act	tcg	gtt	ttg	gtg	691
Thr	Thr	Ala	Gln	Phe	Ser	Phe	Trp	Ser	Ile	Val	Thr	Ser	Val	Leu	Val	
			185						190				195			
ttc	ctc	gga	ata	cct	cta	ctt	gct	gga	gtt	ttc	tcg	cga	att	att	ggc	739
Phe	Leu	Gly	Ile	Pro	Leu	Leu	Ala	Gly	Val	Phe	Ser	Arg	Ile	Ile	Gly	
	200						205					210				
gaa	aag	atc	aag	gga	cgt	gag	tgg	tat	gaa	caa	aag	ttc	ctt	ccg	gca	787
Glu	Lys	Ile	Lys	Gly	Arg	Glu	Trp	Tyr	Glu	Gln	Lys	Phe	Leu	Pro	Ala	
	215					220					225					
atc	tct	cca	ttt	gca	cta	atc	ggc	ctg	ctt	tat	acg	atc	gtc	ttg	ttg	835
Ile	Ser	Pro	Phe	Ala	Leu	Ile	Gly	Leu	Leu	Tyr	Thr	Ile	Val	Leu	Leu	
230					235					240					245	
ttt	tca	ttg	caa	ggc	gat	cag	atc	gtc	tct	caa	cca	tgg	gct	gta	gtt	883
Phe	Ser	Leu	Gln	Gly	Asp	Gln	Ile	Val	Ser	Gln	Pro	Trp	Ala	Val	Val	
			250					255						260		
cgt	ctc	gcg	ata	cca	ttg	gtt	atc	tat	ttc	gtt	gga	atg	ttt	ttc	att	931
Arg	Leu	Ala	Ile	Pro	Leu	Val	Ile	Tyr	Phe	Val	Gly	Met	Phe	Phe	Ile	
			265					270					275			
tca	ctc	att	gcg	tca	aaa	cta	tct	ggc	atg	aac	tat	gca	aag	tct	gca	979
Ser	Leu	Ile	Ala	Ser	Lys	Leu	Ser	Gly	Met	Asn	Tyr	Ala	Lys	Ser	Ala	
		280					285					290				
tcc	gtc	tct	ttc	act	gca	gct	ggc	aac	aat	ttt	gaa	ctt	gcg	att	gcg	1027
Ser	Val	Ser	Phe	Thr	Ala	Ala	Gly	Asn	Asn	Phe	Glu	Leu	Ala	Ile	Ala	
	295					300					305					
gtg	tcg	atc	gga	acg	ttt	ggc	gca	act	tct	gca	cag	gct	atg	gca	gga	1075
Val	Ser	Ile	Gly	Thr	Phe	Gly	Ala	Thr	Ser	Ala	Gln	Ala	Met	Ala	Gly	
310					315					320					325	
acg	att	ggc	ccc	ttg	att	gaa	att	cca	gta	ctt	gtc	ggc	ttg	gtc	tac	1123
Thr	Ile	Gly	Pro	Leu	Ile	Glu	Ile	Pro	Val	Leu	Val	Gly	Leu	Val	Tyr	
			330						335					340		
gcc	atg	ctg	tgg	cta	ggc	ccc	aag	ttg	ttc	cca	aat	gac	ccc	acg	ctg	1171
Ala	Met	Leu	Trp	Leu	Gly	Pro	Lys	Leu	Phe	Pro	Asn	Asp	Pro	Thr	Leu	
		345						350					355			
cca	tca	tca	gct	cgt	tct	acc	agc	caa	atc	atc	aac	tca	tagcgaagga			1220
Pro	Ser	Ser	Ala	Arg	Ser	Thr	Ser	Gln	Ile	Ile	Asn	Ser				

360

365

370

atcaacttca tga

1233

<210> 122

<211> 370

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 122

Met Thr Asn Ser Thr Gln Thr Arg Ala Lys Pro Ala Arg Ile Ser Phe
 1 5 10 15

Leu Asp Lys Tyr Ile Pro Leu Trp Ile Ile Leu Ala Met Ala Phe Gly
 20 25 30

Leu Phe Leu Gly Arg Ser Val Ser Gly Leu Ser Gly Phe Leu Gly Ala
 35 40 45

Met Glu Val Gly Gly Ile Ser Leu Pro Ile Ala Leu Gly Leu Leu Val
 50 55 60

Met Met Tyr Pro Pro Leu Ala Lys Val Arg Tyr Asp Lys Thr Lys Gln
 65 70 75 80

Ile Ala Thr Asp Lys His Leu Met Gly Val Ser Leu Ile Leu Asn Trp
 85 90 95

Val Val Gly Pro Ala Leu Met Phe Ala Leu Ala Trp Leu Phe Leu Pro
 100 105 110

Asp Gln Pro Glu Leu Arg Thr Gly Leu Ile Ile Val Gly Leu Ala Arg
 115 120 125

Cys Ile Ala Met Val Leu Val Trp Ser Asp Met Ser Cys Gly Asp Arg
 130 135 140

Glu Ala Thr Ala Val Leu Val Ala Ile Asn Ser Val Phe Gln Val Ala
 145 150 155 160

Met Phe Gly Ala Leu Gly Trp Phe Tyr Leu Gln Val Leu Pro Ser Trp
 165 170 175

Leu Gly Leu Pro Thr Thr Thr Ala Gln Phe Ser Phe Trp Ser Ile Val
 180 185 190

Thr Ser Val Leu Val Phe Leu Gly Ile Pro Leu Leu Ala Gly Val Phe
 195 200 205

Ser Arg Ile Ile Gly Glu Lys Ile Lys Gly Arg Glu Trp Tyr Glu Gln
 210 215 220

Lys Phe Leu Pro Ala Ile Ser Pro Phe Ala Leu Ile Gly Leu Leu Tyr
 225 230 235 240

Thr Ile Val Leu Leu Phe Ser Leu Gln Gly Asp Gln Ile Val Ser Gln
 245 250 255

Pro Trp Ala Val Val Arg Leu Ala Ile Pro Leu Val Ile Tyr Phe Val
 260 265 270

<400> 123															
cgctgaacta acccaaaacg catagcagtt ttctaattctc acacatcttc aacaccgtta															60
aatctattgg tttccccgta aaatcttcga aaggaagaac															
Met Thr Gly Gln Ala															115
1 5															
gca cca aac ttg cat acc aat att ttg aac cgt atc gca aat gaa ctg															163
Ala Pro Asn Leu His Thr Asn Ile Leu Asn Arg Ile Ala Asn Glu Leu															
10 15 20															
gcg ttg acc tat caa gga gtt ttc tct gca gag act atc aac cgc tat															211
Ala Leu Thr Tyr Gln Gly Val Phe Ser Ala Glu Thr Ile Asn Arg Tyr															
25 30 35															
att ttt gaa tcg tat gtg tcg ttg gcg aga aca gca aaa atc cat acg															259
Ile Phe Glu Ser Tyr Val Ser Leu Ala Arg Thr Ala Lys Ile His Thr															
40 45 50															
cac ctg cca att ttg gca gaa ggt ttt gct aaa gac cgg ctg cac gca															307
His Leu Pro Ile Leu Ala Glu Gly Phe Ala Lys Asp Arg Leu His Ala															
55 60 65															
ctt gcg gta gct gaa ggt aag gtg gct tca cct gtg cct cag gtc cta															355
Leu Ala Val Ala Glu Gly Lys Val Ala Ser Pro Val Pro Gln Val Leu															
70 75 80 85															
ttt att tgc gtc cac aac gca ggt cgt tca caa att gct tcg gcg ttg															403


```
<210> 124
<211> 213
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 124																
Met	Thr	Gly	Gln	Ala	Ala	Pro	Asn	Leu	His	Thr	Asn	Ile	Leu	Asn	Arg	
1				5					10					15		
Ile	Ala	Asn	Glu	Leu	Ala	Leu	Thr	Tyr	Gln	Gly	Val	Phe	Ser	Ala	Glu	
			20					25					30			
Thr	Ile	Asn	Arg	Tyr	Ile	Phe	Glu	Ser	Tyr	Val	Ser	Leu	Ala	Arg	Thr	
		35					40					45				
Ala	Lys	Ile	His	Thr	His	Leu	Pro	Ile	Leu	Ala	Glu	Gly	Phe	Ala	Lys	
	50					55					60					
Asp	Arg	Leu	His	Ala	Leu	Ala	Val	Ala	Glu	Gly	Lys	Val	Ala	Ser	Pro	
65					70					75					80	
Val	Pro	Gln	Val	Leu	Phe	Ile	Cys	Val	His	Asn	Ala	Gly	Arg	Ser	Gln	
				85					90					95		
Ile	Ala	Ser	Ala	Leu	Leu	Ser	His	Tyr	Ala	Gly	Ser	Ser	Val	Glu	Val	
			100					105					110			

Arg Ser Ala Gly Ser Leu Pro Ala Ser Glu Ile His Pro Leu Val Leu
 115 120 125

Glu Ile Leu Ser Glu Arg Gly Val Asn Ile Ser Asp Ala Phe Pro Lys
 130 135 140

Pro Leu Thr Asp Asp Val Ile Arg Ala Ser Asp Tyr Val Ile Thr Met
 145 150 155 160

Gly Cys Gly Asp Val Cys Pro Met Tyr Pro Gly Lys His Tyr Leu Asp
 165 170 175

Trp Glu Leu Ala Asp Pro Ser Asp Glu Gly Glu Asp Lys Ile Gln Glu
 180 185 190

Ile Ile Glu Glu Ile Asp Gly Arg Ile Arg Glu Leu Trp Lys Ser Ile
 195 200 205

Gln Leu Ser Gln Asn
 210

<210> 125

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(979)

<223> RXA02205

<400> 125

gccccaaaccg agcctggata cccgcaaacc acttgaaccg accattcgct gtttcacgcc 60

caccacacta ctgaggtcat aaggtagtagc ggtagatcgg gtg aat gaa gag ata 115
 Val Asn Glu Glu Ile
 1 5

acc ctc cta gcc gca gca gca gat cct gcc gca act gaa aat att ggc 163
 Thr Leu Leu Ala Ala Ala Ala Asp Pro Ala Ala Thr Glu Asn Ile Gly
 10 15 20

tgg gta caa acc att gtg ctc tcc atc gtt caa ggc ctc aca gag ttc 211
 Trp Val Gln Thr Ile Val Leu Ser Ile Val Gln Gly Leu Thr Glu Phe
 25 30 35

ctg ccg atc agc tcc agc gga cac ctc cga atc atc tct gag ctg ttc 259
 Leu Pro Ile Ser Ser Ser Gly His Leu Arg Ile Ile Ser Glu Leu Phe
 40 45 50

tgg ggt gcc gat gcc ggc gcg tcc ttt acc gcc gtg gtt cag ctt ggt 307
 Trp Gly Ala Asp Ala Gly Ala Ser Phe Thr Ala Val Val Gln Leu Gly
 55 60 65

acc gaa gcc gca gtg ctg gtg ttt ttt gcc aag gaa atc tgg caa atc 355
 Thr Glu Ala Ala Val Leu Val Phe Phe Ala Lys Glu Ile Trp Gln Ile
 70 75 80 85

atc aca ggt tgg ttc gct ggc gta ttc aat aag gaa cgc cgc gga ttt 403
 Ile Thr Gly Trp Phe Ala Gly Val Phe Asn Lys Glu Arg Arg Gly Phe

	90	95	100	
gaa tac cgc atg ggc tgg atg atc att gtt gcc acc att ccc gtc gtg				451
Glu Tyr Arg Met Gly Trp Met Ile Ile Val Ala Thr Ile Pro Val Val				
	105	110	115	
atc ttg ggt gtg ttg ggc aag gac ctg atc cgt gag gcg ctg cga aat				499
Ile Leu Gly Val Leu Gly Lys Asp Leu Ile Arg Glu Ala Leu Arg Asn				
	120	125	130	
atg tgg atc act gca tcc gtg ctg atc ctg ttc tcc ctg gtg ttc att				547
Met Trp Ile Thr Ala Ser Val Leu Ile Leu Phe Ser Leu Val Phe Ile				
	135	140	145	
ttg gcc gag aag atg ggc aag aag gaa cgc gac tac gac aaa ctg acc				595
Leu Ala Glu Lys Met Gly Lys Lys Glu Arg Asp Tyr Asp Lys Leu Thr				
	150	155	160	165
atg aaa gat gcc atc atc atg ggt ctt gca cag tgt ctt gcg ctg atc				643
Met Lys Asp Ala Ile Ile Met Gly Leu Ala Gln Cys Leu Ala Leu Ile				
	170	175	180	
cct ggc gtg tct cgc tcc ggc ggc acc atc tct gct ggt ttg ttc ctt				691
Pro Gly Val Ser Arg Ser Gly Gly Thr Ile Ser Ala Gly Leu Phe Leu				
	185	190	195	
ggt ctc aag cgt gaa gta gcc acc aag ttc tcc ttc ctg ctg gca atc				739
Gly Leu Lys Arg Glu Val Ala Thr Lys Phe Ser Phe Leu Leu Ala Ile				
	200	205	210	
cct gca gtg ctt ggc tcc ggt ttg tac tcc ctg cct gac gct ttt gcg				787
Pro Ala Val Leu Gly Ser Gly Leu Tyr Ser Leu Pro Asp Ala Phe Ala				
	215	220	225	
cca agc tcc gga caa gct gcc tcc ggc cta cag ctc acc gtg ggt acc				835
Pro Ser Ser Gly Gln Ala Ala Ser Gly Leu Gln Leu Thr Val Gly Thr				
	230	235	240	245
ctg gtt gcc ttc gta gtt ggc tac att tcc att gcg tgg ctg atg aag				883
Leu Val Ala Phe Val Val Gly Tyr Ile Ser Ile Ala Trp Leu Met Lys				
	250	255	260	
ttc gtg gca aac cac tcc ttc agc tgg ttt gct gca tac cgt att cct				931
Phe Val Ala Asn His Ser Phe Ser Trp Phe Ala Ala Tyr Arg Ile Pro				
	265	270	275	
gca ggt ctg ctc gtg atg ctg ctg ctc gca ctg ggc atg ctc aac cca				979
Ala Gly Leu Leu Val Met Leu Leu Leu Ala Leu Gly Met Leu Asn Pro				
	280	285	290	
taaaattcct gtacatctta aaa				1002

<210> 126

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

Val Asn Glu Glu Ile Thr Leu Leu Ala Ala Ala Ala Asp Pro Ala Ala

1

5

10

15

Thr Glu Asn Ile Gly Trp Val Gln Thr Ile Val Leu Ser Ile Val Gln
 20 25 30
 Gly Leu Thr Glu Phe Leu Pro Ile Ser Ser Ser Gly His Leu Arg Ile
 35 40 45
 Ile Ser Glu Leu Phe Trp Gly Ala Asp Ala Gly Ala Ser Phe Thr Ala
 50 55 60
 Val Val Gln Leu Gly Thr Glu Ala Ala Val Leu Val Phe Phe Ala Lys
 65 70 75 80
 Glu Ile Trp Gln Ile Ile Thr Gly Trp Phe Ala Gly Val Phe Asn Lys
 85 90 95
 Glu Arg Arg Gly Phe Glu Tyr Arg Met Gly Trp Met Ile Ile Val Ala
 100 105 110
 Thr Ile Pro Val Val Ile Leu Gly Val Leu Gly Lys Asp Leu Ile Arg
 115 120 125
 Glu Ala Leu Arg Asn Met Trp Ile Thr Ala Ser Val Leu Ile Leu Phe
 130 135 140
 Ser Leu Val Phe Ile Leu Ala Glu Lys Met Gly Lys Lys Glu Arg Asp
 145 150 155 160
 Tyr Asp Lys Leu Thr Met Lys Asp Ala Ile Ile Met Gly Leu Ala Gln
 165 170 175
 Cys Leu Ala Leu Ile Pro Gly Val Ser Arg Ser Gly Gly Thr Ile Ser
 180 185 190
 Ala Gly Leu Phe Leu Gly Leu Lys Arg Glu Val Ala Thr Lys Phe Ser
 195 200 205
 Phe Leu Leu Ala Ile Pro Ala Val Leu Gly Ser Gly Leu Tyr Ser Leu
 210 215 220
 Pro Asp Ala Phe Ala Pro Ser Ser Gly Gln Ala Ala Ser Gly Leu Gln
 225 230 235 240
 Leu Thr Val Gly Thr Leu Val Ala Phe Val Val Gly Tyr Ile Ser Ile
 245 250 255
 Ala Trp Leu Met Lys Phe Val Ala Asn His Ser Phe Ser Trp Phe Ala
 260 265 270
 Ala Tyr Arg Ile Pro Ala Gly Leu Leu Val Met Leu Leu Leu Ala Leu
 275 280 285
 Gly Met Leu Asn Pro
 290

<210> 127

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(952)

<223> RXA00900

<400> 127

```

gtgcggtggc tgcgctggtc gctagtgtgg tgtgcgcgct ggcgccgctc ataagcgat 60

tagtgatcgc acgcctgggtg caggggcttg gcggcggtgc gtg cgt ggt att gcg 115
Val Arg Gly Ile Ala
1 5

cgc gcg atc gtg cca gac ctt gaa cgc gga caa aag gct gcg cac gcc 163
Arg Ala Ile Val Pro Asp Leu Glu Arg Gly Gln Lys Ala Ala His Ala
10 15 20

ttt gca ctg ctg atg att att cag gga att gct ccc gtg gta gct ccg 211
Phe Ala Leu Leu Met Ile Ile Gln Gly Ile Ala Pro Val Val Ala Pro
25 30 35

ctc att ggt ggt gtg ctg gtc ggg cct ttt ggc tgg cgg gga att ttc 259
Leu Ile Gly Gly Val Leu Val Gly Pro Phe Gly Trp Arg Gly Ile Phe
40 45 50

tgg gca ctt gca ctg gtg aat ttt gcg cag ctg ctt gtt gct ttg ctg 307
Trp Ala Leu Ala Leu Val Asn Phe Ala Gln Leu Leu Val Ala Leu Leu
55 60 65

cag att aag gag tcg aag cca gtt gaa gag cgt acc gca gca gga ctt 355
Gln Ile Lys Glu Ser Lys Pro Val Glu Glu Arg Thr Ala Ala Gly Leu
70 75 80 85

ggc gga atg ctg tcc aac tat gtc ttt gtg ctg aag aat cct caa ttt 403
Gly Gly Met Leu Ser Asn Tyr Val Phe Val Leu Lys Asn Pro Gln Phe
90 95 100

ttg gca tat gta ttc aca ttg ggg ctg tct ttt ggg gcg atg ttc tcc 451
Leu Ala Tyr Val Phe Thr Leu Gly Leu Ser Phe Gly Ala Met Phe Ser
105 110 115

tac att tcg gcg tcg ccg ttc gtg ctg cag aat caa atg ggc att ccg 499
Tyr Ile Ser Ala Ser Pro Phe Val Leu Gln Asn Gln Met Gly Ile Pro
120 125 130

gta ctg ctg tat tcc att att ttc gga gtg aat gct ttt ggt ttg att 547
Val Leu Leu Tyr Ser Ile Ile Phe Gly Val Asn Ala Phe Gly Leu Ile
135 140 145

gtg ggc gga atg gtc aat agg cga ctt ctg cag cgg att cat cca cac 595
Val Gly Gly Met Val Asn Arg Arg Leu Leu Gln Arg Ile His Pro His
150 155 160 165

cgc atc atg caa act gtg ctg gcc agt ttt act gtg ctg tgt gcg ctt 643
Arg Ile Met Gln Thr Val Leu Ala Ser Phe Thr Val Leu Cys Ala Leu
170 175 180

ttg ctg att gaa gtg ctg ttt att aat tgg ata ccg ctg ttc ctg ttg 691
Leu Leu Ile Glu Val Leu Phe Ile Asn Trp Ile Pro Leu Phe Leu Leu
185 190 195

ctg ctg ttt ctt atc gtt tcc cat att ccg atg gtt atg gct aac gcg 739

```

Leu Leu Phe Leu Ile Val Ser His Ile Pro Met Val Met Ala Asn Ala
 200 205 210
 aca gct ctg gga act gaa gtg gtg cga agc agg gcg gga tcg ggt tct 787
 Thr Ala Leu Gly Thr Glu Val Val Arg Ser Arg Ala Gly Ser Gly Ser
 215 220 225
 gca att ttg ggt ttc gtg caa ttc acg atg ggt gct ttg gtg agt tca 835
 Ala Ile Leu Gly Phe Val Gln Phe Thr Met Gly Ala Leu Val Ser Ser
 230 235 240 245
 ctg gtc gga tta ggc tct gat aag gct ttg act atg gga atc gca atg 883
 Leu Val Gly Leu Gly Ser Asp Lys Ala Leu Thr Met Gly Ile Ala Met
 250 255 260
 act gct tgt gca ctg ctg gcg tgt ggg tgt gcg tac ctg gca ggt cga 931
 Thr Ala Cys Ala Leu Leu Ala Cys Gly Cys Ala Tyr Leu Ala Gly Arg
 265 270 275
 aaa ggt att cca gaa atg aag tagctctagg tggcgtttta agg 975
 Lys Gly Ile Pro Glu Met Lys
 280

<210> 128

<211> 284

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 128

Val Arg Gly Ile Ala Arg Ala Ile Val Pro Asp Leu Glu Arg Gly Gln
 1 5 10 15
 Lys Ala Ala His Ala Phe Ala Leu Leu Met Ile Ile Gln Gly Ile Ala
 20 25 30
 Pro Val Val Ala Pro Leu Ile Gly Gly Val Leu Val Gly Pro Phe Gly
 35 40 45
 Trp Arg Gly Ile Phe Trp Ala Leu Ala Leu Val Asn Phe Ala Gln Leu
 50 55 60
 Leu Val Ala Leu Leu Gln Ile Lys Glu Ser Lys Pro Val Glu Glu Arg
 65 70 75 80
 Thr Ala Ala Gly Leu Gly Gly Met Leu Ser Asn Tyr Val Phe Val Leu
 85 90 95
 Lys Asn Pro Gln Phe Leu Ala Tyr Val Phe Thr Leu Gly Leu Ser Phe
 100 105 110
 Gly Ala Met Phe Ser Tyr Ile Ser Ala Ser Pro Phe Val Leu Gln Asn
 115 120 125
 Gln Met Gly Ile Pro Val Leu Leu Tyr Ser Ile Ile Phe Gly Val Asn
 130 135 140
 Ala Phe Gly Leu Ile Val Gly Gly Met Val Asn Arg Arg Leu Leu Gln
 145 150 155 160
 Arg Ile His Pro His Arg Ile Met Gln Thr Val Leu Ala Ser Phe Thr

165								170				175			
Val	Leu	Cys	Ala	Leu	Leu	Leu	Ile	Glu	Val	Leu	Phe	Ile	Asn	Trp	Ile
180								185				190			
Pro	Leu	Phe	Leu	Leu	Leu	Leu	Phe	Leu	Ile	Val	Ser	His	Ile	Pro	Met
195								200				205			
Val	Met	Ala	Asn	Ala	Thr	Ala	Leu	Gly	Thr	Glu	Val	Val	Arg	Ser	Arg
210								215				220			
Ala	Gly	Ser	Gly	Ser	Ala	Ile	Leu	Gly	Phe	Val	Gln	Phe	Thr	Met	Gly
225								230				235			
Ala	Leu	Val	Ser	Ser	Leu	Val	Gly	Leu	Gly	Ser	Asp	Lys	Ala	Leu	Thr
245								250				255			
Met	Gly	Ile	Ala	Met	Thr	Ala	Cys	Ala	Leu	Leu	Ala	Cys	Gly	Cys	Ala
260								265				270			
Tyr	Leu	Ala	Gly	Arg	Lys	Gly	Ile	Pro	Glu	Met	Lys				
275								280							

<210> 129

<211> 537

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(514)

<223> RXN00901

<400> 129

ttttaagtat tgggtgctatc ttccgggtgct gatggtacct gaatgaaaat ttctaattaa 60

aaataccccc	aaatcttcga	tatagatata	cgagacagtg	atg	cag	aaa	aaa	caa	115
				Met	Gln	Lys	Lys	Gln	
				1				5	

cag	ctg	agc	acc	gcc	ctg	att	atg	gga	ttg	gca	tta	ttg	tca	gcc	agc	163
Gln	Leu	Ser	Thr	Ala	Leu	Ile	Met	Gly	Leu	Ala	Leu	Leu	Ser	Ala	Ser	
				10				15						20		

tcc	gcg	cta	gcg	act	gat	atg	tat	ttg	ccg	gca	atg	cct	ggg	att	gcg	211
Ser	Ala	Leu	Ala	Thr	Asp	Met	Tyr	Leu	Pro	Ala	Met	Pro	Gly	Ile	Ala	
				25				30					35			

gaa	gat	ttg	ggg	aca	act	gca	ccg	atg	gtg	cag	tta	act	ctt	tct	tcc	259
Glu	Asp	Leu	Gly	Thr	Thr	Ala	Pro	Met	Val	Gln	Leu	Thr	Leu	Ser	Ser	
				40				45					50			

ttt	atg	gct	gga	atg	gcg	att	ggc	caa	ttg	atc	att	ggg	cct	ttg	tcg	307
Phe	Met	Ala	Gly	Met	Ala	Ile	Gly	Gln	Leu	Ile	Ile	Gly	Pro	Leu	Ser	
				55			60					65				

gat	caa	ttg	gga	agg	aaa	ggc	ctg	ctc	gtt	gca	ggg	gcg	gtg	gct	gcg	355
Asp	Gln	Leu	Gly	Arg	Lys	Gly	Leu	Leu	Val	Ala	Gly	Ala	Val	Ala	Ala	
				70			75				80				85	

```

ctg gtc gct agt gtg gtg tgc gcg ctg gcg ccg tcg ata agc gta tta 403
Leu Val Ala Ser Val Val Cys Ala Leu Ala Pro Ser Ile Ser Val Leu
          90                      95                      100

gtg atc gca cgc ctg gtg cag ggg ctt ggc ggc ggt gcg tgc gtg gta 451
Val Ile Ala Arg Leu Val Gln Gly Leu Gly Gly Gly Ala Cys Val Val
          105                      110                      115

ttg cgc gcg cga tcg tgc cag acc ttg aac gcg gac aaa agg ctg cgc 499
Leu Arg Ala Arg Ser Cys Gln Thr Leu Asn Ala Asp Lys Arg Leu Arg
          120                      125                      130

acg cct ttg cac tgc tgatgattat tcaggggaatt gct 537
Thr Pro Leu His Cys
          135

```

```

<210> 130
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 130
Met Gln Lys Lys Gln Gln Leu Ser Thr Ala Leu Ile Met Gly Leu Ala
  1              5              10              15

Leu Leu Ser Ala Ser Ser Ala Leu Ala Thr Asp Met Tyr Leu Pro Ala
          20              25              30

Met Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala Pro Met Val Gln
          35              40              45

Leu Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile Gly Gln Leu Ile
          50              55              60

Ile Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly Leu Leu Val Ala
          65              70              75              80

Gly Ala Val Ala Ala Leu Val Ala Ser Val Val Cys Ala Leu Ala Pro
          85              90              95

Ser Ile Ser Val Leu Val Ile Ala Arg Leu Val Gln Gly Leu Gly Gly
          100             105             110

Gly Ala Cys Val Val Leu Arg Ala Arg Ser Cys Gln Thr Leu Asn Ala
          115             120             125

Asp Lys Arg Leu Arg Thr Pro Leu His Cys
          130             135

```

```

<210> 131
<211> 501
<212> DNA
<213> Corynebacterium glutamicum

```

```

<220>
<221> CDS
<222> (101)..(478)
<223> FRXA00901

```


<400> 131

```

acctgaatga aaattttctaa ttaaaaatac ccccaaattct tcgatataga tacacgagac 60

agtgatgcag aaaaaacaac agctgagcac cgccctgatt atg gga ttg gca tta 115
                                         Met Gly Leu Ala Leu
                                         1           5

ttg tca gcc agc tcc gcg cta gcg act gat atg tat ttg ccg gca atg 163
Leu Ser Ala Ser Ser Ala Leu Ala Thr Asp Met Tyr Leu Pro Ala Met
                        10                15                20

cct ggt att gcg gaa gat ttg ggg aca act gca ccg atg gtg cag tta 211
Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala Pro Met Val Gln Leu
                        25                30                35

act ctt tct tcc ttt atg gct gga atg gcg att ggc caa ttg atc att 259
Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile Gly Gln Leu Ile Ile
                        40                45                50

ggt cct ttg tcg gat caa ttg gga agg aaa ggc ctg ctc gtt gca ggt 307
Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly Leu Leu Val Ala Gly
                        55                60                65

gcg gtg gct gcg ctg gtc gct agt gtg gtg tgc gcg ctg gcg ccg tcg 355
Ala Val Ala Ala Leu Val Ala Ser Val Val Cys Ala Leu Ala Pro Ser
                        70                75                80                85

ata agc gta tta gtg atc gca cgc ctg gtg cag ggg ctt ggc ggc ggt 403
Ile Ser Val Leu Val Ile Ala Arg Leu Val Gln Gly Leu Gly Gly Gly
                        90                95                100

gcg tgc gtg gta ttg cgc gcg cga tcg tgc cag acc ttg aac gcg gac 451
Ala Cys Val Val Leu Arg Ala Arg Ser Cys Gln Thr Leu Asn Ala Asp
                        105                110                115

aaa agg ctg cgc acg cct ttg cac tgc tgatgattat tcagggaatt 498
Lys Arg Leu Arg Thr Pro Leu His Cys
                        120                125

gct 501

```

<210> 132

<211> 126

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 132

```

Met Gly Leu Ala Leu Leu Ser Ala Ser Ser Ala Leu Ala Thr Asp Met
  1           5           10           15

Tyr Leu Pro Ala Met Pro Gly Ile Ala Glu Asp Leu Gly Thr Thr Ala
      20                25                30

Pro Met Val Gln Leu Thr Leu Ser Ser Phe Met Ala Gly Met Ala Ile
      35                40                45

Gly Gln Leu Ile Ile Gly Pro Leu Ser Asp Gln Leu Gly Arg Lys Gly
      50                55                60

Leu Leu Val Ala Gly Ala Val Ala Ala Leu Val Ala Ser Val Val Cys

```

65	70	75	80
Ala Leu Ala Pro Ser Ile Ser Val Leu Val Ile Ala Arg Leu Val Gln			
	85	90	95
Gly Leu Gly Gly Gly Ala Cys Val Val Leu Arg Ala Arg Ser Cys Gln			
	100	105	110
Thr Leu Asn Ala Asp Lys Arg Leu Arg Thr Pro Leu His Cys			
	115	120	125

<210> 133
 <211> 1299
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1276)
 <223> RXA00289

<400> 133
 cctccccata agttcactca agcaagttct cccgaacaga ttcacccgag aagtcgacag 60

accccat	taa	acagccc	gat	tcaagaa	agg	cttcgcag	cc	atg	agc	acc	acc	acc		115
								Met	Ser	Thr	Thr	Thr		
								1				5		

gcg	ccc	gaa	gca	cgg	ttt	cct	gtc	gtc	cct	ttg	acc	gcc	atg	agt	ttc	163
Ala	Pro	Glu	Ala	Arg	Phe	Pro	Val	Val	Pro	Leu	Thr	Ala	Met	Ser	Phe	
				10					15					20		

gcg	gca	ttt	gtt	tat	gtc	acg	ttc	gag	atg	ttt	gca	gtt	ggc	ctc	atc	211
Ala	Ala	Phe	Val	Tyr	Val	Thr	Phe	Glu	Met	Phe	Ala	Val	Gly	Leu	Ile	
			25					30					35			

aag	ccg	atg	gcc	agc	gat	ctt	gga	gtg	tca	gaa	tcc	agc	atc	ggc	ctg	259
Lys	Pro	Met	Ala	Ser	Asp	Leu	Gly	Val	Ser	Glu	Ser	Ser	Ile	Gly	Leu	
		40					45					50				

ttg	atg	act	gtg	tat	gcg	act	gtc	gtt	gcc	gtg	gtg	acg	atc	cct	gcc	307
Leu	Met	Thr	Val	Tyr	Ala	Thr	Val	Val	Ala	Val	Val	Thr	Ile	Pro	Ala	
	55					60					65					

atg	ttg	tgg	gtt	tct	cga	ttt	aac	aag	cgc	aca	gtt	ttc	ctg	att	act	355
Met	Leu	Trp	Val	Ser	Arg	Phe	Asn	Lys	Arg	Thr	Val	Phe	Leu	Ile	Thr	
	70				75					80				85		

ctg	gca	ttt	ttg	gcc	acg	ggc	att	gtt	gtt	cag	gca	ctg	acc	gtt	aat	403
Leu	Ala	Phe	Leu	Ala	Thr	Gly	Ile	Val	Val	Gln	Ala	Leu	Thr	Val	Asn	
				90					95					100		

tat	gga	atg	cta	gcc	atc	ggc	cgc	act	atc	gca	gca	ttg	act	cac	ggg	451
Tyr	Gly	Met	Leu	Ala	Ile	Gly	Arg	Thr	Ile	Ala	Ala	Leu	Thr	His	Gly	
			105					110					115			

gtg	ttt	tgg	gca	ctt	gtt	ggg	cca	atg	gca	gcg	cgt	atg	tcc	cca	ggg	499
Val	Phe	Trp	Ala	Leu	Val	Gly	Pro	Met	Ala	Ala	Arg	Met	Ser	Pro	Gly	
			120				125					130				

cac	act	ggt	cgt	gca	gta	ggc	gtt	gtg	tcg	att	gga	tca	acc	atg	gcg	547
His	Thr	Gly	Arg	Ala	Val	Gly	Val	Val	Ser	Ile	Gly	Ser	Thr	Met	Ala	
	135					140					145					
ctg	gtc	gtt	ggt	tct	ccg	ctg	gca	aca	tgg	atc	ggt	gaa	ctc	atc	gga	595
Leu	Val	Val	Gly	Ser	Pro	Leu	Ala	Thr	Trp	Ile	Gly	Glu	Leu	Ile	Gly	
150					155					160					165	
tgg	cgt	cct	gcc	acc	tgg	att	ctt	ggt	gcg	ctg	acc	att	gcg	gcc	gtg	643
Trp	Arg	Pro	Ala	Thr	Trp	Ile	Leu	Gly	Ala	Leu	Thr	Ile	Ala	Ala	Val	
			170						175					180		
gct	gta	ctc	att	cca	acc	gtt	cca	tca	ctg	cca	cca	ctt	cca	gac	acg	691
Ala	Val	Leu	Ile	Pro	Thr	Val	Pro	Ser	Leu	Pro	Pro	Leu	Pro	Asp	Thr	
			185					190					195			
gaa	tca	gag	tcc	aaa	gaa	aag	aaa	tcc	ctt	cca	tgg	ggt	ctc	att	tcc	739
Glu	Ser	Glu	Ser	Lys	Glu	Lys	Lys	Ser	Leu	Pro	Trp	Gly	Leu	Ile	Ser	
	200						205					210				
ctg	gtc	att	ttc	ctt	ctc	ctt	gcc	gtc	acc	ggt	gtt	ttt	gct	gcc	tac	787
Leu	Val	Ile	Phe	Leu	Leu	Leu	Ala	Val	Thr	Gly	Val	Phe	Ala	Ala	Tyr	
	215					220					225					
acc	tac	ctt	ggc	ctc	atc	atc	gct	gaa	aca	gca	ggg	gac	agc	ttc	gtg	835
Thr	Tyr	Leu	Gly	Leu	Ile	Ile	Ala	Glu	Thr	Ala	Gly	Asp	Ser	Phe	Val	
230					235					240					245	
tcc	att	ggc	ttg	ttc	gcc	ttc	ggt	gca	ctc	gga	ctc	att	ggc	gtg	aca	883
Ser	Ile	Gly	Leu	Phe	Ala	Phe	Gly	Ala	Leu	Gly	Leu	Ile	Gly	Val	Thr	
				250					255					260		
gtg	gca	acc	cga	act	gtg	gat	caa	cgc	atg	ctg	cgt	gga	agt	gtt	cac	931
Val	Ala	Thr	Arg	Thr	Val	Asp	Gln	Arg	Met	Leu	Arg	Gly	Ser	Val	His	
			265					270					275			
acc	acc	act	ttg	ttt	gtc	att	gct	gca	att	ctc	gga	cag	atc	gca	ttc	979
Thr	Thr	Thr	Leu	Phe	Val	Ile	Ala	Ala	Ile	Leu	Gly	Gln	Ile	Ala	Phe	
			280				285					290				
gga	tta	gag	ggc	aca	cta	gcc	gta	gta	gct	atc	ttc	ctt	gca	gtc	acc	1027
Gly	Leu	Glu	Gly	Thr	Leu	Ala	Val	Val	Ala	Ile	Phe	Leu	Ala	Val	Thr	
	295					300					305					
gtg	ttt	ggt	gga	gca	tac	ggc	gct	ctc	cca	acc	ctg	gga	acc	acc	atc	1075
Val	Phe	Gly	Gly	Ala	Tyr	Gly	Ala	Leu	Pro	Thr	Leu	Gly	Thr	Thr	Ile	
310					315					320					325	
ttc	ctc	cat	gcg	ggt	cgc	gac	cac	cca	gat	act	gca	tcc	tcc	att	tat	1123
Phe	Leu	His	Ala	Gly	Arg	Asp	His	Pro	Asp	Thr	Ala	Ser	Ser	Ile	Tyr	
				330					335					340		
gtg	gtc	act	tac	caa	gtg	ggt	atc	gcg	tct	ggc	gcg	gca	ctt	ggc	gcg	1171
Val	Val	Thr	Tyr	Gln	Val	Gly	Ile	Ala	Ser	Gly	Ala	Ala	Leu	Gly	Ala	
			345					350					355			
atg	gct	gtg	gat	gcc	gat	tgg	gtt	gct	ggc	act	ttg	tgg	atc	atg	gct	1219
Met	Ala	Val	Asp	Ala	Asp	Trp	Val	Ala	Gly	Thr	Leu	Trp	Ile	Met	Ala	
	360						365					370				
gga	ctg	tca	ttg	gct	tcc	acg	ttg	gcc	ttg	gcg	ctg	tgg	tcc	cgc	ccg	1267

Gly Leu Ser Leu Ala Ser Thr Leu Ala Leu Ala Leu Trp Ser Arg Pro
 375 380 385

cta ctg aag tagcagccca aattcagccc act
 Leu Leu Lys
 390

1299

<210> 134

<211> 392

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 134

Met Ser Thr Thr Thr Ala Pro Glu Ala Arg Phe Pro Val Val Pro Leu
 1 5 10 15

Thr Ala Met Ser Phe Ala Ala Phe Val Tyr Val Thr Phe Glu Met Phe
 20 25 30

Ala Val Gly Leu Ile Lys Pro Met Ala Ser Asp Leu Gly Val Ser Glu
 35 40 45

Ser Ser Ile Gly Leu Leu Met Thr Val Tyr Ala Thr Val Val Ala Val
 50 55 60

Val Thr Ile Pro Ala Met Leu Trp Val Ser Arg Phe Asn Lys Arg Thr
 65 70 75 80

Val Phe Leu Ile Thr Leu Ala Phe Leu Ala Thr Gly Ile Val Val Gln
 85 90 95

Ala Leu Thr Val Asn Tyr Gly Met Leu Ala Ile Gly Arg Thr Ile Ala
 100 105 110

Ala Leu Thr His Gly Val Phe Trp Ala Leu Val Gly Pro Met Ala Ala
 115 120 125

Arg Met Ser Pro Gly His Thr Gly Arg Ala Val Gly Val Val Ser Ile
 130 135 140

Gly Ser Thr Met Ala Leu Val Val Gly Ser Pro Leu Ala Thr Trp Ile
 145 150 155 160

Gly Glu Leu Ile Gly Trp Arg Pro Ala Thr Trp Ile Leu Gly Ala Leu
 165 170 175

Thr Ile Ala Ala Val Ala Val Leu Ile Pro Thr Val Pro Ser Leu Pro
 180 185 190

Pro Leu Pro Asp Thr Glu Ser Glu Ser Lys Glu Lys Lys Ser Leu Pro
 195 200 205

Trp Gly Leu Ile Ser Leu Val Ile Phe Leu Leu Leu Ala Val Thr Gly
 210 215 220

Val Phe Ala Ala Tyr Thr Tyr Leu Gly Leu Ile Ile Ala Glu Thr Ala
 225 230 235 240

Gly Asp Ser Phe Val Ser Ile Gly Leu Phe Ala Phe Gly Ala Leu Gly
 245 250 255

Leu Ile Gly Val Thr Val Ala Thr Arg Thr Val Asp Gln Arg Met Leu
 260 265 270
 Arg Gly Ser Val His Thr Thr Thr Leu Phe Val Ile Ala Ala Ile Leu
 275 280 285
 Gly Gln Ile Ala Phe Gly Leu Glu Gly Thr Leu Ala Val Val Ala Ile
 290 295 300
 Phe Leu Ala Val Thr Val Phe Gly Gly Ala Tyr Gly Ala Leu Pro Thr
 305 310 315 320
 Leu Gly Thr Thr Ile Phe Leu His Ala Gly Arg Asp His Pro Asp Thr
 325 330 335
 Ala Ser Ser Ile Tyr Val Val Thr Tyr Gln Val Gly Ile Ala Ser Gly
 340 345 350
 Ala Ala Leu Gly Ala Met Ala Val Asp Ala Asp Trp Val Ala Gly Thr
 355 360 365
 Leu Trp Ile Met Ala Gly Leu Ser Leu Ala Ser Thr Leu Ala Leu Ala
 370 375 380
 Leu Trp Ser Arg Pro Leu Leu Lys
 385 390

<210> 135

<211> 420

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(397)

<223> RXN01984

<400> 135

aggaaatgtc tcacgtcaca accttttgaa aggtggctaa gtacgcacat ttgttgctctg 60

caatagtgcc ggtgagggag ctgtccgata ttgtgcttac atg cac gaa tct gga 115
 Met His Glu Ser Gly
 1 5

aaa aat cct gtc aag gtt gtc gac tcg cag gca cca caa gga cgc ggt 163
 Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala Pro Gln Gly Arg Gly
 10 15 20

ggg cat atc ggc gga cat atc aaa cgc cgc ccg att cct agg caa acg 211
 Gly His Ile Gly Gly His Ile Lys Arg Arg Pro Ile Pro Arg Gln Thr
 25 30 35

gaa att tcc gag gtt cgt cga tat atc gtc atg act gcc ctc gca ctc 259
 Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met Thr Ala Leu Ala Leu
 40 45 50

ggt ggc ttc gcc atc ggt gtg acg gaa ttt gtc tcc atg ggt ctg ctc 307
 Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val Ser Met Gly Leu Leu
 55 60 65

agc gcg atc gcc tcc gac ttt gag atc tcc gaa gac caa gcc gga cac 355
 Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu Asp Gln Ala Gly His
 70 75 80 85

atc atc acc atc tac gcc ctc gcg tgg ttg tgg gtg ccc cgc 397
 Ile Ile Thr Ile Tyr Ala Leu Ala Trp Leu Trp Val Pro Arg
 90 95

tgatcacagc gtttaccggc aaa 420

<210> 136

<211> 99

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

Met His Glu Ser Gly Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala
 1 5 10 15

Pro Gln Gly Arg Gly Gly His Ile Gly Gly His Ile Lys Arg Arg Pro
 20 25 30

Ile Pro Arg Gln Thr Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met
 35 40 45

Thr Ala Leu Ala Leu Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val
 50 55 60

Ser Met Gly Leu Leu Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu
 65 70 75 80

Asp Gln Ala Gly His Ile Ile Thr Ile Tyr Ala Leu Ala Trp Leu Trp
 85 90 95

Val Pro Arg

<210> 137

<211> 379

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(379)

<223> FRXA01984

<400> 137

aggaaatgtc tcacgtcaca acctttttgaa aggtgggctaa gtacgcacat ttgttgctctg 60

caatagtgcc ggtgagggag ctgtccgata ttgtgcttac atg cac gaa tct gga 115
 Met His Glu Ser Gly
 1 5

aaa aat cct gtc aag gtt gtc gac tcg cag gca cca caa gga cgc ggt 163
 Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala Pro Gln Gly Arg Gly
 10 15 20

```

ggg cat atc ggc gga cat atc aaa cgc cgc ccg att cct agg caa acg 211
Gly His Ile Gly Gly His Ile Lys Arg Arg Pro Ile Pro Arg Gln Thr
                25                      30                      35

gaa att tcc gag gtt cgt cga tat atc gtc atg act gcc ctc gca ctc 259
Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met Thr Ala Leu Ala Leu
                40                      45                      50

ggg ggc ttc gcc atc ggt gtg acg gaa ttt gtc tcc atg ggt ctg ctc 307
Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val Ser Met Gly Leu Leu
                55                      60                      65

agc gcg atc gcc tcc gac ttt gag atc tcc gaa gac caa gcc gga cac 355
Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu Asp Gln Ala Gly His
                70                      75                      80                      85

atc atc acc atc tac gcc ctc gcg 379
Ile Ile Thr Ile Tyr Ala Leu Ala
                90

```

<210> 138
 <211> 93
 <212> PRT
 <213> Corynebacterium glutamicum

```

<400> 138
Met His Glu Ser Gly Lys Asn Pro Val Lys Val Val Asp Ser Gln Ala
  1              5              10              15

Pro Gln Gly Arg Gly Gly His Ile Gly Gly His Ile Lys Arg Arg Pro
      20              25              30

Ile Pro Arg Gln Thr Glu Ile Ser Glu Val Arg Arg Tyr Ile Val Met
      35              40              45

Thr Ala Leu Ala Leu Gly Gly Phe Ala Ile Gly Val Thr Glu Phe Val
      50              55              60

Ser Met Gly Leu Leu Ser Ala Ile Ala Ser Asp Phe Glu Ile Ser Glu
      65              70              75              80

Asp Gln Ala Gly His Ile Ile Thr Ile Tyr Ala Leu Ala
      85              90

```

<210> 139
 <211> 735
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(712)
 <223> RXA00109

```

<400> 139
aagtggggga agatttcgac aactaaccgg gcgcaaagat gaaactaatg cgtccgacca 60

cggcgaaaag gaagtttcgc ccatctatga gaggttgaat gtg gct tca gag aag 115
                Val Ala Ser Glu Lys

```

	1	5	
aat cta aaa ttg cgt acc ttg gcg gca gct gct ggg gtg ttg ggc gtt			163
Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Ala Gly Val Leu Gly Val			
	10	20	
ggc gcg atg tcg atg ctc gtg gct ccg cag gct gct gcc cat gat gtg			211
Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala Ala Ala His Asp Val			
	25	35	
gtg gtg gat tct aat cct gaa aat ggc agt gtc gtt gat gag ttc ccg			259
Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val Val Asp Glu Phe Pro			
	40	50	
gag acc att gag ttg gag ttt tcc ggt att cct cag gat ctg ttc aca			307
Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro Gln Asp Leu Phe Thr			
	55	65	
aca gtt gca ttg agc aat gcg gat tcc gga gag gtg tta act tct gga			355
Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu Val Leu Thr Ser Gly			
	70	85	
act cct cag ctt gag ggg cag cac ttg agc tat gaa gtg cca tct gat			403
Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr Glu Val Pro Ser Asp			
	90	100	
gtg cag acg gga gct ggt aac tac att ttg ggt ttc cag atc act tct			451
Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly Phe Gln Ile Thr Ser			
	105	115	
tct gat ggt cac gct act aaa ggt tca atc tct ttt gag gtg aca ggc			499
Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser Phe Glu Val Thr Gly			
	120	130	
tct gct gaa acg aca aca gag aca aca gca gag acg aca act gag tca			547
Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu Thr Thr Thr Glu Ser			
	135	145	
gca gca acc act gac acc tca gag acc acc gaa gca gag aca act gaa			595
Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu Ala Glu Thr Thr Glu			
	150	165	
act gct gat gaa act tct gga att cct gcg ccg tgg aat tgg gtt ttg			643
Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro Trp Asn Trp Val Leu			
	170	180	
agc atc gtg gcg gtg ctt gtt gtt gca agt gcc atc gtc atg atg att			691
Ser Ile Val Ala Val Leu Val Val Ala Ser Ala Ile Val Met Met Ile			
	185	195	
gca aag aat cgt aac cag aaa taagagggtt tattcaccat gaa			735
Ala Lys Asn Arg Asn Gln Lys			
	200		

<210> 140

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 140

Val Ala Ser Glu Lys Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Ala
 1 5 10 15
 Gly Val Leu Gly Val Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala
 20 25 30
 Ala Ala His Asp Val Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val
 35 40 45
 Val Asp Glu Phe Pro Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro
 50 55 60
 Gln Asp Leu Phe Thr Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu
 65 70 75 80
 Val Leu Thr Ser Gly Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr
 85 90 95
 Glu Val Pro Ser Asp Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly
 100 105 110
 Phe Gln Ile Thr Ser Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser
 115 120 125
 Phe Glu Val Thr Gly Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu
 130 135 140
 Thr Thr Thr Glu Ser Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu
 145 150 155 160
 Ala Glu Thr Thr Glu Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro
 165 170 175
 Trp Asn Trp Val Leu Ser Ile Val Ala Val Leu Val Val Ala Ser Ala
 180 185 190
 Ile Val Met Met Ile Ala Lys Asn Arg Asn Gln Lys
 195 200

<210> 141
 <211> 735
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(712)
 <223> RXA00109

<400> 141
 aagtggggga agatttcgac aactaaccgg gcgcaaagat gaaactaatg cgtccgacca 60
 cggcgaaaag gaagtttcgc ccatctatga gaggttgaat gtg gct tca gag aag 115
 Val Ala Ser Glu Lys
 1 5
 aat cta aaa ttg cgt acc ttg gcg gca gct gct ggg gtg ttg ggc gtt 163
 Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Gly Val Leu Gly Val
 10 15 20

```

ggc gcg atg tcg atg ctc gtg gct ccg cag gct gct gcc cat gat gtg 211
Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala Ala Ala His Asp Val
      25                      30                      35

gtg gtg gat tct aat cct gaa aat ggc agt gtc gtt gat gag ttc ccg 259
Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val Val Asp Glu Phe Pro
      40                      45                      50

gag acc att gag ttg gag ttt tcc ggt att cct cag gat ctg ttc aca 307
Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro Gln Asp Leu Phe Thr
      55                      60                      65

aca gtt gca ttg agc aat gcg gat tcc gga gag gtg tta act tct gga 355
Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu Val Leu Thr Ser Gly
      70                      75                      80                      85

act cct cag ctt gag ggg cag cac ttg agc tat gaa gtg cca tct gat 403
Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr Glu Val Pro Ser Asp
      90                      95                      100

gtg cag acg gga gct ggt aac tac att ttg ggt ttc cag atc act tct 451
Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly Phe Gln Ile Thr Ser
      105                      110                      115

tct gat ggt cac gct act aaa ggt tca atc tct ttt gag gtg aca ggc 499
Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser Phe Glu Val Thr Gly
      120                      125                      130

tct gct gaa acg aca aca gag aca aca gca gag acg aca act gag tca 547
Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu Thr Thr Thr Glu Ser
      135                      140                      145

gca gca acc act gac acc tca gag acc acc gaa gca gag aca act gaa 595
Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu Ala Glu Thr Thr Glu
      150                      155                      160                      165

act gct gat gaa act tct gga att cct gcg ccg tgg aat tgg gtt ttg 643
Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro Trp Asn Trp Val Leu
      170                      175                      180

agc atc gtg gcg gtg ctt gtt gtt gca agt gcc atc gtc atg atg att 691
Ser Ile Val Ala Val Leu Val Val Ala Ser Ala Ile Val Met Met Ile
      185                      190                      195

gca aag aat cgt aac cag aaa taagagggtt tattcaccat gaa 735
Ala Lys Asn Arg Asn Gln Lys
      200

```

<210> 142

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 142

```

Val Ala Ser Glu Lys Asn Leu Lys Leu Arg Thr Leu Ala Ala Ala Ala
  1                      5                      10                      15

```

```

Gly Val Leu Gly Val Gly Ala Met Ser Met Leu Val Ala Pro Gln Ala
      20                      25                      30

```

Ala Ala His Asp Val Val Val Asp Ser Asn Pro Glu Asn Gly Ser Val
 35 40 45

Val Asp Glu Phe Pro Glu Thr Ile Glu Leu Glu Phe Ser Gly Ile Pro
 50 55 60

Gln Asp Leu Phe Thr Thr Val Ala Leu Ser Asn Ala Asp Ser Gly Glu
 65 70 75 80

Val Leu Thr Ser Gly Thr Pro Gln Leu Glu Gly Gln His Leu Ser Tyr
 85 90 95

Glu Val Pro Ser Asp Val Gln Thr Gly Ala Gly Asn Tyr Ile Leu Gly
 100 105 110

Phe Gln Ile Thr Ser Ser Asp Gly His Ala Thr Lys Gly Ser Ile Ser
 115 120 125

Phe Glu Val Thr Gly Ser Ala Glu Thr Thr Thr Glu Thr Thr Ala Glu
 130 135 140

Thr Thr Thr Glu Ser Ala Ala Thr Thr Asp Thr Ser Glu Thr Thr Glu
 145 150 155 160

Ala Glu Thr Thr Glu Thr Ala Asp Glu Thr Ser Gly Ile Pro Ala Pro
 165 170 175

Trp Asn Trp Val Leu Ser Ile Val Ala Val Leu Val Val Ala Ser Ala
 180 185 190

Ile Val Met Met Ile Ala Lys Asn Arg Asn Gln Lys
 195 200

<210> 143

<211> 864

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(841)

<223> RXA00996

<400> 143

atcttaagcc ttttgtccaa ggctctgagt tcttagtggc ggtatttacc aagaagtaac 60

acctctatct tgcacctgat ctggcgtaga ctcataagtt atg agc acc gta acg 115
 Met Ser Thr Val Thr
 1 5

gca gtg cag gtc aac ggc cta aaa gtt tcc ata tcg tcc ggt ttt tca 163
 Ala Val Gln Val Asn Gly Leu Lys Val Ser Ile Ser Ser Gly Phe Ser
 10 15 20

cgc aag aaa aca aaa acg atc ttg cat gat ctc gat ttc acc gta gag 211
 Arg Lys Lys Thr Lys Thr Ile Leu His Asp Leu Asp Phe Thr Val Glu
 25 30 35

acc gga aag atc acg gga ttg ctg ggg cca tcg ggc agc ggc aag aca 259
 Thr Gly Lys Ile Thr Gly Leu Leu Gly Pro Ser Gly Ser Gly Lys Thr

40	45	50	
act ttg atg cgc gcg att gtg gga gtg caa aac ttc gac ggc acc ctt			307
Thr Leu Met Arg Ala Ile Val Gly Val Gln Asn Phe Asp Gly Thr Leu			
55	60	65	
gag gtg ttt gat cag ccc gca ggt gct gcc tct ctg cgc ggg aaa atc			355
Glu Val Phe Asp Gln Pro Ala Gly Ala Ala Ser Leu Arg Gly Lys Ile			
70	75	80	85
ggc tat gtc acc caa aac gcc agc gta tat cac gat ctg tcg gtg ata			403
Gly Tyr Val Thr Gln Asn Ala Ser Val Tyr His Asp Leu Ser Val Ile			
	90	95	100
gaa aac ctc aag tat ttc ggg gct ctg gct aaa gga acc tcc act cca			451
Glu Asn Leu Lys Tyr Phe Gly Ala Leu Ala Lys Gly Thr Ser Thr Pro			
	105	110	115
cgc acc ccg gaa aag att ctg gag gtc tta gac atc gca gat ctt gct			499
Arg Thr Pro Glu Lys Ile Leu Glu Val Leu Asp Ile Ala Asp Leu Ala			
	120	125	130
caa cgc caa gta tca aca cta tct ggt ggg cag cgc ggc cga gtc tcc			547
Gln Arg Gln Val Ser Thr Leu Ser Gly Gly Gln Arg Gly Arg Val Ser			
	135	140	145
ctt gga tgt gcg ctt att gcc tca cca gaa ctc ttg gtg atg gat gag			595
Leu Gly Cys Ala Leu Ile Ala Ser Pro Glu Leu Leu Val Met Asp Glu			
150	155	160	165
cca acc gtg ggt ttg gat ccc att acc cgg caa gca ctg tgg gaa gag			643
Pro Thr Val Gly Leu Asp Pro Ile Thr Arg Gln Ala Leu Trp Glu Glu			
	170	175	180
ttc acc acc atc gca aaa gca ggt gct gga gtg gtt atc tcc agt cac			691
Phe Thr Thr Ile Ala Lys Ala Gly Ala Gly Val Val Ile Ser Ser His			
	185	190	195
gtg ttg gag gaa gcc gcg cgg tgc gac aac ctc att ttg ttg cgt gat			739
Val Leu Glu Glu Ala Ala Arg Cys Asp Asn Leu Ile Leu Leu Arg Asp			
200	205	210	
ggt cgg atc atc tgg agg gga aca ccc aca cgc ctt cta gaa gat aca			787
Gly Arg Ile Ile Trp Arg Gly Thr Pro Thr Arg Leu Leu Glu Asp Thr			
215	220	225	
ggc aaa agc tca tac gaa gat gct ttc ttg gct gcc att gac ggg gta			835
Gly Lys Ser Ser Tyr Glu Asp Ala Phe Leu Ala Ala Ile Asp Gly Val			
230	235	240	245
agg tca tgaacctca ctatctgctt gcc			864
Arg Ser			

<210> 144

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

Met Ser Thr Val Thr Ala Val Gln Val Asn Gly Leu Lys Val Ser Ile
 1 5 10 15
 Ser Ser Gly Phe Ser Arg Lys Lys Thr Lys Thr Ile Leu His Asp Leu
 20 25 30
 Asp Phe Thr Val Glu Thr Gly Lys Ile Thr Gly Leu Leu Gly Pro Ser
 35 40 45
 Gly Ser Gly Lys Thr Thr Leu Met Arg Ala Ile Val Gly Val Gln Asn
 50 55 60
 Phe Asp Gly Thr Leu Glu Val Phe Asp Gln Pro Ala Gly Ala Ala Ser
 65 70 75 80
 Leu Arg Gly Lys Ile Gly Tyr Val Thr Gln Asn Ala Ser Val Tyr His
 85 90 95
 Asp Leu Ser Val Ile Glu Asn Leu Lys Tyr Phe Gly Ala Leu Ala Lys
 100 105 110
 Gly Thr Ser Thr Pro Arg Thr Pro Glu Lys Ile Leu Glu Val Leu Asp
 115 120 125
 Ile Ala Asp Leu Ala Gln Arg Gln Val Ser Thr Leu Ser Gly Gly Gln
 130 135 140
 Arg Gly Arg Val Ser Leu Gly Cys Ala Leu Ile Ala Ser Pro Glu Leu
 145 150 155 160
 Leu Val Met Asp Glu Pro Thr Val Gly Leu Asp Pro Ile Thr Arg Gln
 165 170 175
 Ala Leu Trp Glu Glu Phe Thr Thr Ile Ala Lys Ala Gly Ala Gly Val
 180 185 190
 Val Ile Ser Ser His Val Leu Glu Glu Ala Ala Arg Cys Asp Asn Leu
 195 200 205
 Ile Leu Leu Arg Asp Gly Arg Ile Ile Trp Arg Gly Thr Pro Thr Arg
 210 215 220
 Leu Leu Glu Asp Thr Gly Lys Ser Ser Tyr Glu Asp Ala Phe Leu Ala
 225 230 235 240
 Ala Ile Asp Gly Val Arg Ser
 245

<210> 145

<211> 2463

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2440)

<223> RXN00829

<400> 145

tggttttagcc atggacccca tactagggag agttttggtt tggtgctaga aaaggttcac 60

caagcgcgaa caggcctatg caaacggtac gatatgacac	atg	caa	aaa	gct	gat	115
	Met	Gln	Lys	Ala	Asp	
	1				5	
tcc cat gat tgg att tcg gtc cac ggt gcg aat gaa aac aac ctc aaa						163
Ser His Asp Trp Ile Ser Val His Gly Ala Asn Glu Asn Asn Leu Lys						
	10			15	20	
aat gtg tcg gtg cgc atc cct aaa agg cgt ctc acc gtg ttc acg ggt						211
Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu Thr Val Phe Thr Gly						
	25			30	35	
gtg tcg gga tct ggc aag tcc tcg ctg gtg ttc ggc aca att gct gcg						259
Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe Gly Thr Ile Ala Ala						
	40			45	50	
gaa tca cgc cgg ttg atc aac gaa acc tat agc act ttt gtg caa ggt						307
Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser Thr Phe Val Gln Gly						
	55			60	65	
ttc atg ccg tcg atg gca agg ccc gat gtt gac cat ttg gaa ggc atc						355
Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp His Leu Glu Gly Ile						
	70			75	80	85
acc acg gcg atc atc gtc gat cag gag cag atg ggc gca aac cca cgg						403
Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met Gly Ala Asn Pro Arg						
	90			95	100	
tct acg gtg ggt acc gca act gat gcc acc gcg atg ttg cgc att ttg						451
Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala Met Leu Arg Ile Leu						
	105			110	115	
ttt tcc cga atc gcg gaa cct aac gcg ggt ggc ccg gga gct tat tcc						499
Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly Pro Gly Ala Tyr Ser						
	120			125	130	
ttc aac gtc ccc tct gtt tcc gca tcc ggc gcc atc acg gtg gaa aag						547
Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala Ile Thr Val Glu Lys						
	135			140	145	
ggc gga aac acc aag cgg gag aaa gct acc ttc aaa cgc acg ggt ggc						595
Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe Lys Arg Thr Gly Gly						
	150			155	160	165
atg tgc cca gcg tgc gag ggc atg ggc agg gcc tca gac atc gac ctc						643
Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala Ser Asp Ile Asp Leu						
	170			175	180	
aaa gag ctt ttc gac gcc tcc ctc tcc ctc aac gac ggc gcc ctg acc						691
Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn Asp Gly Ala Leu Thr						
	185			190	195	
atc ccc ggt tac acc cca ggt gga tgg agt tat cgg atg tat tca gaa						739
Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr Arg Met Tyr Ser Glu						
	200			205	210	
tcg ggc ctt ttt gat gct gcc aag ccg att aag gat ttc acc gag gaa						787
Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys Asp Phe Thr Glu Glu						
	215			220	225	

gaa cgc cac aac ttc ctt tat ctt gag ccc acc aag atg aag atc gct	835
Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr Lys Met Lys Ile Ala	
230 235 240 245	
ggc atc aac atg acc tat gag ggt ctt atc ccc cgc att cag aaa tcc	883
Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro Arg Ile Gln Lys Ser	
250 255 260	
atg ttg tct aag gat cgc gaa ggc atg cag aag cat att cgt gcg ttc	931
Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys His Ile Arg Ala Phe	
265 270 275	
gtg gat cga gcg gtt acc ttc att cct tgc cct gcg tgt ggt gga act	979
Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro Ala Cys Gly Gly Thr	
280 285 290	
cga tta gcg cca cat gcc ttg gag tcc aag atc aat ggc aaa aac atc	1027
Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile Asn Gly Lys Asn Ile	
295 300 305	
gct gag ttg tgc gcg atg gag gtc cgt gat ttg gcc aag tgg atc aaa	1075
Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu Ala Lys Trp Ile Lys	
310 315 320 325	
acg gtg gaa gcc ccc tcg gtt gct ccc ctg ctc acc gca ctg act gaa	1123
Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu Thr Ala Leu Thr Glu	
330 335 340	
acc ctg gat aac ttc gtg gag atc ggt ttg ggc tat atc caa ctc gat	1171
Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly Tyr Ile Gln Leu Asp	
345 350 355	
cgc ccc gct ggc acg ttg tct ggt ggt gag gca cag cgc acc aag atg	1219
Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala Gln Arg Thr Lys Met	
360 365 370	
atc cgc cat ttg ggc tct gca ttg act gac gtc acc tat gtt ttt gat	1267
Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val Thr Tyr Val Phe Asp	
375 380 385	
gaa ccc acc gcc ggt ttg cac gcc tac gac att gaa cgc atg aac aag	1315
Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile Glu Arg Met Asn Lys	
390 395 400 405	
ttg ctg ctc gat ctt cgc gat aaa ggc aat acc gtt tta gtc gtg gag	1363
Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr Val Leu Val Val Glu	
410 415 420	
cac aag ccg gaa acc atc gcc att gca gat cat gtg gtg gac ctt ggg	1411
His Lys Pro Glu Thr Ile Ala Ile Ala Asp His Val Val Asp Leu Gly	
425 430 435	
cca ggt gca ggc gcg ggt gga ggt gaa att cgg ttt gag ggg agc gtc	1459
Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg Phe Glu Gly Ser Val	
440 445 450	
gac aag ctt aaa gac agc gac acc gtg act ggc ctc cat ttt aat gac	1507
Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly Leu His Phe Asn Asp	
455 460 465	
cgg gcg tca ttg aag gaa tcc gtg cgt gcg ccg cat ggc gcc ctg gag	1555

Arg	Ala	Ser	Leu	Lys	Glu	Ser	Val	Arg	Ala	Pro	His	Gly	Ala	Leu	Glu	
470					475					480					485	
atc	cgc	ggg	gcc	gat	cga	aat	aat	ttg	aac	aat	gtg	gat	gtc	gat	att	1603
Ile	Arg	Gly	Ala	Asp	Arg	Asn	Asn	Leu	Asn	Asn	Val	Asp	Val	Asp	Ile	
				490					495						500	
ccg	ctc	ggc	gtg	ttc	acg	gcg	att	tcc	ggc	gtt	gca	ggg	tcg	ggg	aag	1651
Pro	Leu	Gly	Val	Phe	Thr	Ala	Ile	Ser	Gly	Val	Ala	Gly	Ser	Gly	Lys	
			505					510					515			
tcc	tcg	ttg	att	cat	gag	att	ccg	cgt	gat	gag	tcg	gtt	gtg	ttt	gtc	1699
Ser	Ser	Leu	Ile	His	Glu	Ile	Pro	Arg	Asp	Glu	Ser	Val	Val	Phe	Val	
		520					525					530				
gat	caa	acc	gca	atc	cac	ggg	tct	aat	cgt	tcc	aat	cct	gcg	aca	tat	1747
Asp	Gln	Thr	Ala	Ile	His	Gly	Ser	Asn	Arg	Ser	Asn	Pro	Ala	Thr	Tyr	
	535					540					545					
aca	ggc	atg	ctg	gat	tcg	att	cgc	aag	gct	ttt	gcc	aag	gcc	aat	gat	1795
Thr	Gly	Met	Leu	Asp	Ser	Ile	Arg	Lys	Ala	Phe	Ala	Lys	Ala	Asn	Asp	
550					555				560						565	
gtg	aaa	ccg	gcg	ctg	ttc	tcc	ccc	aat	tct	gaa	ggc	gcg	tgc	cca	aac	1843
Val	Lys	Pro	Ala	Leu	Phe	Ser	Pro	Asn	Ser	Glu	Gly	Ala	Cys	Pro	Asn	
				570					575					580		
tgt	aag	ggc	gcc	ggc	tcg	gtc	tat	gtc	gat	ttg	ggc	atg	atg	gct	ggg	1891
Cys	Lys	Gly	Ala	Gly	Ser	Val	Tyr	Val	Asp	Leu	Gly	Met	Met	Ala	Gly	
			585					590					595			
gta	tct	tcg	ccg	tgt	gag	gtg	tgc	gag	ggc	aag	cgt	ttt	gat	gag	tcc	1939
Val	Ser	Ser	Pro	Cys	Glu	Val	Cys	Glu	Gly	Lys	Arg	Phe	Asp	Glu	Ser	
			600				605					610				
gtg	ttg	gac	tac	cac	ttt	ggg	ggc	aag	gac	atc	gca	gac	gtg	ttg	ggg	1987
Val	Leu	Asp	Tyr	His	Phe	Gly	Gly	Lys	Asp	Ile	Ala	Asp	Val	Leu	Gly	
	615					620					625					
ctg	tcg	gct	gcc	aat	gcg	tat	gag	ttt	ttc	gcg	gcg	aaa	gat	tca	aag	2035
Leu	Ser	Ala	Ala	Asn	Ala	Tyr	Glu	Phe	Phe	Ala	Ala	Lys	Asp	Ser	Lys	
630					635					640					645	
att	ttg	cct	gcg	gca	aag	atc	gca	aag	agg	ctt	gtc	gac	gtc	ggc	ctc	2083
Ile	Leu	Pro	Ala	Ala	Lys	Ile	Ala	Lys	Arg	Leu	Val	Asp	Val	Gly	Leu	
				650					655					660		
ggc	tac	atc	acc	ctc	ggc	cag	ccg	ctc	acc	acg	ttg	tcc	ggc	ggg	gaa	2131
Gly	Tyr	Ile	Thr	Leu	Gly	Gln	Pro	Leu	Thr	Thr	Leu	Ser	Gly	Gly	Glu	
			665					670					675			
cgc	cag	cgt	ttg	aag	ctc	gcc	acc	cac	atg	gca	gac	aag	gcc	acc	acc	2179
Arg	Gln	Arg	Leu	Lys	Leu	Ala	Thr	His	Met	Ala	Asp	Lys	Ala	Thr	Thr	
			680				685					690				
ttt	att	ttg	gat	gag	ccc	acc	aca	ggc	ctg	cac	ctc	gct	gat	gtg	aaa	2227
Phe	Ile	Leu	Asp	Glu	Pro	Thr	Thr	Gly	Leu	His	Leu	Ala	Asp	Val	Lys	
	695					700					705					
acc	ttg	ctg	gat	ctt	ttt	gat	caa	ctg	gtt	gat	gac	ggc	aag	tct	gtc	2275
Thr	Leu	Leu	Asp	Leu	Phe	Asp	Gln	Leu	Val	Asp	Asp	Gly	Lys	Ser	Val	

710	715	720	725	
atc gtc atc gaa cac cac ctc ggc gtg ctc gct cac gct gac cac atc				2323
Ile Val Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile	730	735	740	
att gat gtc ggc cct ggt gca ggt tct gat ggt ggc tcg att gta ttc				2371
Ile Asp Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe	745	750	755	
gag ggc agc ccc gcg gaa ctc atc aaa act gat act cca aca gga cgc				2419
Glu Gly Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg	760	765	770	
cac ctt aaa gct tat gta gat tagttttctta tggaaaaccc tgg				2463
His Leu Lys Ala Tyr Val Asp	775	780		

<210> 146

<211> 780

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 146

Met Gln Lys Ala Asp Ser His Asp Trp Ile Ser Val His Gly Ala Asn	
1 5 10 15	

Glu Asn Asn Leu Lys Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu	
20 25 30	

Thr Val Phe Thr Gly Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe	
35 40 45	

Gly Thr Ile Ala Ala Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser	
50 55 60	

Thr Phe Val Gln Gly Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp	
65 70 75 80	

His Leu Glu Gly Ile Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met	
85 90 95	

Gly Ala Asn Pro Arg Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala	
100 105 110	

Met Leu Arg Ile Leu Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly	
115 120 125	

Pro Gly Ala Tyr Ser Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala	
130 135 140	

Ile Thr Val Glu Lys Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe	
145 150 155 160	

Lys Arg Thr Gly Gly Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala	
165 170 175	

Ser Asp Ile Asp Leu Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn	
180 185 190	

Asp Gly Ala Leu Thr Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr
 195 200 205
 Arg Met Tyr Ser Glu Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys
 210 215 220
 Asp Phe Thr Glu Glu Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr
 225 230 235 240
 Lys Met Lys Ile Ala Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro
 245 250 255
 Arg Ile Gln Lys Ser Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys
 260 265 270
 His Ile Arg Ala Phe Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro
 275 280 285
 Ala Cys Gly Gly Thr Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile
 290 295 300
 Asn Gly Lys Asn Ile Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu
 305 310 315 320
 Ala Lys Trp Ile Lys Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu
 325 330 335
 Thr Ala Leu Thr Glu Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly
 340 345 350
 Tyr Ile Gln Leu Asp Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala
 355 360 365
 Gln Arg Thr Lys Met Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val
 370 375 380
 Thr Tyr Val Phe Asp Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile
 385 390 395 400
 Glu Arg Met Asn Lys Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr
 405 410 415
 Val Leu Val Val Glu His Lys Pro Glu Thr Ile Ala Ile Ala Asp His
 420 425 430
 Val Val Asp Leu Gly Pro Gly Ala Gly Ala Gly Gly Glu Ile Arg
 435 440 445
 Phe Glu Gly Ser Val Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly
 450 455 460
 Leu His Phe Asn Asp Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro
 465 470 475 480
 His Gly Ala Leu Glu Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn
 485 490 495
 Val Asp Val Asp Ile Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val
 500 505 510
 Ala Gly Ser Gly Lys Ser Ser Leu Ile His Glu Ile Pro Arg Asp Glu

515					520					525					
Ser	Val	Val	Phe	Val	Asp	Gln	Thr	Ala	Ile	His	Gly	Ser	Asn	Arg	Ser
530						535					540				
Asn	Pro	Ala	Thr	Tyr	Thr	Gly	Met	Leu	Asp	Ser	Ile	Arg	Lys	Ala	Phe
545					550					555					560
Ala	Lys	Ala	Asn	Asp	Val	Lys	Pro	Ala	Leu	Phe	Ser	Pro	Asn	Ser	Glu
			565						570					575	
Gly	Ala	Cys	Pro	Asn	Cys	Lys	Gly	Ala	Gly	Ser	Val	Tyr	Val	Asp	Leu
			580					585					590		
Gly	Met	Met	Ala	Gly	Val	Ser	Ser	Pro	Cys	Glu	Val	Cys	Glu	Gly	Lys
		595					600					605			
Arg	Phe	Asp	Glu	Ser	Val	Leu	Asp	Tyr	His	Phe	Gly	Gly	Lys	Asp	Ile
	610					615					620				
Ala	Asp	Val	Leu	Gly	Leu	Ser	Ala	Ala	Asn	Ala	Tyr	Glu	Phe	Phe	Ala
625					630					635					640
Ala	Lys	Asp	Ser	Lys	Ile	Leu	Pro	Ala	Ala	Lys	Ile	Ala	Lys	Arg	Leu
				645						650				655	
Val	Asp	Val	Gly	Leu	Gly	Tyr	Ile	Thr	Leu	Gly	Gln	Pro	Leu	Thr	Thr
			660					665					670		
Leu	Ser	Gly	Gly	Glu	Arg	Gln	Arg	Leu	Lys	Leu	Ala	Thr	His	Met	Ala
		675					680					685			
Asp	Lys	Ala	Thr	Thr	Phe	Ile	Leu	Asp	Glu	Pro	Thr	Thr	Gly	Leu	His
	690					695					700				
Leu	Ala	Asp	Val	Lys	Thr	Leu	Leu	Asp	Leu	Phe	Asp	Gln	Leu	Val	Asp
705					710					715					720
Asp	Gly	Lys	Ser	Val	Ile	Val	Ile	Glu	His	His	Leu	Gly	Val	Leu	Ala
				725					730					735	
His	Ala	Asp	His	Ile	Ile	Asp	Val	Gly	Pro	Gly	Ala	Gly	Ser	Asp	Gly
			740					745					750		
Gly	Ser	Ile	Val	Phe	Glu	Gly	Ser	Pro	Ala	Glu	Leu	Ile	Lys	Thr	Asp
		755					760					765			
Thr	Pro	Thr	Gly	Arg	His	Leu	Lys	Ala	Tyr	Val	Asp				
	770					775					780				

<210> 147

<211> 278

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(255)

<223> FRXA00829

<400> 147

ttg gat gag ccc acc aca ggc ctg cac ctc gct gat gtg aaa acc ttg 48
 Leu Asp Glu Pro Thr Thr Gly Leu His Leu Ala Asp Val Lys Thr Leu
 1 5 10 15

ctg gat ctt ttt gat caa ctg gtt gat gac ggc aag tct gtc atc gtc 96
 Leu Asp Leu Phe Asp Gln Leu Val Asp Asp Gly Lys Ser Val Ile Val
 20 25 30

atc gaa cac cac ctc ggc gtg ctc gct cac gct gac cac atc att gat 144
 Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile Ile Asp
 35 40 45

gtc ggc cct ggt gca ggt tct gat ggt ggc tcg att gta ttc gag ggc 192
 Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe Glu Gly
 50 55 60

agc ccc gcg gaa ctc atc aaa act gat act cca aca gga cgc cac ctt 240
 Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg His Leu
 65 70 75 80

aaa gct tat gta gat tagtttctta tggaaaaccc tgg 278
 Lys Ala Tyr Val Asp
 85

<210> 148

<211> 85

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 148

Leu Asp Glu Pro Thr Thr Gly Leu His Leu Ala Asp Val Lys Thr Leu
 1 5 10 15

Leu Asp Leu Phe Asp Gln Leu Val Asp Asp Gly Lys Ser Val Ile Val
 20 25 30

Ile Glu His His Leu Gly Val Leu Ala His Ala Asp His Ile Ile Asp
 35 40 45

Val Gly Pro Gly Ala Gly Ser Asp Gly Gly Ser Ile Val Phe Glu Gly
 50 55 60

Ser Pro Ala Glu Leu Ile Lys Thr Asp Thr Pro Thr Gly Arg His Leu
 65 70 75 80

Lys Ala Tyr Val Asp
 85

<210> 149

<211> 1663

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1663)

<223> FRXA00834

<400> 149

```

tgttttagcc atggaccca tactagggag agttttgttt tggtgctaga aaaggttcac 60

caagcgcgaa caggcctatg caaacggtac gatatgacac atg caa aaa gct gat 115
                                         Met Gln Lys Ala Asp
                                         1      5

tcc cat gat tgg att tcg gtc cac ggt gcg aat gaa aac aac ctc aaa 163
Ser His Asp Trp Ile Ser Val His Gly Ala Asn Glu Asn Asn Leu Lys
              10              15              20

aat gtg tcg gtg cgc atc cct aaa agg cgt ctc acc gtg ttc acg ggt 211
Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu Thr Val Phe Thr Gly
              25              30              35

gtg tcg gga tct ggc aag tcc tcg ctg gtg ttc ggc aca att gct gcg 259
Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe Gly Thr Ile Ala Ala
              40              45              50

gaa tca cgc cgg ttg atc aac gaa acc tat agc act ttt gtg caa ggt 307
Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser Thr Phe Val Gln Gly
              55              60              65

ttc atg ccg tcg atg gca agg ccc gat gtt gac cat ttg gaa ggc atc 355
Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp His Leu Glu Gly Ile
              70              75              80              85

acc acg gcg atc atc gtc gat cag gag cag atg ggc gca aac cca cgg 403
Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met Gly Ala Asn Pro Arg
              90              95              100

tct acg gtg ggt acc gca act gat gcc acc gcg atg ttg cgc att ttg 451
Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala Met Leu Arg Ile Leu
              105              110              115

ttt tcc cga atc gcg gaa cct aac gcg ggt ggc ccg gga gct tat tcc 499
Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly Pro Gly Ala Tyr Ser
              120              125              130

ttc aac gtc ccc tct gtt tcc gca tcc ggc gcc atc acg gtg gaa aag 547
Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala Ile Thr Val Glu Lys
              135              140              145

ggc gga aac acc aag cgg gag aaa gct acc ttc aaa cgc acg ggt ggc 595
Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe Lys Arg Thr Gly Gly
              150              155              160              165

atg tgc cca gcg tgc gag ggc atg ggc agg gcc tca gac atc gac ctc 643
Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala Ser Asp Ile Asp Leu
              170              175              180

aaa gag ctt ttc gac gcc tcc ctc tcc ctc aac gac ggc gcc ctg acc 691
Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn Asp Gly Ala Leu Thr
              185              190              195

atc ccc ggt tac acc cca ggt gga tgg agt tat cgg atg tat tca gaa 739
Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr Arg Met Tyr Ser Glu
              200              205              210

tcg ggc ctt ttt gat gct gcc aag ccg att aag gat ttc acc gag gaa 787
Ser Gly Leu Phe Asp Ala Ala Lys Pro Ile Lys Asp Phe Thr Glu Glu

```

215	220	225	
gaa cgc cac aac ttc ctt tat ctt gag ccc acc aag atg aag atc gct			835
Glu Arg His Asn Phe Leu Tyr Leu Glu Pro Thr Lys Met Lys Ile Ala			
230	235	240	245
ggc atc aac atg acc tat gag ggt ctt atc ccc cgc att cag aaa tcc			883
Gly Ile Asn Met Thr Tyr Glu Gly Leu Ile Pro Arg Ile Gln Lys Ser			
	250	255	260
atg ttg tct aag gat cgc gaa ggc atg cag aag cat att cgt gcg ttc			931
Met Leu Ser Lys Asp Arg Glu Gly Met Gln Lys His Ile Arg Ala Phe			
	265	270	275
gtg gat cga gcg gtt acc ttc att cct tgc cct gcg tgt ggt gga act			979
Val Asp Arg Ala Val Thr Phe Ile Pro Cys Pro Ala Cys Gly Gly Thr			
	280	285	290
cga tta gcg cca cat gcc ttg gag tcc aag atc aat ggc aaa aac atc			1027
Arg Leu Ala Pro His Ala Leu Glu Ser Lys Ile Asn Gly Lys Asn Ile			
	295	300	305
gct gag ttg tgc gcg atg gag gtc cgt gat ttg gcc aag tgg atc aaa			1075
Ala Glu Leu Cys Ala Met Glu Val Arg Asp Leu Ala Lys Trp Ile Lys			
310	315	320	325
acg gtg gaa gcc ccc tcg gtt gct ccc ctg ctc acc gca ctg act gaa			1123
Thr Val Glu Ala Pro Ser Val Ala Pro Leu Leu Thr Ala Leu Thr Glu			
	330	335	340
acc ctg gat aac ttc gtg gag atc ggt ttg ggc tat atc caa ctc gat			1171
Thr Leu Asp Asn Phe Val Glu Ile Gly Leu Gly Tyr Ile Gln Leu Asp			
	345	350	355
cgc ccc gct ggc acg ttg tct ggt ggt gag gca cag cgc acc aag atg			1219
Arg Pro Ala Gly Thr Leu Ser Gly Gly Glu Ala Gln Arg Thr Lys Met			
	360	365	370
atc cgc cat ttg ggc tct gca ttg act gac gtc acc tat gtt ttt gat			1267
Ile Arg His Leu Gly Ser Ala Leu Thr Asp Val Thr Tyr Val Phe Asp			
	375	380	385
gaa ccc acc gcc ggt ttg cac gcc tac gac att gaa cgc atg aac aag			1315
Glu Pro Thr Ala Gly Leu His Ala Tyr Asp Ile Glu Arg Met Asn Lys			
390	395	400	405
ttg ctg ctc gat ctt cgc gat aaa ggc aat acc gtt tta gtc gtg gag			1363
Leu Leu Leu Asp Leu Arg Asp Lys Gly Asn Thr Val Leu Val Val Glu			
	410	415	420
cac aag ccg gaa acc atc gcc att gca gat cat gtg gtg gac ctt ggg			1411
His Lys Pro Glu Thr Ile Ala Ile Ala Asp His Val Val Asp Leu Gly			
	425	430	435
cca ggt gca ggc gcg ggt gga ggt gaa att cgg ttt gag ggg agc gtc			1459
Pro Gly Ala Gly Ala Gly Gly Gly Glu Ile Arg Phe Glu Gly Ser Val			
	440	445	450
gac aag ctt aaa gac agc gac acc gtg act ggc ctc cat ttt aat gac			1507
Asp Lys Leu Lys Asp Ser Asp Thr Val Thr Gly Leu His Phe Asn Asp			
	455	460	465

cgg gcg tca ttg aag gaa tcc gtg cgt gcg ccg cat ggc gcc ctg gag 1555
 Arg Ala Ser Leu Lys Glu Ser Val Arg Ala Pro His Gly Ala Leu Glu
 470 475 480 485

 atc cgc ggg gcc gat cga aat aat ttg aac aat gtg gat gtc gat att 1603
 Ile Arg Gly Ala Asp Arg Asn Asn Leu Asn Asn Val Asp Val Asp Ile
 490 495 500

 ccg ctc ggc gtg ttc acg gcg att tcc ggc gtt gca ggt tcg ggt aag 1651
 Pro Leu Gly Val Phe Thr Ala Ile Ser Gly Val Ala Gly Ser Gly Lys
 505 510 515

 tcc tcg ttg att 1663
 Ser Ser Leu Ile
 520

<210> 150

<211> 521

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 150

Met Gln Lys Ala Asp Ser His Asp Trp Ile Ser Val His Gly Ala Asn
 1 5 10 15

 Glu Asn Asn Leu Lys Asn Val Ser Val Arg Ile Pro Lys Arg Arg Leu
 20 25 30

 Thr Val Phe Thr Gly Val Ser Gly Ser Gly Lys Ser Ser Leu Val Phe
 35 40 45

 Gly Thr Ile Ala Ala Glu Ser Arg Arg Leu Ile Asn Glu Thr Tyr Ser
 50 55 60

 Thr Phe Val Gln Gly Phe Met Pro Ser Met Ala Arg Pro Asp Val Asp
 65 70 75 80

 His Leu Glu Gly Ile Thr Thr Ala Ile Ile Val Asp Gln Glu Gln Met
 85 90 95

 Gly Ala Asn Pro Arg Ser Thr Val Gly Thr Ala Thr Asp Ala Thr Ala
 100 105 110

 Met Leu Arg Ile Leu Phe Ser Arg Ile Ala Glu Pro Asn Ala Gly Gly
 115 120 125

 Pro Gly Ala Tyr Ser Phe Asn Val Pro Ser Val Ser Ala Ser Gly Ala
 130 135 140

 Ile Thr Val Glu Lys Gly Gly Asn Thr Lys Arg Glu Lys Ala Thr Phe
 145 150 155 160

 Lys Arg Thr Gly Gly Met Cys Pro Ala Cys Glu Gly Met Gly Arg Ala
 165 170 175

 Ser Asp Ile Asp Leu Lys Glu Leu Phe Asp Ala Ser Leu Ser Leu Asn
 180 185 190

 Asp Gly Ala Leu Thr Ile Pro Gly Tyr Thr Pro Gly Gly Trp Ser Tyr

195					200					205					
Arg	Met	Tyr	Ser	Glu	Ser	Gly	Leu	Phe	Asp	Ala	Ala	Lys	Pro	Ile	Lys
210						215					220				
Asp	Phe	Thr	Glu	Glu	Glu	Arg	His	Asn	Phe	Leu	Tyr	Leu	Glu	Pro	Thr
225					230					235					240
Lys	Met	Lys	Ile	Ala	Gly	Ile	Asn	Met	Thr	Tyr	Glu	Gly	Leu	Ile	Pro
				245					250					255	
Arg	Ile	Gln	Lys	Ser	Met	Leu	Ser	Lys	Asp	Arg	Glu	Gly	Met	Gln	Lys
			260					265					270		
His	Ile	Arg	Ala	Phe	Val	Asp	Arg	Ala	Val	Thr	Phe	Ile	Pro	Cys	Pro
			275					280					285		
Ala	Cys	Gly	Gly	Thr	Arg	Leu	Ala	Pro	His	Ala	Leu	Glu	Ser	Lys	Ile
	290					295					300				
Asn	Gly	Lys	Asn	Ile	Ala	Glu	Leu	Cys	Ala	Met	Glu	Val	Arg	Asp	Leu
305					310					315					320
Ala	Lys	Trp	Ile	Lys	Thr	Val	Glu	Ala	Pro	Ser	Val	Ala	Pro	Leu	Leu
				325					330					335	
Thr	Ala	Leu	Thr	Glu	Thr	Leu	Asp	Asn	Phe	Val	Glu	Ile	Gly	Leu	Gly
			340					345					350		
Tyr	Ile	Gln	Leu	Asp	Arg	Pro	Ala	Gly	Thr	Leu	Ser	Gly	Gly	Glu	Ala
		355					360					365			
Gln	Arg	Thr	Lys	Met	Ile	Arg	His	Leu	Gly	Ser	Ala	Leu	Thr	Asp	Val
	370					375					380				
Thr	Tyr	Val	Phe	Asp	Glu	Pro	Thr	Ala	Gly	Leu	His	Ala	Tyr	Asp	Ile
385					390					395					400
Glu	Arg	Met	Asn	Lys	Leu	Leu	Leu	Asp	Leu	Arg	Asp	Lys	Gly	Asn	Thr
				405					410					415	
Val	Leu	Val	Val	Glu	His	Lys	Pro	Glu	Thr	Ile	Ala	Ile	Ala	Asp	His
			420					425					430		
Val	Val	Asp	Leu	Gly	Pro	Gly	Ala	Gly	Ala	Gly	Gly	Gly	Glu	Ile	Arg
		435					440					445			
Phe	Glu	Gly	Ser	Val	Asp	Lys	Leu	Lys	Asp	Ser	Asp	Thr	Val	Thr	Gly
	450					455					460				
Leu	His	Phe	Asn	Asp	Arg	Ala	Ser	Leu	Lys	Glu	Ser	Val	Arg	Ala	Pro
465					470					475					480
His	Gly	Ala	Leu	Glu	Ile	Arg	Gly	Ala	Asp	Arg	Asn	Asn	Leu	Asn	Asn
				485					490					495	
Val	Asp	Val	Asp	Ile	Pro	Leu	Gly	Val	Phe	Thr	Ala	Ile	Ser	Gly	Val
			500					505					510		
Ala	Gly	Ser	Gly	Lys	Ser	Ser	Leu	Ile							
	515						520								


```
<220>  
<221> CDS  
<222> (101) .. (841)  
<223> RXA00995
```

<400> 151																
gtcggatcat ctggagggga acacccacac gccttctaga agatacaggc aaaagctcat 60																
acgaagatgc tttcttggct gccattgacg gggtaaggtc atg aac cct cac tat 115																
Met Asn Pro His Tyr 5																
ctg ctt gcc acg gtc aaa cga gtc ctg ctg cag ctg aaa gcc gat aaa 163																
Leu Leu Ala Thr Val Lys Arg Val Leu Leu Gln Leu Lys Ala Asp Lys 20																
cgt tcc atc gcg ctg att ctt cta gca ccc gtg gcg ttg atg tcg ctg 211																
Arg Ser Ile Ala Leu Ile Leu Leu Ala Pro Val Ala Leu Met Ser Leu 35																
ttt tat tac atg tat tcc tcc aca ccg gca ggc acc cag ctg ttt aag 259																
Phe Tyr Tyr Met Tyr Ser Ser Thr Pro Ala Gly Thr Gln Leu Phe Lys 50																
acc att tcc acg gtc atg atc gca gtg ttc ccc ttg atg ctc atg ttt 307																
Thr Ile Ser Thr Val Met Ile Ala Val Phe Pro Leu Met Leu Met Phe 65																
ttg atg acg tcg gtg acg atg caa aga gaa cgc aac gct gga acg ctc 355																
Leu Met Thr Ser Val Thr Met Gln Arg Glu Arg Asn Ala Gly Thr Leu 85																
gag cgc ttg tgg acc acg aac att cac cgc gtt gat ttg atc ggt ggc 403																
Glu Arg Leu Trp Thr Thr Asn Ile His Arg Val Asp Leu Ile Gly Gly 100																
tac ggg gtg gcc ttc ggc atc atg gcg gtg gcg caa tct ttg ctc atg 451																
Tyr Gly Val Ala Phe Gly Ile Met Ala Val Ala Gln Ser Leu Leu Met 115																
gtg ctc acc ctt cgg tat ctc ctg ggt gtg gaa acc gaa tcg gag tgg 499																
Val Leu Thr Leu Arg Tyr Leu Leu Gly Val Glu Thr Glu Ser Glu Trp 130																
tgg att tct acg ctc att gct gcg atc acc ggt ctt atc gga gtg tct 547																
Trp Ile Ser Thr Leu Ile Ala Ala Ile Thr Gly Leu Ile Gly Val Ser 145																
ctt ggc ctg ttg agc tct gcg ttt gcc agc act gag ttc caa gct atc 595																
Leu Gly Leu Leu Ser Ser Ala Phe Ala Ser Thr Glu Phe Gln Ala Ile 165																
caa acg ctg ccg ttg ctt att ttg ccc cag ttc cta ttg tgc ggt ttg 643																
Gln Thr Leu Pro Leu Leu Ile Leu Pro Gln Phe Leu Leu Cys Gly Leu																

170										175					180					
ctg	atc	cca	cgg	gat	gat	ctg	ccg	gat	gtg	ttg	cgc	tgg	gtt	tct	aat	691				
Leu	Ile	Pro	Arg	Asp	Asp	Leu	Pro	Asp	Val	Leu	Arg	Trp	Val	Ser	Asn					
			185				190						195							
gtg	ttg	ccg	ctg	tcc	tat	gca	gtt	gat	gca	gcg	ctt	gag	gcc	tca	cgg	739				
Val	Leu	Pro	Leu	Ser	Tyr	Ala	Val	Asp	Ala	Ala	Leu	Glu	Ala	Ser	Arg					
			200				205						210							
acg	gga	atc	gga	cag	caa	gta	gtg	gtc	aac	att	gcc	atc	tgc	gcc	gcg	787				
Thr	Gly	Ile	Gly	Gln	Gln	Val	Val	Val	Asn	Ile	Ala	Ile	Cys	Ala	Ala					
			215				220						225							
ttt	gcc	gtg	agc	ttc	ctg	ctg	gtg	gcg	gcg	cta	tcg	atg	ccg	aga	atg	835				
Phe	Ala	Val	Ser	Phe	Leu	Leu	Val	Ala	Ala	Leu	Ser	Met	Pro	Arg	Met					
			230				235						240							
acc cgc tagattactc ttccagcgag gtg															864					
Thr Arg																				

<210> 152

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

Met	Asn	Pro	His	Tyr	Leu	Leu	Ala	Thr	Val	Lys	Arg	Val	Leu	Leu	Gln
1				5					10					15	

Leu	Lys	Ala	Asp	Lys	Arg	Ser	Ile	Ala	Leu	Ile	Leu	Leu	Ala	Pro	Val
			20					25					30		

Ala	Leu	Met	Ser	Leu	Phe	Tyr	Tyr	Met	Tyr	Ser	Ser	Thr	Pro	Ala	Gly
		35					40					45			

Thr	Gln	Leu	Phe	Lys	Thr	Ile	Ser	Thr	Val	Met	Ile	Ala	Val	Phe	Pro
	50					55					60				

Leu	Met	Leu	Met	Phe	Leu	Met	Thr	Ser	Val	Thr	Met	Gln	Arg	Glu	Arg
65					70					75					80

Asn	Ala	Gly	Thr	Leu	Glu	Arg	Leu	Trp	Thr	Thr	Asn	Ile	His	Arg	Val
				85					90					95	

Asp	Leu	Ile	Gly	Gly	Tyr	Gly	Val	Ala	Phe	Gly	Ile	Met	Ala	Val	Ala
			100					105					110		

Gln	Ser	Leu	Leu	Met	Val	Leu	Thr	Leu	Arg	Tyr	Leu	Leu	Gly	Val	Glu
		115					120					125			

Thr	Glu	Ser	Glu	Trp	Trp	Ile	Ser	Thr	Leu	Ile	Ala	Ala	Ile	Thr	Gly
	130					135					140				

Leu	Ile	Gly	Val	Ser	Leu	Gly	Leu	Leu	Ser	Ser	Ala	Phe	Ala	Ser	Thr
145					150					155					160

Glu	Phe	Gln	Ala	Ile	Gln	Thr	Leu	Pro	Leu	Leu	Ile	Leu	Pro	Gln	Phe
				165					170					175	

Leu Leu Cys Gly Leu Leu Ile Pro Arg Asp Asp Leu Pro Asp Val Leu
 180 185 190
 Arg Trp Val Ser Asn Val Leu Pro Leu Ser Tyr Ala Val Asp Ala Ala
 195 200 205
 Leu Glu Ala Ser Arg Thr Gly Ile Gly Gln Gln Val Val Val Asn Ile
 210 215 220
 Ala Ile Cys Ala Ala Phe Ala Val Ser Phe Leu Leu Val Ala Ala Leu
 225 230 235 240
 Ser Met Pro Arg Met Thr Arg
 245

<210> 153
 <211> 1353
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1330)
 <223> RXN00803

<400> 153
 tcatccttcc ttagctcgcg tgagcttccc aagcgtaagc acccccgtgt gagggcataa 60
 cggccgttct gttaaagatt ggtctggcca tttcctccat atg ggg gtg tcc gcg 115
 Met Gly Val Ser Ala
 1 5
 ctt aac atg tct gac atg gtg gcg aac aaa cgg gca cag cgt aaa gtc 163
 Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg Ala Gln Arg Lys Val
 10 15 20
 tgg cta gcg gta gct tta tcg gtc ttt acg gtc gcg tgg ggt ggc aat 211
 Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val Ala Trp Gly Gly Asn
 25 30 35
 gaa ttc act ccc ttg ctg gtg ttt tac cga ggt gaa ggg ttc ttt agc 259
 Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly Glu Gly Phe Phe Ser
 40 45 50
 aac ctg ttc atc gac ctt ttg ctg gtg ttt tat gcc atc gga gta gcg 307
 Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr Ala Ile Gly Val Ala
 55 60 65
 gta ggt ttg ctg gca gct ggt cct tta tct gac cgc tat ggc cga cgt 355
 Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp Arg Tyr Gly Arg Arg
 70 75 80 85
 gcc gtc atg ttg cct gcg cca ttg atc gcg atc ttg ggt tcc gcg ttg 403
 Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile Leu Gly Ser Ala Leu
 90 95 100
 att gcc tcg ggt gaa gaa acc gcc atc ctg att gcc att ggt cga gtg 451
 Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile Ala Ile Gly Arg Val
 105 110 115

ctg	tcg	gga	att	tcg	gtg	ggc	atg	gtg	atg	aca	gcg	gga	ggg	tcc	tgg	499
Leu	Ser	Gly	Ile	Ser	Val	Gly	Met	Val	Met	Thr	Ala	Gly	Gly	Ser	Trp	
		120					125						130			
att	aag	gag	ctt	tca	tcg	tcg	cgg	ttt	gag	cca	ggg	gtg	aaa	acc	agt	547
Ile	Lys	Glu	Leu	Ser	Ser	Ser	Arg	Phe	Glu	Pro	Gly	Val	Lys	Thr	Ser	
	135						140					145				
gct	ggg	gca	aaa	cgc	gca	tcg	atg	tct	ttg	acc	ggg	ggg	ttt	gcg	ctc	595
Ala	Gly	Ala	Lys	Arg	Ala	Ser	Met	Ser	Leu	Thr	Gly	Gly	Phe	Ala	Leu	
150					155					160					165	
ggc	cca	gcg	ctt	gct	ggg	gtg	atg	gca	cag	tgg	ctg	cca	cta	cct	gga	643
Gly	Pro	Ala	Leu	Ala	Gly	Val	Met	Ala	Gln	Trp	Leu	Pro	Leu	Pro	Gly	
			170						175						180	
cag	ttg	gca	tat	gtt	ttg	cac	att	att	ctc	act	ctg	att	ttg	ttc	ccg	691
Gln	Leu	Ala	Tyr	Val	Leu	His	Ile	Ile	Leu	Thr	Leu	Ile	Leu	Phe	Pro	
		185						190					195			
ttg	ctt	att	aca	gcg	ccg	gaa	act	cgt	caa	tca	gcg	cac	ctg	aaa	act	739
Leu	Leu	Ile	Thr	Ala	Pro	Glu	Thr	Arg	Gln	Ser	Ala	His	Leu	Lys	Thr	
		200					205					210				
aag	gga	tca	ttc	tgg	tca	gat	gtg	ctt	gtg	cca	tct	gca	cta	gac	aag	787
Lys	Gly	Ser	Phe	Trp	Ser	Asp	Val	Leu	Val	Pro	Ser	Ala	Leu	Asp	Lys	
	215					220					225					
cga	ttc	ttg	ttt	gtg	gtt	gct	cca	att	gga	ccg	tgg	gtt	ttc	ggg	gcg	835
Arg	Phe	Leu	Phe	Val	Val	Ala	Pro	Ile	Gly	Pro	Trp	Val	Phe	Gly	Ala	
230					235					240					245	
gcc	ttc	act	gcc	tac	gca	gtt	ttg	ccg	tcg	cag	ctg	cgt	gac	atg	gtt	883
Ala	Phe	Thr	Ala	Tyr	Ala	Val	Leu	Pro	Ser	Gln	Leu	Arg	Asp	Met	Val	
			250						255					260		
tct	gca	ccc	gtt	gcg	tat	tct	gcg	ctg	atc	gct	ttg	gtt	acc	tta	ggg	931
Ser	Ala	Pro	Val	Ala	Tyr	Ser	Ala	Leu	Ile	Ala	Leu	Val	Thr	Leu	Gly	
		265						270					275			
tct	gga	ttt	ggg	atc	caa	caa	ttc	ggg	cct	caa	atc	atg	ggc	acc	tct	979
Ser	Gly	Phe	Gly	Ile	Gln	Gln	Phe	Gly	Pro	Gln	Ile	Met	Gly	Thr	Ser	
		280					285					290				
aaa	act	cgc	ggg	ccg	att	ttg	gcc	atg	ttc	gtc	aca	gtc	atc	ggc	atg	1027
Lys	Thr	Arg	Gly	Pro	Ile	Leu	Ala	Met	Phe	Val	Thr	Val	Ile	Gly	Met	
	295					300					305					
atc	ggc	gcg	gtg	atc	gtg	gtg	atg	aac	cct	cat	cca	tgg	tgg	gcg	cta	1075
Ile	Gly	Ala	Val	Ile	Val	Val	Met	Asn	Pro	His	Pro	Trp	Trp	Ala	Leu	
310					315					320					325	
gtt	ggc	tgc	atg	gcc	ctc	ggc	ctg	tct	tat	ggc	ctg	tgt	atg	ttc	atg	1123
Val	Gly	Cys	Met	Ala	Leu	Gly	Leu	Ser	Tyr	Gly	Leu	Cys	Met	Phe	Met	
				330					335					340		
ggg	ttg	gcg	gaa	act	caa	aac	att	gct	cca	cct	att	gat	atg	gca	ggc	1171
Gly	Leu	Ala	Glu	Thr	Gln	Asn	Ile	Ala	Pro	Pro	Ile	Asp	Met	Ala	Gly	
			345					350					355			

ctg acg ggt att ttc tac tgc ctg acg tac gta ggt atg gtc ttt cca 1219
 Leu Thr Gly Ile Phe Tyr Cys Leu Thr Tyr Val Gly Met Val Phe Pro
 360 365 370
 gcc ttg atg acc tgg ttg aat caa tgg ctc agt tac ccg ttc atg ctg 1267
 Ala Leu Met Thr Trp Leu Asn Gln Trp Leu Ser Tyr Pro Phe Met Leu
 375 380 385
 ggc ttt ggt gcg gtg atg gca act att tgt ctg atc att gtg agt ttt 1315
 Gly Phe Gly Ala Val Met Ala Thr Ile Cys Leu Ile Ile Val Ser Phe
 390 395 400 405
 agt gca cgc cga ttc tgagaaacaa ctaaagtggag cca 1353
 Ser Ala Arg Arg Phe
 410

<210> 154

<211> 410

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 154

Met Gly Val Ser Ala Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg
 1 5 10 15
 Ala Gln Arg Lys Val Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val
 20 25 30
 Ala Trp Gly Gly Asn Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly
 35 40 45
 Glu Gly Phe Phe Ser Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr
 50 55 60
 Ala Ile Gly Val Ala Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp
 65 70 75 80
 Arg Tyr Gly Arg Arg Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile
 85 90 95
 Leu Gly Ser Ala Leu Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile
 100 105 110
 Ala Ile Gly Arg Val Leu Ser Gly Ile Ser Val Gly Met Val Met Thr
 115 120 125
 Ala Gly Gly Ser Trp Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro
 130 135 140
 Gly Val Lys Thr Ser Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr
 145 150 155 160
 Gly Gly Phe Ala Leu Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp
 165 170 175
 Leu Pro Leu Pro Gly Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr
 180 185 190
 Leu Ile Leu Phe Pro Leu Leu Ile Thr Ala Pro Glu Thr Arg Gln Ser
 195 200 205

Ala His Leu Lys Thr Lys Gly Ser Phe Trp Ser Asp Val Leu Val Pro
 210 215 220
 Ser Ala Leu Asp Lys Arg Phe Leu Phe Val Val Ala Pro Ile Gly Pro
 225 230 235 240
 Trp Val Phe Gly Ala Ala Phe Thr Ala Tyr Ala Val Leu Pro Ser Gln
 245 250 255
 Leu Arg Asp Met Val Ser Ala Pro Val Ala Tyr Ser Ala Leu Ile Ala
 260 265 270
 Leu Val Thr Leu Gly Ser Gly Phe Gly Ile Gln Gln Phe Gly Pro Gln
 275 280 285
 Ile Met Gly Thr Ser Lys Thr Arg Gly Pro Ile Leu Ala Met Phe Val
 290 295 300
 Thr Val Ile Gly Met Ile Gly Ala Val Ile Val Val Met Asn Pro His
 305 310 315 320
 Pro Trp Trp Ala Leu Val Gly Cys Met Ala Leu Gly Leu Ser Tyr Gly
 325 330 335
 Leu Cys Met Phe Met Gly Leu Ala Glu Thr Gln Asn Ile Ala Pro Pro
 340 345 350
 Ile Asp Met Ala Gly Leu Thr Gly Ile Phe Tyr Cys Leu Thr Tyr Val
 355 360 365
 Gly Met Val Phe Pro Ala Leu Met Thr Trp Leu Asn Gln Trp Leu Ser
 370 375 380
 Tyr Pro Phe Met Leu Gly Phe Gly Ala Val Met Ala Thr Ile Cys Leu
 385 390 395 400
 Ile Ile Val Ser Phe Ser Ala Arg Arg Phe
 405 410

<210> 155

<211> 703

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(703)

<223> FRXA00803

<400> 155

tcatccttcc ttagctcgcg tgagcttccc aagcgtaagc acccccgtgt gagggcataa 60

cggccgttct gttaaagatt ggtctggcca tttcctccat atg ggg gtg tcc gcg 115
 Met Gly Val Ser Ala
 1 5

ctt aac atg tct gac atg gtg gcg aac aaa cgg gca cag cgt aaa gtc 163
 Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg Ala Gln Arg Lys Val
 10 15 20

tgg cta gcg gta gct tta tcg gtc ttt acg gtc gcg tgg ggt ggc aat 211
 Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val Ala Trp Gly Gly Asn
 25 30 35

gaa ttc act ccc ttg ctg gtg ttt tac cga ggt gaa ggg ttc ttt agc 259
 Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly Glu Gly Phe Phe Ser
 40 45 50

aac ctg ttc atc gac ctt ttg ctg gtg ttt tat gcc atc gga gta gcg 307
 Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr Ala Ile Gly Val Ala
 55 60 65

gta ggt ttg ctg gca gct ggt cct tta tct gac cgc tat ggc cga cgt 355
 Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp Arg Tyr Gly Arg Arg
 70 75 80 85

gcc gtc atg ttg cct gcg cca ttg atc gcg atc ttg ggt tcc gcg ttg 403
 Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile Leu Gly Ser Ala Leu
 90 95 100

att gcc tcg ggt gaa gaa acc gcc atc ctg att gcc att ggt cga gtg 451
 Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile Ala Ile Gly Arg Val
 105 110 115

ctg tcg gga att tcg gtg ggc atg gtg atg aca gcg gga ggt tcc tgg 499
 Leu Ser Gly Ile Ser Val Gly Met Val Met Thr Ala Gly Gly Ser Trp
 120 125 130

att aag gag ctt tca tcg tcg cgg ttt gag cca ggg gtg aaa acc agt 547
 Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro Gly Val Lys Thr Ser
 135 140 145

gct ggt gca aaa cgc gca tcg atg tct ttg acc ggt ggt ttt gcg ctc 595
 Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr Gly Gly Phe Ala Leu
 150 155 160 165

ggc cca gcg ctt gct ggt gtg atg gca cag tgg ctg cca caa cct gga 643
 Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp Leu Pro Gln Pro Gly
 170 175 180

cag ttg gca tat gtt ttg cac att att ctc act ctg att ttg ttc ccg 691
 Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr Leu Ile Leu Phe Pro
 185 190 195

ttg ctt att aca 703
 Leu Leu Ile Thr
 200

<210> 156

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

Met Gly Val Ser Ala Leu Asn Met Ser Asp Met Val Ala Asn Lys Arg
 1 5 10 15

Ala Gln Arg Lys Val Trp Leu Ala Val Ala Leu Ser Val Phe Thr Val
 20 25 30

Ala Trp Gly Gly Asn Glu Phe Thr Pro Leu Leu Val Phe Tyr Arg Gly
 35 40 45

Glu Gly Phe Phe Ser Asn Leu Phe Ile Asp Leu Leu Leu Val Phe Tyr
 50 55 60

Ala Ile Gly Val Ala Val Gly Leu Leu Ala Ala Gly Pro Leu Ser Asp
 65 70 75 80

Arg Tyr Gly Arg Arg Ala Val Met Leu Pro Ala Pro Leu Ile Ala Ile
 85 90 95

Leu Gly Ser Ala Leu Ile Ala Ser Gly Glu Glu Thr Ala Ile Leu Ile
 100 105 110

Ala Ile Gly Arg Val Leu Ser Gly Ile Ser Val Gly Met Val Met Thr
 115 120 125

Ala Gly Gly Ser Trp Ile Lys Glu Leu Ser Ser Ser Arg Phe Glu Pro
 130 135 140

Gly Val Lys Thr Ser Ala Gly Ala Lys Arg Ala Ser Met Ser Leu Thr
 145 150 155 160

Gly Gly Phe Ala Leu Gly Pro Ala Leu Ala Gly Val Met Ala Gln Trp
 165 170 175

Leu Pro Gln Pro Gly Gln Leu Ala Tyr Val Leu His Ile Ile Leu Thr
 180 185 190

Leu Ile Leu Phe Pro Leu Leu Ile Thr
 195 200

<210> 157

<211> 1014

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(991)

<223> RXA01407

<400> 157

atccgggggaa cggatcccaa agatctcctt gatgccatcg cggtttttaac ctggccagct 60

ctggttgccc cagtgatcgc ccacttctg ggaggtcttc ttg caa gat acc att 115
 Leu Gln Asp Thr Ile
 1 5

ggt tgc cga tgg atc ttc ctc ctc aac gtg ccc tta gga atc atc gcg 163
 Gly Cys Arg Trp Ile Phe Leu Leu Asn Val Pro Leu Gly Ile Ile Ala
 10 15 20

atc atg gct gga cta ttc atc cag ccc aag aac acg gcc gtg aat gtg 211
 Ile Met Ala Gly Leu Phe Ile Gln Pro Lys Asn Thr Ala Val Asn Val
 25 30 35

aag cga ttt gat cgg cca ggt ttc ctc ggc gca atg ctg gtg atg gtg 259

Lys	Arg	Phe	Asp	Arg	Pro	Gly	Phe	Leu	Gly	Ala	Met	Leu	Val	Met	Val	
		40					45					50				
gcg	caa	gcc	gtg	att	gcg	gag	tta	att	tgc	agc	aga	agt	ccg	gcc	gca	307
Ala	Gln	Ala	Val	Ile	Ala	Glu	Leu	Ile	Cys	Ser	Arg	Ser	Pro	Ala	Ala	
	55					60				65						
ctt	act	atc	tgt	gca	tgc	ctc	gtc	tta	agt	gct	gcg	gtg	gta	tgc	ggc	355
Leu	Thr	Ile	Cys	Ala	Cys	Leu	Val	Leu	Ser	Ala	Ala	Val	Val	Cys	Gly	
	70				75					80					85	
ttt	gta	gtg	cgc	tgg	ctg	cga	gtt	cca	ggc	cga	ctt	ttt	gat	ctc	agc	403
Phe	Val	Val	Arg	Trp	Leu	Arg	Val	Pro	Gly	Arg	Leu	Phe	Asp	Leu	Ser	
				90					95					100		
atc	atg	cgc	atc	cca	ggc	ttc	cga	gtg	ggc	aat	tcc	tcc	gga	agt	atc	451
Ile	Met	Arg	Ile	Pro	Gly	Phe	Arg	Val	Gly	Asn	Ser	Ser	Gly	Ser	Ile	
			105					110					115			
tac	cgc	ttg	gta	atc	acc	gca	gca	cca	ttc	atg	ttc	act	ttg	ctc	ttc	499
Tyr	Arg	Leu	Val	Ile	Thr	Ala	Ala	Pro	Phe	Met	Phe	Thr	Leu	Leu	Phe	
		120					125					130				
caa	gtg	gcg	ttt	ggg	tgg	tct	gca	aca	tta	gcg	ggc	gcc	atg	gtg	gtc	547
Gln	Val	Ala	Phe	Gly	Trp	Ser	Ala	Thr	Leu	Ala	Gly	Ala	Met	Val	Val	
	135					140					145					
gca	cta	ttc	gca	ggc	aac	gtg	gca	atc	aaa	cct	ttc	acc	acg	ccg	atc	595
Ala	Leu	Phe	Ala	Gly	Asn	Val	Ala	Ile	Lys	Pro	Phe	Thr	Thr	Pro	Ile	
	150				155					160					165	
att	aaa	cgc	tgg	aat	ttc	aaa	cca	gta	ctg	gtc	ttt	tct	aac	gct	gct	643
Ile	Lys	Arg	Trp	Asn	Phe	Lys	Pro	Val	Leu	Val	Phe	Ser	Asn	Ala	Ala	
				170					175					180		
ggc	gcc	ttg	gta	ttg	gca	act	ttt	ttg	ttc	gtt	cgt	gca	gat	acc	cca	691
Gly	Ala	Leu	Val	Leu	Ala	Thr	Phe	Leu	Phe	Val	Arg	Ala	Asp	Thr	Pro	
			185					190					195			
ctg	gtt	ctc	atc	gtg	ctg	ctg	ctc	ttt	gtt	tcg	ggc	gca	tta	agg	tcc	739
Leu	Val	Leu	Ile	Val	Leu	Leu	Leu	Phe	Val	Ser	Gly	Ala	Leu	Arg	Ser	
		200					205					210				
ctc	ggc	ttc	agc	gcc	tac	aac	acc	ttg	cag	ttt	gtc	gat	atc	tca	cca	787
Leu	Gly	Phe	Ser	Ala	Tyr	Asn	Thr	Leu	Gln	Phe	Val	Asp	Ile	Ser	Pro	
	215					220					225					
gaa	caa	acc	agc	aac	gcc	aac	gtg	tta	tca	gca	acc	ctg	cac	caa	cta	835
Glu	Gln	Thr	Ser	Asn	Ala	Asn	Val	Leu	Ser	Ala	Thr	Leu	His	Gln	Leu	
	230				235					240					245	
ggc	atg	tct	ttg	ggc	att	gcg	gta	gca	gtc	atc	gcc	atg	tcc	ctt	gca	883
Gly	Met	Ser	Leu	Gly	Ile	Ala	Val	Ala	Val	Ile	Ala	Met	Ser	Leu	Ala	
				250					255					260		
ccc	acc	gcc	aac	tgg	gca	ttc	cca	ctg	gca	gca	gcg	ttg	ttc	ctc	att	931
Pro	Thr	Ala	Asn	Trp	Ala	Phe	Pro	Leu	Ala	Ala	Ala	Leu	Phe	Leu	Ile	
			265					270					275			
cct	cta	atc	ggc	gca	cta	tct	ttg	cct	cgc	gac	ggc	ggc	gcc	cga	gcc	979
Pro	Leu	Ile	Gly	Ala	Leu	Ser	Leu	Pro	Arg	Asp	Gly	Gly	Ala	Arg	Ala	

280 285 290
 ttt tcc tcc tct tagaaaccca cttctgaaag gta 1014
 Phe Ser Ser Ser
 295

 <210> 158
 <211> 297
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 158
 Leu Gln Asp Thr Ile Gly Cys Arg Trp Ile Phe Leu Leu Asn Val Pro
 1 5 10 15
 Leu Gly Ile Ile Ala Ile Met Ala Gly Leu Phe Ile Gln Pro Lys Asn
 20 25 30
 Thr Ala Val Asn Val Lys Arg Phe Asp Arg Pro Gly Phe Leu Gly Ala
 35 40 45
 Met Leu Val Met Val Ala Gln Ala Val Ile Ala Glu Leu Ile Cys Ser
 50 55 60
 Arg Ser Pro Ala Ala Leu Thr Ile Cys Ala Cys Leu Val Leu Ser Ala
 65 70 75 80
 Ala Val Val Cys Gly Phe Val Val Arg Trp Leu Arg Val Pro Gly Arg
 85 90 95
 Leu Phe Asp Leu Ser Ile Met Arg Ile Pro Gly Phe Arg Val Gly Asn
 100 105 110
 Ser Ser Gly Ser Ile Tyr Arg Leu Val Ile Thr Ala Ala Pro Phe Met
 115 120 125
 Phe Thr Leu Leu Phe Gln Val Ala Phe Gly Trp Ser Ala Thr Leu Ala
 130 135 140
 Gly Ala Met Val Val Ala Leu Phe Ala Gly Asn Val Ala Ile Lys Pro
 145 150 155 160
 Phe Thr Thr Pro Ile Ile Lys Arg Trp Asn Phe Lys Pro Val Leu Val
 165 170 175
 Phe Ser Asn Ala Ala Gly Ala Leu Val Leu Ala Thr Phe Leu Phe Val
 180 185 190
 Arg Ala Asp Thr Pro Leu Val Leu Ile Val Leu Leu Leu Phe Val Ser
 195 200 205
 Gly Ala Leu Arg Ser Leu Gly Phe Ser Ala Tyr Asn Thr Leu Gln Phe
 210 215 220
 Val Asp Ile Ser Pro Glu Gln Thr Ser Asn Ala Asn Val Leu Ser Ala
 225 230 235 240
 Thr Leu His Gln Leu Gly Met Ser Leu Gly Ile Ala Val Ala Val Ile
 245 250 255

Ala Met Ser Leu Ala Pro Thr Ala Asn Trp Ala Phe Pro Leu Ala Ala
 260 265 270

Ala Leu Phe Leu Ile Pro Leu Ile Gly Ala Leu Ser Leu Pro Arg Asp
 275 280 285

Gly Gly Ala Arg Ala Phe Ser Ser Ser
 290 295

<210> 159

<211> 324

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(301)

<223> RXA01408

<400> 159

cgcatagagt tatctcgaaa ctaccaagac gggtttctttt ctttagatct aaggaggaga 60

gaccgtcttt caccctttca tctgattgga catcgacgcc atg cgc aat gat cgg 115
 Met Arg Asn Asp Arg
 1 5

tcc ttt agc gtt ccc att gcg cta ctt gcc gcg gga gca ctg ttt cta 163
 Ser Phe Ser Val Pro Ile Ala Leu Leu Ala Ala Gly Ala Leu Phe Leu
 10 15 20

gaa atc ctc gac ggc acc atc ctg aca acc gca gtg cca gct att gct 211
 Glu Ile Leu Asp Gly Thr Ile Leu Thr Thr Ala Val Pro Ala Ile Ala
 25 30 35

cgt gac ttc ggt att gac gcc gtg gat gtc agc att gca ctg gtt gct 259
 Arg Asp Phe Gly Ile Asp Ala Val Asp Val Ser Ile Ala Leu Val Ala
 40 45 50

tac ttg gca gcc gca gca gct ggc att ccg ctg cag ggt ggc 301
 Tyr Leu Ala Ala Ala Ala Gly Ile Pro Leu Gln Gly Gly
 55 60 65

tagcggatcg atttgggtgtg cgc 324

<210> 160

<211> 67

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

Met Arg Asn Asp Arg Ser Phe Ser Val Pro Ile Ala Leu Leu Ala Ala
 1 5 10 15

Gly Ala Leu Phe Leu Glu Ile Leu Asp Gly Thr Ile Leu Thr Thr Ala
 20 25 30

Val Pro Ala Ile Ala Arg Asp Phe Gly Ile Asp Ala Val Asp Val Ser
 35 40 45

Ile Ala Leu Val Ala Tyr Leu Ala Ala Ala Ala Ala Gly Ile Pro Leu
 50 55 60

Gln Gly Gly
 65

<210> 161

<211> 1275

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1252)

<223> RXN01922

<400> 161

acactccttt ggtcacctgg ttggttgag ggaaacagac cgccaagaa cccaagaaat 60

cccaagaaaa catgctgctt atgaattaaa gtgagcaccc atg aga tca gga aac 115
 Met Arg Ser Gly Asn
 1 5

gcc aat cgc gtc ttc ata ggt gtt acc atc ctg ctg ttt act gca gga 163
 Ala Asn Arg Val Phe Ile Gly Val Thr Ile Leu Leu Phe Thr Ala Gly
 10 15 20

tgg gca gcc aat cat ttc gcg tca gtg ttg gtg ttg atc cgt gaa caa 211
 Trp Ala Ala Asn His Phe Ala Ser Val Leu Val Leu Ile Arg Glu Gln
 25 30 35

tta gac gta tca agc gtg ctg gtc aac ggc gct ttt ggt att tat gca 259
 Leu Asp Val Ser Ser Val Leu Val Asn Gly Ala Phe Gly Ile Tyr Ala
 40 45 50

ctg gga ctt ctt cca agt ttg ctc gca ggc ggt gtg ctt gcc gac cgt 307
 Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly Gly Val Leu Ala Asp Arg
 55 60 65

ttt ggt gcc cgc atg gtg gta ctc acc gga ggt gta ctt tct gcg ctt 355
 Phe Gly Ala Arg Met Val Val Leu Thr Gly Gly Val Leu Ser Ala Leu
 70 75 80 85

gga aac ctt tct ctt tta gcg ttt cat gat ggt cct tcc ctc ctg gta 403
 Gly Asn Leu Ser Leu Leu Ala Phe His Asp Gly Pro Ser Leu Leu Val
 90 95 100

gga cga ttc atc gtt ggt ctg ggc gtt gga tta gtc gtc agc gcg ggc 451
 Gly Arg Phe Ile Val Gly Leu Gly Val Gly Leu Val Val Ser Ala Gly
 105 110 115

acc gca tgg gcg ggc aga ttg cgc gga gca agc ggc gtg aca ttg gcc 499
 Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala Ser Gly Val Thr Leu Ala
 120 125 130

ggc att att ctg acc gcc ggt ttc atg atg ggg ccg att gtg aca agt 547
 Gly Ile Ile Leu Thr Ala Gly Phe Met Met Gly Pro Ile Val Thr Ser
 135 140 145

ggg ttg ggg atg gcg tcg aca agc att att acg ccc ttt gcc ata agc 595

gaa

<210> 162

<211> 384

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 162

Met Arg Ser Gly Asn Ala Asn Arg Val Phe Ile Gly Val Thr Ile Leu
 1 5 10 15

Leu Phe Thr Ala Gly Trp Ala Ala Asn His Phe Ala Ser Val Leu Val
 20 25 30

Leu Ile Arg Glu Gln Leu Asp Val Ser Ser Val Leu Val Asn Gly Ala
 35 40 45

Phe Gly Ile Tyr Ala Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly Gly
 50 55 60

Val Leu Ala Asp Arg Phe Gly Ala Arg Met Val Val Leu Thr Gly Gly
 65 70 75 80

Val Leu Ser Ala Leu Gly Asn Leu Ser Leu Leu Ala Phe His Asp Gly
 85 90 95

Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly Leu
 100 105 110

Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala Ser
 115 120 125

Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met Gly
 130 135 140

Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile Thr
 145 150 155 160

Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val Gly
 165 170 175

Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala Ser
 180 185 190

Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val Ser
 195 200 205

Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu Ile
 210 215 220

Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu Leu
 225 230 235 240

Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala Gln
 245 250 255

Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val Gly
 260 265 270

Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly Asp
 275 280 285

Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly Thr
 290 295 300

Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr Tyr
 305 310 315 320

Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val Phe
 325 330 335

Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu Pro
 340 345 350

His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala Leu
 355 360 365

Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val Val
 370 375 380

<210> 163
 <211> 1130
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1107)
 <223> FRXA01922

<400> 163

ctg	ctg	ttt	act	gca	gga	tgg	gca	gcc	aat	cat	ttc	gcg	tca	gtg	ttg	48
Leu	Leu	Phe	Thr	Ala	Gly	Trp	Ala	Ala	Asn	His	Phe	Ala	Ser	Val	Leu	
1				5					10					15		
gtg	ttg	atc	cgt	gaa	caa	tta	gac	gta	tca	agc	gtg	ctg	gtc	aac	ggc	96
Val	Leu	Ile	Arg	Glu	Gln	Leu	Asp	Val	Ser	Ser	Val	Leu	Val	Asn	Gly	
			20					25					30			
gct	ttt	ggt	att	tat	gca	ctg	gga	ctt	ctt	cca	agt	ttg	ctc	gca	ggc	144
Ala	Phe	Gly	Ile	Tyr	Ala	Leu	Gly	Leu	Leu	Pro	Ser	Leu	Leu	Ala	Gly	
			35				40					45				
ggt	gtg	ctt	gcc	gac	cgt	ttt	ggt	gcc	cgc	atg	gtg	gta	ctc	acc	gga	192
Gly	Val	Leu	Ala	Asp	Arg	Phe	Gly	Ala	Arg	Met	Val	Val	Leu	Thr	Gly	
	50					55				60						
ggt	gta	ctt	tct	gcg	ctt	gga	aac	ctt	tct	ctt	tta	gcg	ttt	cat	gat	240
Gly	Val	Leu	Ser	Ala	Leu	Gly	Asn	Leu	Ser	Leu	Leu	Ala	Phe	His	Asp	
65					70				75					80		
ggt	cct	tcc	ctc	ctg	gta	gga	cga	ttc	atc	gtt	ggt	ctg	ggc	gtt	gga	288
Gly	Pro	Ser	Leu	Leu	Val	Gly	Arg	Phe	Ile	Val	Gly	Leu	Gly	Val	Gly	
			85						90					95		
tta	gtc	gtc	agc	gcg	ggc	acc	gca	tgg	gcg	ggc	aga	ttg	cgc	gga	gca	336
Leu	Val	Val	Ser	Ala	Gly	Thr	Ala	Trp	Ala	Gly	Arg	Leu	Arg	Gly	Ala	
			100					105				110				
agc	ggc	gtg	aca	ttg	gcc	ggc	att	att	ctg	acc	gcc	ggt	ttc	atg	atg	384
Ser	Gly	Val	Thr	Leu	Ala	Gly	Ile	Ile	Leu	Thr	Ala	Gly	Phe	Met	Met	
		115					120					125				

ggg ccg att gtg aca agt ggg ttg ggg atg gcg tcg aca agc att att	432
Gly Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile	
130 135 140	
acg ccc ttt gcc ata agc gtt gcc ctc tcg ctg atc gcg gtg gtt gtg	480
Thr Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val	
145 150 155 160	
gga ttt gcg ctt ggc gat gcc cgc agc acc ccg agc gca ctt ggc gca	528
Gly Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala	
165 170 175	
tcc agc gga atc aaa cac gaa cga agc atg aaa aag gcc ctc gcg gtg	576
Ser Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val	
180 185 190	
tcc ttg ccg atg gca att tgg gtg ttc agc tgc atc acc acc tcc ctg	624
Ser Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu	
195 200 205	
atc gtg atg tcc gcg cgc atc gac tcc acc ttc ggc aac gcc att ctt	672
Ile Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu	
210 215 220	
ctc ccc gga atc ggc gcg gcg atc gcc ttc agc gca ggc ctg atc gca	720
Leu Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala	
225 230 235 240	
caa ttt tta ggt agg aaa ttc gcg tgg ggt cgt ggc tcc gga atc gtg	768
Gln Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val	
245 250 255	
ggc gcg ctg tgt gcc ctc gcg ggt ttt gcg ctg gca gct ttt ggt ggc	816
Gly Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly	
260 265 270	
gac tcc att cca gtg tgg ctt ttc gtt atc gcc tcg atc ctg ttc ggc	864
Asp Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly	
275 280 285	
acc gca tat ggc ctc tgc ctg cgc gaa ggc ctc ctc agc atc gaa act	912
Thr Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr	
290 295 300	
tac acg cca ctc aac cga cgt ggc acc ggc atc ggc atc tat tat gtg	960
Tyr Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val	
305 310 315 320	
ttc acg tat ttg gga ttc ggg ctg cca gtg ctt ctc gac gcc ctc ctc	1008
Phe Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu	
325 330 335	
ccg cac ctt ggc gcc tcc att ccg ctg tac gcg ctg gcg gcg ctc gcc	1056
Pro His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala	
340 345 350	
ctt ggc tcc gca gta atc cgc ggc gta caa atc aag cgc ggg tat gtg	1104
Leu Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val	
355 360 365	

gtt tagatttcta cctacgacct gaa
Val

1130

<210> 164

<211> 369

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 164

Leu Leu Phe Thr Ala Gly Trp Ala Ala Asn His Phe Ala Ser Val Leu
1 5 10 15

Val Leu Ile Arg Glu Gln Leu Asp Val Ser Ser Val Leu Val Asn Gly
20 25 30

Ala Phe Gly Ile Tyr Ala Leu Gly Leu Leu Pro Ser Leu Leu Ala Gly
35 40 45

Gly Val Leu Ala Asp Arg Phe Gly Ala Arg Met Val Val Leu Thr Gly
50 55 60

Gly Val Leu Ser Ala Leu Gly Asn Leu Ser Leu Leu Ala Phe His Asp
65 70 75 80

Gly Pro Ser Leu Leu Val Gly Arg Phe Ile Val Gly Leu Gly Val Gly
85 90 95

Leu Val Val Ser Ala Gly Thr Ala Trp Ala Gly Arg Leu Arg Gly Ala
100 105 110

Ser Gly Val Thr Leu Ala Gly Ile Ile Leu Thr Ala Gly Phe Met Met
115 120 125

Gly Pro Ile Val Thr Ser Gly Leu Gly Met Ala Ser Thr Ser Ile Ile
130 135 140

Thr Pro Phe Ala Ile Ser Val Ala Leu Ser Leu Ile Ala Val Val Val
145 150 155 160

Gly Phe Ala Leu Gly Asp Ala Arg Ser Thr Pro Ser Ala Leu Gly Ala
165 170 175

Ser Ser Gly Ile Lys His Glu Arg Ser Met Lys Lys Ala Leu Ala Val
180 185 190

Ser Leu Pro Met Ala Ile Trp Val Phe Ser Cys Ile Thr Thr Ser Leu
195 200 205

Ile Val Met Ser Ala Arg Ile Asp Ser Thr Phe Gly Asn Ala Ile Leu
210 215 220

Leu Pro Gly Ile Gly Ala Ala Ile Ala Phe Ser Ala Gly Leu Ile Ala
225 230 235 240

Gln Phe Leu Gly Arg Lys Phe Ala Trp Gly Arg Gly Ser Gly Ile Val
245 250 255

Gly Ala Leu Cys Ala Leu Ala Gly Phe Ala Leu Ala Ala Phe Gly Gly
260 265 270

Asp Ser Ile Pro Val Trp Leu Phe Val Ile Ala Ser Ile Leu Phe Gly
 275 280 285
 Thr Ala Tyr Gly Leu Cys Leu Arg Glu Gly Leu Leu Ser Ile Glu Thr
 290 295 300
 Tyr Thr Pro Leu Asn Arg Arg Gly Thr Gly Ile Gly Ile Tyr Tyr Val
 305 310 315 320
 Phe Thr Tyr Leu Gly Phe Gly Leu Pro Val Leu Leu Asp Ala Leu Leu
 325 330 335
 Pro His Leu Gly Ala Ser Ile Pro Leu Tyr Ala Leu Ala Ala Leu Ala
 340 345 350
 Leu Gly Ser Ala Val Ile Arg Gly Val Gln Ile Lys Arg Gly Tyr Val
 355 360 365

Val

<210> 165
 <211> 362
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(339)
 <223> RXA02060

<400> 165
 gaa ttt gcc cgc att ttg aag cca aag gga cag gtc atc gtg ctt acc 48
 Glu Phe Ala Arg Ile Leu Lys Pro Lys Gly Gln Val Ile Val Leu Thr
 1 5 10 15
 gca gat acc ggc cac ttg gct gag ctt cgt gaa cca ctg ggc atc att 96
 Ala Asp Thr Gly His Leu Ala Glu Leu Arg Glu Pro Leu Gly Ile Ile
 20 25 30
 gat gtg gag gcc ggc aaa gtt gat cgc atg atc gaa caa gcg gca ggc 144
 Asp Val Glu Ala Gly Lys Val Asp Arg Met Ile Glu Gln Ala Ala Gly
 35 40 45
 cac ctc aag cca gtt ggc gaa aga gac ttg gtg gaa ttt gaa atg ctg 192
 His Leu Lys Pro Val Gly Glu Arg Asp Leu Val Glu Phe Glu Met Leu
 50 55 60
 ctg gat caa aaa tcc att gca tct cag atc ggt atg agc cct tct gca 240
 Leu Asp Gln Lys Ser Ile Ala Ser Gln Ile Gly Met Ser Pro Ser Ala
 65 70 75 80
 cgc cac att aag cct gag gct ttg gcg gaa cgc atc gcc gct cta cca 288
 Arg His Ile Lys Pro Glu Ala Leu Ala Glu Arg Ile Ala Ala Leu Pro
 85 90 95
 gaa caa atg aag gtt aca gcc cgg gcc aag atc acc agg ctg gaa cgc 336
 Glu Gln Met Lys Val Thr Ala Arg Ala Lys Ile Thr Arg Leu Glu Arg
 100 105 110

atc taactcttat ctcaactgggc ctt
Ile

362

<210> 166
<211> 113
<212> PRT
<213> Corynebacterium glutamicum

<400> 166
Glu Phe Ala Arg Ile Leu Lys Pro Lys Gly Gln Val Ile Val Leu Thr
1 5 10 15
Ala Asp Thr Gly His Leu Ala Glu Leu Arg Glu Pro Leu Gly Ile Ile
20 25 30
Asp Val Glu Ala Gly Lys Val Asp Arg Met Ile Glu Gln Ala Ala Gly
35 40 45
His Leu Lys Pro Val Gly Glu Arg Asp Leu Val Glu Phe Glu Met Leu
50 55 60
Leu Asp Gln Lys Ser Ile Ala Ser Gln Ile Gly Met Ser Pro Ser Ala
65 70 75 80
Arg His Ile Lys Pro Glu Ala Leu Ala Glu Arg Ile Ala Ala Leu Pro
85 90 95
Glu Gln Met Lys Val Thr Ala Arg Ala Lys Ile Thr Arg Leu Glu Arg
100 105 110
Ile

<210> 167
<211> 1395
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1372)
<223> RXN01936

<400> 167
gcgcggtgac accacagccg ttgtcagcgg cgcttgggtct gtggaggatc gccgaggtta 60
ctaacaaata ggccaacaa agagggtctaa gctctacctg gtg agt ttc cga gat 115
Val Ser Phe Arg Asp
1 5
att ttc gct gac acc aga ccg ctg aaa gaa ccg gcc ttc aaa cgc ctc 163
Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro Ala Phe Lys Arg Leu
10 15 20
tgg ctt ggc aat gtt gcc acc gtc att ggt gcc caa tta act gtt gtt 211
Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala Gln Leu Thr Val Val
25 30 35

gcc gtt ccg gtg cag att tac caa atg act ggg tcc tcc ggc tat gtg	259
Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly Ser Ser Gly Tyr Val	
40 45 50	
ggc ttg acc ggg ctt ttt ggc ctt att cct ttg gtt att ttt ggc ctt	307
Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu Val Ile Phe Gly Leu	
55 60 65	
tat ggt gga tcc att gcg gat gct ttt gat aaa cgc atc gtg ctg atc	355
Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys Arg Ile Val Leu Ile	
70 75 80 85	
tgc acc acg atc ggc atg tgt gtc acc act gcc ggt ttt tgg gtg ctg	403
Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala Gly Phe Trp Val Leu	
90 95 100	
acc att tta ggc aat gag aat att tgg ctc ctg tta ata aac ttt tct	451
Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu Leu Ile Asn Phe Ser	
105 110 115	
tta cag cag gca ttt ttc gcg gtg aat caa ccc acc cga acg gcg atc	499
Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro Thr Arg Thr Ala Ile	
120 125 130	
ctt cga agt att ttg ccg att gat caa tta gcg tcg gca aca tca ctg	547
Leu Arg Ser Ile Leu Pro Ile Asp Gln Leu Ala Ser Ala Thr Ser Leu	
135 140 145	
aat atg ctg ctc atg cag acc ggc gca atc gtt ggc ccg ctg atc gca	595
Asn Met Leu Leu Met Gln Thr Gly Ala Ile Val Gly Pro Leu Ile Ala	
150 155 160 165	
ggt gcg ttg att ccg ctg atc ggt ttc ggg tgg ctg tat ttc ctt gat	643
Gly Ala Leu Ile Pro Leu Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp	
170 175 180	
gtt gtc tcc atc atc ccc aca ctg tgg gct gta tgg tca ctg cct tcg	691
Val Val Ser Ile Ile Pro Thr Leu Trp Ala Val Trp Ser Leu Pro Ser	
185 190 195	
atc aag cca tcc ggc aag gtg atg aag gct ggt ttc gcc agt gtg gtg	739
Ile Lys Pro Ser Gly Lys Val Met Lys Ala Gly Phe Ala Ser Val Val	
200 205 210	
gat ggc ctg aag tat ttg gct ggc caa ccc gtg ttg ttg atg gtg atg	787
Asp Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val Leu Leu Met Val Met	
215 220 225	
gtg ctg gat ctt atc gcc atg att ttc ggc atg cca cgt gcg ctt tac	835
Val Leu Asp Leu Ile Ala Met Ile Phe Gly Met Pro Arg Ala Leu Tyr	
230 235 240 245	
ccc gag atc gca gaa gtg aac ttc ggt ggg ggt gac gcc ggt gca acg	883
Pro Glu Ile Ala Glu Val Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr	
250 255 260	
atg ctg gcg ttc atg tac tca tcc atg gct gtt ggc gca gtt ctt ggc	931
Met Leu Ala Phe Met Tyr Ser Ser Met Ala Val Gly Ala Val Leu Gly	
265 270 275	

ggc gtg ctg tct ggt tgg gtg gcc cgg att agc cgc cag ggt gtt gca 979
 Gly Val Leu Ser Gly Trp Val Ala Arg Ile Ser Arg Gln Gly Val Ala
 280 285 290

gtt tat tgg tgc atc atc gcc tgg ggc gca gcc gtt gct ttg ggt ggt 1027
 Val Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala Val Ala Leu Gly Gly
 295 300 305

gtg gca att gtt gtc agc ccc ggc gcg gtg act gcg tgg gcg tgg atg 1075
 Val Ala Ile Val Val Ser Pro Gly Ala Val Thr Ala Trp Ala Trp Met
 310 315 320 325

ttc atc atc atg atg gtc att ggt ggc atg gct gac atg ttc agc tcg 1123
 Phe Ile Ile Met Met Val Ile Gly Gly Met Ala Asp Met Phe Ser Ser
 330 335 340

gca gtt cga aac gct att ttg cag cag tct gct gcg gaa cat gtg cag 1171
 Ala Val Arg Asn Ala Ile Leu Gln Gln Ser Ala Ala Glu His Val Gln
 345 350 355

ggc cga atc caa ggt gtg tgg atc atc gtc gtg gtg ggt gga cct cgt 1219
 Gly Arg Ile Gln Gly Val Trp Ile Ile Val Val Val Gly Gly Pro Arg
 360 365 370

tta gct gac gtc ctt cac ggt tgg gcc gct gag ccc ctc ggc gca ggt 1267
 Leu Ala Asp Val Leu His Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly
 375 380 385

tgg acg gta tta tgg ggc gga gta gcg gtg gtt gta ctc act gca att 1315
 Trp Thr Val Leu Trp Gly Gly Val Ala Val Val Val Leu Thr Ala Ile
 390 395 400 405

tgt atg gtg gcg gtg cct aaa ttc tgg aaa tac gag aaa cca aaa att 1363
 Cys Met Val Ala Val Pro Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile
 410 415 420

acc ggc atc taaataactta tccatgccca ttt 1395
 Thr Gly Ile

<210> 168

<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

Val Ser Phe Arg Asp Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro
 1 5 10 15

Ala Phe Lys Arg Leu Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala
 20 25 30

Gln Leu Thr Val Val Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly
 35 40 45

Ser Ser Gly Tyr Val Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu
 50 55 60

Val Ile Phe Gly Leu Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys
 65 70 75 80

Arg	Ile	Val	Leu	Ile	Cys	Thr	Thr	Ile	Gly	Met	Cys	Val	Thr	Thr	Ala	
				85					90						95	
Gly	Phe	Trp	Val	Leu	Thr	Ile	Leu	Gly	Asn	Glu	Asn	Ile	Trp	Leu	Leu	
			100					105					110			
Leu	Ile	Asn	Phe	Ser	Leu	Gln	Gln	Ala	Phe	Phe	Ala	Val	Asn	Gln	Pro	
		115					120					125				
Thr	Arg	Thr	Ala	Ile	Leu	Arg	Ser	Ile	Leu	Pro	Ile	Asp	Gln	Leu	Ala	
	130					135					140					
Ser	Ala	Thr	Ser	Leu	Asn	Met	Leu	Leu	Met	Gln	Thr	Gly	Ala	Ile	Val	
145					150					155					160	
Gly	Pro	Leu	Ile	Ala	Gly	Ala	Leu	Ile	Pro	Leu	Ile	Gly	Phe	Gly	Trp	
				165					170					175		
Leu	Tyr	Phe	Leu	Asp	Val	Val	Ser	Ile	Ile	Pro	Thr	Leu	Trp	Ala	Val	
			180					185					190			
Trp	Ser	Leu	Pro	Ser	Ile	Lys	Pro	Ser	Gly	Lys	Val	Met	Lys	Ala	Gly	
		195					200					205				
Phe	Ala	Ser	Val	Val	Asp	Gly	Leu	Lys	Tyr	Leu	Ala	Gly	Gln	Pro	Val	
	210					215					220					
Leu	Leu	Met	Val	Met	Val	Leu	Asp	Leu	Ile	Ala	Met	Ile	Phe	Gly	Met	
225					230					235					240	
Pro	Arg	Ala	Leu	Tyr	Pro	Glu	Ile	Ala	Glu	Val	Asn	Phe	Gly	Gly	Gly	
				245					250					255		
Asp	Ala	Gly	Ala	Thr	Met	Leu	Ala	Phe	Met	Tyr	Ser	Ser	Met	Ala	Val	
			260					265					270			
Gly	Ala	Val	Leu	Gly	Gly	Val	Leu	Ser	Gly	Trp	Val	Ala	Arg	Ile	Ser	
		275					280					285				
Arg	Gln	Gly	Val	Ala	Val	Tyr	Trp	Cys	Ile	Ile	Ala	Trp	Gly	Ala	Ala	
	290					295					300					
Val	Ala	Leu	Gly	Gly	Val	Ala	Ile	Val	Val	Ser	Pro	Gly	Ala	Val	Thr	
305					310					315					320	
Ala	Trp	Ala	Trp	Met	Phe	Ile	Ile	Met	Met	Val	Ile	Gly	Gly	Met	Ala	
				325					330					335		
Asp	Met	Phe	Ser	Ser	Ala	Val	Arg	Asn	Ala	Ile	Leu	Gln	Gln	Ser	Ala	
			340					345					350			
Ala	Glu	His	Val	Gln	Gly	Arg	Ile	Gln	Gly	Val	Trp	Ile	Ile	Val	Val	
		355					360					365				
Val	Gly	Gly	Pro	Arg	Leu	Ala	Asp	Val	Leu	His	Gly	Trp	Ala	Ala	Glu	
	370					375					380					
Pro	Leu	Gly	Ala	Gly	Trp	Thr	Val	Leu	Trp	Gly	Gly	Val	Ala	Val	Val	
385					390					395					400	

Val Leu Thr Ala Ile Cys Met Val Ala Val Pro Lys Phe Trp Lys Tyr
 405 410 415

Glu Lys Pro Lys Ile Thr Gly Ile
 420

<210> 169

<211> 945

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(922)

<223> FRXA01936

<400> 169

tttacagcag gcattttttcg cgggtgaatca acccaccgga acggcgatcc ttcgaagtat 60

tttgccgatt gatcaataag cgtcggcaac atcactgaat atg ctg ctc atg cag 115
 Met Leu Leu Met Gln
 1 5

acc ggc gca atc gtt ggc ccg ctg atc gca ggt gcg ttg att ccg ctg 163
 Thr Gly Ala Ile Val Gly Pro Leu Ile Ala Gly Ala Leu Ile Pro Leu
 10 15 20

atc ggt ttc ggg tgg ctg tat ttc ctt gat gtt gtc tcc atc atc ccc 211
 Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp Val Val Ser Ile Ile Pro
 25 30 35

aca ctg tgg gct gta tgg tca ctg cct tcg atc aag cca tcc ggc aag 259
 Thr Leu Trp Ala Val Trp Ser Leu Pro Ser Ile Lys Pro Ser Gly Lys
 40 45 50

gtg atg aag gct ggt ttc gcc agt gtg gtg gat ggc ctg aag tat ttg 307
 Val Met Lys Ala Gly Phe Ala Ser Val Val Asp Gly Leu Lys Tyr Leu
 55 60 65

gct ggc caa ccc gtg ttg ttg atg gtg atg gtg ctg gat ctt atc gcc 355
 Ala Gly Gln Pro Val Leu Leu Met Val Met Val Leu Asp Leu Ile Ala
 70 75 80 85

atg att ttc ggc atg cca cgt gcg ctt tac ccc gag atc gca gaa gtg 403
 Met Ile Phe Gly Met Pro Arg Ala Leu Tyr Pro Glu Ile Ala Glu Val
 90 95 100

aac ttc ggt ggg ggt gac gcc ggt gca acg atg ctg gcg ttc atg tac 451
 Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr Met Leu Ala Phe Met Tyr
 105 110 115

tca tcc atg gct gtt ggc gca gtt ctt ggc ggc gtg ctg tct ggt tgg 499
 Ser Ser Met Ala Val Gly Ala Val Leu Gly Gly Val Leu Ser Gly Trp
 120 125 130

gtg gcc cgg att agc cgc cag ggt gtt gca gtt tat tgg tgc atc atc 547
 Val Ala Arg Ile Ser Arg Gln Gly Val Ala Val Tyr Trp Cys Ile Ile
 135 140 145

gcc tgg ggc gca gcc gtt gct ttg ggt ggt gtg gca att gtt gtc agc 595

Ala Trp Gly Ala Ala Val Ala Leu Gly Gly Val Ala Ile Val Val Ser
 150 155 160 165

ccc ggc gcg gtg act gcg tgg gcg tgg atg ttc atc atc atg atg gtc 643
 Pro Gly Ala Val Thr Ala Trp Ala Trp Met Phe Ile Ile Met Met Val
 170 175 180

att ggt ggc atg gct gac atg ttc agc tcg gca gtt cga aac gct att 691
 Ile Gly Gly Met Ala Asp Met Phe Ser Ser Ala Val Arg Asn Ala Ile
 185 190 195

ttg cag cag tct gct gcg gaa cat gtg cag ggc cga atc caa ggt gtg 739
 Leu Gln Gln Ser Ala Ala Glu His Val Gln Gly Arg Ile Gln Gly Val
 200 205 210

tgg atc atc gtc gtg gtg ggt gga cct cgt tta gct gac gtc ctt cac 787
 Trp Ile Ile Val Val Val Gly Gly Pro Arg Leu Ala Asp Val Leu His
 215 220 225

ggt tgg gcc gct gag ccc ctc ggc gca ggt tgg acg gta tta tgg ggc 835
 Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly Trp Thr Val Leu Trp Gly
 230 235 240 245

gga gta gcg gtg gtt gta ctc act gca att tgt atg gtg gcg gtg cct 883
 Gly Val Ala Val Val Val Leu Thr Ala Ile Cys Met Val Ala Val Pro
 250 255 260

aaa ttc tgg aaa tac gag aaa cca aaa att acc ggc atc taaataactta 932
 Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile Thr Gly Ile
 265 270

tccatgccca ttt 945

<210> 170

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

Met Leu Leu Met Gln Thr Gly Ala Ile Val Gly Pro Leu Ile Ala Gly
 1 5 10 15

Ala Leu Ile Pro Leu Ile Gly Phe Gly Trp Leu Tyr Phe Leu Asp Val
 20 25 30

Val Ser Ile Ile Pro Thr Leu Trp Ala Val Trp Ser Leu Pro Ser Ile
 35 40 45

Lys Pro Ser Gly Lys Val Met Lys Ala Gly Phe Ala Ser Val Val Asp
 50 55 60

Gly Leu Lys Tyr Leu Ala Gly Gln Pro Val Leu Leu Met Val Met Val
 65 70 75 80

Leu Asp Leu Ile Ala Met Ile Phe Gly Met Pro Arg Ala Leu Tyr Pro
 85 90 95

Glu Ile Ala Glu Val Asn Phe Gly Gly Gly Asp Ala Gly Ala Thr Met
 100 105 110

Leu Ala Phe Met Tyr Ser Ser Met Ala Val Gly Ala Val Leu Gly Gly
 115 120 125
 Val Leu Ser Gly Trp Val Ala Arg Ile Ser Arg Gln Gly Val Ala Val
 130 135 140
 Tyr Trp Cys Ile Ile Ala Trp Gly Ala Ala Val Ala Leu Gly Gly Val
 145 150 155 160
 Ala Ile Val Val Ser Pro Gly Ala Val Thr Ala Trp Ala Trp Met Phe
 165 170 175
 Ile Ile Met Met Val Ile Gly Gly Met Ala Asp Met Phe Ser Ser Ala
 180 185 190
 Val Arg Asn Ala Ile Leu Gln Gln Ser Ala Ala Glu His Val Gln Gly
 195 200 205
 Arg Ile Gln Gly Val Trp Ile Ile Val Val Val Gly Gly Pro Arg Leu
 210 215 220
 Ala Asp Val Leu His Gly Trp Ala Ala Glu Pro Leu Gly Ala Gly Trp
 225 230 235 240
 Thr Val Leu Trp Gly Gly Val Ala Val Val Val Leu Thr Ala Ile Cys
 245 250 255
 Met Val Ala Val Pro Lys Phe Trp Lys Tyr Glu Lys Pro Lys Ile Thr
 260 265 270

Gly Ile

<210> 171
 <211> 549
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(526)
 <223> FRXA01937

<400> 171
 gcgcggtgac accacagccg ttgtcagcgg cgcttgggtct gtggaggatc gccgaggtta 60
 ctaacaaata ggcccaacaa agaggtctaa gctctacctg gtg agt ttc cga gat 115
 Val Ser Phe Arg Asp 5
 att ttc gct gac acc aga ccg ctg aaa gaa ccg gcc ttc aaa cgc ctc 163
 Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro Ala Phe Lys Arg Leu 20
 10 15
 tgg ctt ggc aat gtt gcc acc gtc att ggt gcc caa tta act gtt gtt 211
 Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala Gln Leu Thr Val Val 35
 25 30
 gcc gtt ccg gtg cag att tac caa atg act ggg tcc tcc ggc tat gtg 259
 Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly Ser Ser Gly Tyr Val

40	45	50	
ggc ttg acc ggg ctt ttt	ggc ctt att cct ttg gtt att ttt ggc ctt		307
Gly Leu Thr Gly Leu Phe	Gly Leu Ile Pro Leu Val Ile Phe Gly Leu		
55	60	65	
tat ggt gga tcc att gcg gat gct ttt gat aaa cgc atc gtg ctg atc			355
Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys Arg Ile Val Leu Ile			
70	75	80	85
tgc acc acg atc ggc atg tgt gtc acc act gcc ggt ttt tgg gtg ctg			403
Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala Gly Phe Trp Val Leu			
90	95	100	
acc att tta ggc aat gag aat att tgg ctc ctg tta ata aac ttt tct			451
Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu Leu Ile Asn Phe Ser			
105	110	115	
tta cag cag gca ttt ttc gcg gtg aat caa ccc acc cga acg gcg atc			499
Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro Thr Arg Thr Ala Ile			
120	125	130	
ctt cga agt att ttg ccg att gat caa taagcgctcgg caacatcact			546
Leu Arg Ser Ile Leu Pro Ile Asp Gln			
135	140		
gaa			549

<210> 172

<211> 142

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

Val Ser Phe Arg Asp	Ile Phe Ala Asp Thr Arg Pro Leu Lys Glu Pro
1	5 10 15

Ala Phe Lys Arg Leu Trp Leu Gly Asn Val Ala Thr Val Ile Gly Ala
20 25 30

Gln Leu Thr Val Val Ala Val Pro Val Gln Ile Tyr Gln Met Thr Gly
35 40 45

Ser Ser Gly Tyr Val Gly Leu Thr Gly Leu Phe Gly Leu Ile Pro Leu
50 55 60

Val Ile Phe Gly Leu Tyr Gly Gly Ser Ile Ala Asp Ala Phe Asp Lys
65 70 75 80

Arg Ile Val Leu Ile Cys Thr Thr Ile Gly Met Cys Val Thr Thr Ala
85 90 95

Gly Phe Trp Val Leu Thr Ile Leu Gly Asn Glu Asn Ile Trp Leu Leu
100 105 110

Leu Ile Asn Phe Ser Leu Gln Gln Ala Phe Phe Ala Val Asn Gln Pro
115 120 125

Thr Arg Thr Ala Ile Leu Arg Ser Ile Leu Pro Ile Asp Gln
130 135 140

<400> 173															
gtgccaaagc gtttctgtga aaacgcataa ccccgaatac cccctgtttc cagatccaaa 60															
aaaagatctg gcaggggggtt taggcataga ttaggaactt atg aag aaa ctg caa 115															
Met Lys Lys Leu Gln 5															
atg ccg gcc att ttg gtc gga ggc ttt gtg ggg ccg ttt act ggc caa 163															
Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly Pro Phe Thr Gly Gln 20															
gct cta tca gtg gtc ttg ccg gaa ttt gca gac acc ttt gat atc agt 211															
Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp Thr Phe Asp Ile Ser 35															
gtc agc cag gca gcg ctg acc atg acc gca tac ttg ttg ccc ttt gcc 259															
Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr Leu Leu Pro Phe Ala 50															
acc atg atg ttg ttt tcg ggg cgc atc acc aga aag atc cat ccg cat 307															
Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg Lys Ile His Pro His 65															
aag gtg gtg cag gcg gct tat att gtc aca ctg cca ctt gcg ctg ttg 355															
Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu Pro Leu Ala Leu Leu 85															
ctc cta gtt aca cca tcg tgg ggg ctg ttt atg gct gcg tat gcc acg 403															
Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met Ala Ala Tyr Ala Thr 100															
att ggt atc gct aat gca ttt acc act ccg gtg ctg caa att atg ttg 451															
Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val Leu Gln Ile Met Leu 115															
cgt gag ctt gtt ccg ccg cgt tct ttg ggt aag gca ttg ggc acc tat 499															
Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys Ala Leu Gly Thr Tyr 130															
gct gcg atg caa tca ctc ggc atg ttg tcg gcg cca ctg atc gca ggt 547															
Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala Pro Leu Ile Ala Gly 145															
gtg tct tcg gtg gtg tcg tgg agg ttg acc ttc ctg gtc act gca gca 595															
Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe Leu Val Thr Ala Ala 165															
gcg tca ctg ttt att ttg gtg gcg cga ctc ccc gtt gtt cca cca cca 643															
Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro Val Val Pro Pro Pro															

170	175	180	
tca gca tcg aag caa aac gtt agt ggc aag gtg cag tgg gga ccg acc			691
Ser Ala Ser Lys Gln Asn Val Ser Gly Lys Val Gln Trp Gly Pro Thr			
185	190	195	
atc atc cac atg gtt tcc ggc ttt gtg gtg ggc atc ggc atc atc ggc			739
Ile Ile His Met Val Ser Gly Phe Val Val Gly Ile Gly Ile Ile Gly			
200	205	210	
att gga ttc atg aca tcg ctg cac gtt ggc gag caa ttc gga ctt gat			787
Ile Gly Phe Met Thr Ser Leu His Val Gly Glu Gln Phe Gly Leu Asp			
215	220	225	
gct gca gcg cgt ggt ttg gtg gtc atg tgt ggt ggc ctg gct gcg ttc			835
Ala Ala Ala Arg Gly Leu Val Val Met Cys Gly Gly Leu Ala Ala Phe			
230	235	240	245
ttt gcc tcc cgc aag att ggc gat ttg gca gac aaa ttt ggt gtg cgc			883
Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp Lys Phe Gly Val Arg			
250	255	260	
gcg gtg ctc att gtc agt gct gtc atc ggt acc atc gca ctc gca ctg			931
Ala Val Leu Ile Val Ser Ala Val Ile Gly Thr Ile Ala Leu Ala Leu			
265	270	275	
ctg ccg atc gca ccg tgg atc att gtg gtg gcc gta ctg tgg gcc ttc			979
Leu Pro Ile Ala Pro Trp Ile Ile Val Val Ala Val Leu Trp Ala Phe			
280	285	290	
gca gta gca gca gca caa gga atc caa gca acc gtc aac ttg gct gtc			1027
Ala Val Ala Ala Ala Gln Gly Ile Gln Ala Thr Val Asn Leu Ala Val			
295	300	305	
atc gga agc ccc ggt gga tca tcg ctg ctt tct acc gtg cag gct ttc			1075
Ile Gly Ser Pro Gly Gly Ser Ser Leu Leu Ser Thr Val Gln Ala Phe			
310	315	320	325
cga ttc ttc gga tca gcg gca gca cca gtg aca ttc ctt cct atc tat			1123
Arg Phe Phe Gly Ser Ala Ala Ala Pro Val Thr Phe Leu Pro Ile Tyr			
330	335	340	
atg ggc atc ggc tcg ggg gcg ttt tgg gtc agc gcg gta gcg ctg ttc			1171
Met Gly Ile Gly Ser Gly Ala Phe Trp Val Ser Ala Val Ala Leu Phe			
345	350	355	
ttc gtt gcc atc gcc cag tgg ctc aac ccg cag cgg gtg gag cgg ggc			1219
Phe Val Ala Ile Ala Gln Trp Leu Asn Pro Gln Arg Val Glu Arg Gly			
360	365	370	
tgaggagac gtcgagaagc gtc			1242

<210> 174

<211> 373

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

Met Lys Lys Leu Gln Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly

1

5

10

15

Pro Phe Thr Gly Gln Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp
 20 25 30
 Thr Phe Asp Ile Ser Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr
 35 40 45
 Leu Leu Pro Phe Ala Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg
 50 55 60
 Lys Ile His Pro His Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu
 65 70 75 80
 Pro Leu Ala Leu Leu Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met
 85 90 95
 Ala Ala Tyr Ala Thr Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val
 100 105 110
 Leu Gln Ile Met Leu Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys
 115 120 125
 Ala Leu Gly Thr Tyr Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala
 130 135 140
 Pro Leu Ile Ala Gly Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe
 145 150 155 160
 Leu Val Thr Ala Ala Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro
 165 170 175
 Val Val Pro Pro Pro Ser Ala Ser Lys Gln Asn Val Ser Gly Lys Val
 180 185 190
 Gln Trp Gly Pro Thr Ile Ile His Met Val Ser Gly Phe Val Val Gly
 195 200 205
 Ile Gly Ile Ile Gly Ile Gly Phe Met Thr Ser Leu His Val Gly Glu
 210 215 220
 Gln Phe Gly Leu Asp Ala Ala Ala Arg Gly Leu Val Val Met Cys Gly
 225 230 235 240
 Gly Leu Ala Ala Phe Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp
 245 250 255
 Lys Phe Gly Val Arg Ala Val Leu Ile Val Ser Ala Val Ile Gly Thr
 260 265 270
 Ile Ala Leu Ala Leu Leu Pro Ile Ala Pro Trp Ile Ile Val Val Ala
 275 280 285
 Val Leu Trp Ala Phe Ala Val Ala Ala Ala Gln Gly Ile Gln Ala Thr
 290 295 300
 Val Asn Leu Ala Val Ile Gly Ser Pro Gly Gly Ser Ser Leu Leu Ser
 305 310 315 320
 Thr Val Gln Ala Phe Arg Phe Phe Gly Ser Ala Ala Ala Pro Val Thr
 325 330 335

Phe Leu Pro Ile Tyr Met Gly Ile Gly Ser Gly Ala Phe Trp Val Ser
 340 345 350
 Ala Val Ala Leu Phe Phe Val Ala Ile Ala Gln Trp Leu Asn Pro Gln
 355 360 365
 Arg Val Glu Arg Gly
 370

<210> 175
 <211> 871
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(871)
 <223> FRXA01010

<400> 175
 gtgccaaagc gtttcctgta aaacgcataa ccccgaaatac cccctgtttc cagatccaaa 60
 aaaagatctg gcaggggggtt taggcataga ttaggaactt atg aag aaa ctg caa 115
 Met Lys Lys Leu Gln
 1 5
 atg ccg gcc att ttg gtc gga ggc ttt gtg ggg ccg ttt act ggc caa 163
 Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly Pro Phe Thr Gly Gln
 10 15 20
 gct cta tca gtg gtc ttg ccg gaa ttt gca gac acc ttt gat atc agt 211
 Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp Thr Phe Asp Ile Ser
 25 30 35
 gtc agc cag gca gcg ctg acc atg acc gca tac ttg ttg ccc ttt gcc 259
 Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr Leu Leu Pro Phe Ala
 40 45 50
 acc atg atg ttg ttt tcg ggg cgc atc acc aga aag atc cat ccg cat 307
 Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg Lys Ile His Pro His
 55 60 65
 aag gtg gtg cag gcg gct tat att gtc aca ctg cca ctt gcg ctg ttg 355
 Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu Pro Leu Ala Leu Leu
 70 75 80 85
 ctc cta gtt aca cca tcg tgg ggg ctg ttt atg gct gcg tat gcc acg 403
 Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met Ala Ala Tyr Ala Thr
 90 95 100
 att ggt atc gct aat gca ttt acc act ccg gtg ctg caa att atg ttg 451
 Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val Leu Gln Ile Met Leu
 105 110 115
 cgt gag ctt gtt ccg ccg cgt tct ttg ggt aag gca ttg ggc acc tat 499
 Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys Ala Leu Gly Thr Tyr
 120 125 130
 gct gcg atg caa tca ctc ggc atg ttg tcg gcg cca ctg atc gca ggt 547
 Ala Ala Met Gln Ser Leu Gly Met Leu Ser Ala Pro Leu Ile Ala Gly

135	140	145	
gtg tct tcg gtg gtg tcg tgg agg ttg acc ttc ctg gtc act gca gca			595
Val Ser Ser Val Val Ser Trp Arg Leu Thr Phe Leu Val Thr Ala Ala			
150	155	160	165
gcg tca ctg ttt att ttg gtg gcg cga ctc ccc gtt gtt cca cca cca			643
Ala Ser Leu Phe Ile Leu Val Ala Arg Leu Pro Val Val Pro Pro Pro			
	170	175	180
tca gca ttg aag caa aac gtt agt ggc aag gtg cag tgg gga ccg acc			691
Ser Ala Leu Lys Gln Asn Val Ser Gly Lys Val Gln Trp Gly Pro Thr			
	185	190	195
atc atc cac atg gtt tcc ggc ttt gtg gtg ggc atc ggc atc atc ggc			739
Ile Ile His Met Val Ser Gly Phe Val Val Gly Ile Gly Ile Ile Gly			
	200	205	210
att gga ttc atg aca tcg ctg cac gtt ggc gag caa ttc gga ctt aat			787
Ile Gly Phe Met Thr Ser Leu His Val Gly Glu Gln Phe Gly Leu Asn			
	215	220	225
act gca gcg cgt ggt ttg gtg gtc atg tgt ggt ggc cgg gct gcg ttc			835
Thr Ala Ala Arg Gly Leu Val Val Met Cys Gly Gly Arg Ala Ala Phe			
	230	235	240
ttt gcc tcc cgc aag ata ggc gat ttg gca gac aaa			871
Phe Ala Ser Arg Lys Ile Gly Asp Leu Ala Asp Lys			
	250	255	

<210> 176

<211> 257

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

Met Lys Lys Leu Gln Met Pro Ala Ile Leu Val Gly Gly Phe Val Gly
1 5 10 15

Pro Phe Thr Gly Gln Ala Leu Ser Val Val Leu Pro Glu Phe Ala Asp
20 25 30

Thr Phe Asp Ile Ser Val Ser Gln Ala Ala Leu Thr Met Thr Ala Tyr
35 40 45

Leu Leu Pro Phe Ala Thr Met Met Leu Phe Ser Gly Arg Ile Thr Arg
50 55 60

Lys Ile His Pro His Lys Val Val Gln Ala Ala Tyr Ile Val Thr Leu
65 70 75 80

Pro Leu Ala Leu Leu Leu Val Thr Pro Ser Trp Gly Leu Phe Met
85 90 95

Ala Ala Tyr Ala Thr Ile Gly Ile Ala Asn Ala Phe Thr Thr Pro Val
100 105 110

Leu Gln Ile Met Leu Arg Glu Leu Val Pro Pro Arg Ser Leu Gly Lys
115 120 125

Ala	Leu	Gly	Thr	Tyr	Ala	Ala	Met	Gln	Ser	Leu	Gly	Met	Leu	Ser	Ala
130						135					140				
Pro	Leu	Ile	Ala	Gly	Val	Ser	Ser	Val	Val	Ser	Trp	Arg	Leu	Thr	Phe
145					150					155					160
Leu	Val	Thr	Ala	Ala	Ala	Ser	Leu	Phe	Ile	Leu	Val	Ala	Arg	Leu	Pro
				165					170					175	
Val	Val	Pro	Pro	Pro	Ser	Ala	Leu	Lys	Gln	Asn	Val	Ser	Gly	Lys	Val
			180					185					190		
Gln	Trp	Gly	Pro	Thr	Ile	Ile	His	Met	Val	Ser	Gly	Phe	Val	Val	Gly
		195					200					205			
Ile	Gly	Ile	Ile	Gly	Ile	Gly	Phe	Met	Thr	Ser	Leu	His	Val	Gly	Glu
	210					215					220				
Gln	Phe	Gly	Leu	Asn	Thr	Ala	Ala	Arg	Gly	Leu	Val	Val	Met	Cys	Gly
225					230					235					240
Gly	Arg	Ala	Ala	Phe	Phe	Ala	Ser	Arg	Lys	Ile	Gly	Asp	Leu	Ala	Asp
				245					250					255	

Lys

<210> 177
 <211> 1266
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1243)
 <223> RXN03142

<400> 177
 gcaatttggc caatcaacaa cataggagga ctgcgtggcg gtcaccgcaa gaacggacat 60
 aaaaccacac ccacgcgaac caacggcact gttcactcca gtg ttt att ttg ggc 115
 Val Phe Ile Leu Gly
 1 5
 tgg ctc gtc aac ttg acc cag tac ttg agc ttc tac ttc ctg atc aca 163
 Trp Leu Val Asn Leu Thr Gln Tyr Leu Ser Phe Tyr Phe Leu Ile Thr
 10 15 20
 gtc atg gcg ctg tat gcg atg gaa agc ttc gcc gtt tca gag gcc gct 211
 Val Met Ala Leu Tyr Ala Met Glu Ser Phe Ala Val Ser Glu Ala Ala
 25 30 35
 gtc gga ttt gcg gcc agc tcc ttt gtt atc ggc gca acc gtg gct cgt 259
 Val Gly Phe Ala Ala Ser Ser Phe Val Ile Gly Ala Thr Val Ala Arg
 40 45 50
 gtg ttc gcg gga tgg acg tcc gac cgt ttt ggt aaa aaa cag atc ctg 307
 Val Phe Ala Gly Trp Thr Ser Asp Arg Phe Gly Lys Lys Gln Ile Leu
 55 60 65

ctc atc ttt gtc ggc ttg gaa gcg gta gca tca cta ttc tat att cca	355
Leu Ile Phe Val Gly Leu Glu Ala Val Ala Ser Leu Phe Tyr Ile Pro	
70 75 80 85	
gct gcc tca cta cca gcg ctg gtt gct gtg cgt ttt gtt cac ggt ttt	403
Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg Phe Val His Gly Phe	
90 95 100	
tct tat tct ctt gct tcc acc gct gtg atg gca ctt gtg cag tcc gtg	451
Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala Leu Val Gln Ser Val	
105 110 115	
att cct gca agc cgt agg gca gag ggc acc ggc tac ttc gcg ctc gga	499
Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu Gly	
120 125 130	
tcc aca ctg gct aca gct ttc ggc cca gca att gcg ctg ttt gtt atc	547
Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile Ala Leu Phe Val Ile	
135 140 145	
gat gac ttc aac tac aac acc ctg ttc tgg att acc act gcg acc agt	595
Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr Ser	
150 155 160 165	
gtt ttc ggc ctg atc ctc acc gtt ttg atc cgc aag ccg gag ttc att	643
Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe Ile	
170 175 180	
aag aat gcg gaa cac ggc aga gta aag cca gtc tgg tct atc aag act	691
Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys Thr	
185 190 195	
gtt gtg cac cca tcg gtc atg ctc att gga ttc ttc atg ctc gct gtc	739
Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala Val	
200 205 210	
gga ctg gct tac gca ggc gtg atc acc ttc ctc aac ggc ttc gcg caa	787
Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala Gln	
215 220 225	
gac act ggc ctc acc gcc gga gcg ggt ctt ttc ttt atc gct tat gcg	835
Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala	
230 235 240 245	
gtt gcg atg ctg gtc atg cgt ttc ttc ctt gga cgc att cag gac aaa	883
Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp Lys	
250 255 260	
cat ggt gac aac ccg gtt att tac ttc ggt ttg atc agc ttc gcc ctc	931
His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala Leu	
265 270 275	
gcg ctg ggg ctt atg gct ttg gcg act gaa gac tgg cac att gtt ctc	979
Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val Leu	
280 285 290	
gct ggc gca ctc acc ggt ttg ggc tat ggc acc atc atg ccg gcc gca	1027
Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala Ala	
295 300 305	
caa gcc att gct gtc gat tca gtt cca agc act cag gtt ggt tcc ggt	1075

Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser Gly
 310 315 320 325
 att tct acg ctt ttc ctg ttc acc gac atc ggc att ggc tta ggc cca 1123
 Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly Pro
 330 335 340
 atc ctg ctg ggt gga ttg gtt gca gcg acc gga tac aac gtc atg tac 1171
 Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met Tyr
 345 350 355
 gca gct ttg gcc gca gtg att gtt gtg gcg ggc gtg ctc tac ctg gtt 1219
 Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu Val
 360 365 370
 gct ttg ggt agg aaa gct agc cac taagtttagag cattttattg agc 1266
 Ala Leu Gly Arg Lys Ala Ser His
 375 380

<210> 178

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

Val Phe Ile Leu Gly Trp Leu Val Asn Leu Thr Gln Tyr Leu Ser Phe
 1 5 10 15
 Tyr Phe Leu Ile Thr Val Met Ala Leu Tyr Ala Met Glu Ser Phe Ala
 20 25 30
 Val Ser Glu Ala Ala Val Gly Phe Ala Ala Ser Ser Phe Val Ile Gly
 35 40 45
 Ala Thr Val Ala Arg Val Phe Ala Gly Trp Thr Ser Asp Arg Phe Gly
 50 55 60
 Lys Lys Gln Ile Leu Leu Ile Phe Val Gly Leu Glu Ala Val Ala Ser
 65 70 75 80
 Leu Phe Tyr Ile Pro Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg
 85 90 95
 Phe Val His Gly Phe Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala
 100 105 110
 Leu Val Gln Ser Val Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly
 115 120 125
 Tyr Phe Ala Leu Gly Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile
 130 135 140
 Ala Leu Phe Val Ile Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile
 145 150 155 160
 Thr Thr Ala Thr Ser Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg
 165 170 175
 Lys Pro Glu Phe Ile Lys Asn Ala Glu His Gly Arg Val Lys Pro Val
 180 185 190

Trp Ser Ile Lys Thr Val Val His Pro Ser Val Met Leu Ile Gly Phe
 195 200 205
 Phe Met Leu Ala Val Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu
 210 215 220
 Asn Gly Phe Ala Gln Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe
 225 230 235 240
 Phe Ile Ala Tyr Ala Val Ala Met Leu Val Met Arg Phe Phe Leu Gly
 245 250 255
 Arg Ile Gln Asp Lys His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu
 260 265 270
 Ile Ser Phe Ala Leu Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp
 275 280 285
 Trp His Ile Val Leu Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr
 290 295 300
 Ile Met Pro Ala Ala Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr
 305 310 315 320
 Gln Val Gly Ser Gly Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly
 325 330 335
 Ile Gly Leu Gly Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly
 340 345 350
 Tyr Asn Val Met Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly
 355 360 365
 Val Leu Tyr Leu Val Ala Leu Gly Arg Lys Ala Ser His
 370 375 380

<210> 179

<211> 914

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(891)

<223> FRXA01150

<400> 179

cca gct gcc tca cta cca gcg ctg gtt gct gtg cgt ttt gtt cac ggt	48
Pro Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg Phe Val His Gly	
1 5 10 15	
ttt tct tat tct ctt gct tcc acc gct gtg atg gca ctt gtg cag tcc	96
Phe Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala Leu Val Gln Ser	
20 25 30	
gtg att cct gca agc cgt agg gca gag ggc acc ggc tac ttc gcg ctc	144
Val Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu	
35 40 45	

gga tcc aca ctg gct aca gct ttc ggc cca gca att gcg ctg ttt gtt	192
Gly Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile Ala Leu Phe Val	
50 55 60	
atc gat gac ttc aac tac aac acc ctg ttc tgg att acc act gcg acc	240
Ile Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr	
65 70 75 80	
agt gtt ttc ggc ctg atc ctc acc gtt ttg atc cgc aag ccg gag ttc	288
Ser Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe	
85 90 95	
att aag aat gcg gaa cac ggc aga gta aag cca gtc tgg tct atc aag	336
Ile Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys	
100 105 110	
act gtt gtg cac cca tcg gtc atg ctc att gga ttc ttc atg ctc gct	384
Thr Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala	
115 120 125	
gtc gga ctg gct tac gca ggc gtg atc acc ttc ctc aac ggc ttc gcg	432
Val Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala	
130 135 140	
caa gac act ggc ctc acc gcc gga gcg ggt ctt ttc ttt atc gct tat	480
Gln Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr	
145 150 155 160	
gcg gtt gcg atg ctg gtc atg cgt ttc ttc ctt gga cgc att cag gac	528
Ala Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp	
165 170 175	
aaa cat ggt gac aac ccg gtt att tac ttc ggt ttg atc agc ttc gcc	576
Lys His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala	
180 185 190	
ctc gcg ctg ggg ctt atg gct ttg gcg act gaa gac tgg cac att gtt	624
Leu Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val	
195 200 205	
ctc gct ggc gca ctc acc ggt ttg ggc tat ggc acc atc atg ccg gcc	672
Leu Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala	
210 215 220	
gca caa gcc att gct gtc gat tca gtt cca agc act cag gtt ggt tcc	720
Ala Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser	
225 230 235 240	
ggt att tct acg ctt ttc ctg ttc acc gac atc ggc att ggc tta ggc	768
Gly Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly	
245 250 255	
cca atc ctg ctg ggt gga ttg gtt gca gcg acc gga tac aac gtc atg	816
Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met	
260 265 270	
tac gca gct ttg gcc gca gtg att gtt gtg gcg ggc gtg ctc tac ctg	864
Tyr Ala Ala Leu Ala Ala Val Ile Val Val Ala Gly Val Leu Tyr Leu	
275 280 285	
ggt gct ttg ggt agg aaa gct agc cac taagttagag cattttattg	911

Val Ala Leu Gly Arg Lys Ala Ser His
 290 295

agc

914

<210> 180
 <211> 297
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 180
 Pro Ala Ala Ser Leu Pro Ala Leu Val Ala Val Arg Phe Val His Gly
 1 5 10 15
 Phe Ser Tyr Ser Leu Ala Ser Thr Ala Val Met Ala Leu Val Gln Ser
 20 25 30
 Val Ile Pro Ala Ser Arg Arg Ala Glu Gly Thr Gly Tyr Phe Ala Leu
 35 40 45
 Gly Ser Thr Leu Ala Thr Ala Phe Gly Pro Ala Ile Ala Leu Phe Val
 50 55 60
 Ile Asp Asp Phe Asn Tyr Asn Thr Leu Phe Trp Ile Thr Thr Ala Thr
 65 70 75 80
 Ser Val Phe Gly Leu Ile Leu Thr Val Leu Ile Arg Lys Pro Glu Phe
 85 90 95
 Ile Lys Asn Ala Glu His Gly Arg Val Lys Pro Val Trp Ser Ile Lys
 100 105 110
 Thr Val Val His Pro Ser Val Met Leu Ile Gly Phe Phe Met Leu Ala
 115 120 125
 Val Gly Leu Ala Tyr Ala Gly Val Ile Thr Phe Leu Asn Gly Phe Ala
 130 135 140
 Gln Asp Thr Gly Leu Thr Ala Gly Ala Gly Leu Phe Phe Ile Ala Tyr
 145 150 155 160
 Ala Val Ala Met Leu Val Met Arg Phe Phe Leu Gly Arg Ile Gln Asp
 165 170 175
 Lys His Gly Asp Asn Pro Val Ile Tyr Phe Gly Leu Ile Ser Phe Ala
 180 185 190
 Leu Ala Leu Gly Leu Met Ala Leu Ala Thr Glu Asp Trp His Ile Val
 195 200 205
 Leu Ala Gly Ala Leu Thr Gly Leu Gly Tyr Gly Thr Ile Met Pro Ala
 210 215 220
 Ala Gln Ala Ile Ala Val Asp Ser Val Pro Ser Thr Gln Val Gly Ser
 225 230 235 240
 Gly Ile Ser Thr Leu Phe Leu Phe Thr Asp Ile Gly Ile Gly Leu Gly
 245 250 255
 Pro Ile Leu Leu Gly Gly Leu Val Ala Ala Thr Gly Tyr Asn Val Met

260	265	270
Tyr Ala Ala Leu Ala Ala Val	Ile Val Val Ala Gly	Val Leu Tyr Leu
275	280	285
Val Ala Leu Gly Arg Lys Ala Ser His		
290	295	

<210> 181
 <211> 1341
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1318)
 <223> RXN02964

<400> 181
 ttttatatcc tagcaagggt gttgcatgat gcaataaacg tggtagtttg tgttcataac 60
 aaaattgcat gatgcaataa tttcgattta aaggagaaca gtg tcc gta gct gaa 115
 Val Ser Val Ala Glu
 1 5
 gaa ggg aaa ctt ttt aca cca acg ttt gtc atg gga tgg ttt gcc aac 163
 Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met Gly Trp Phe Ala Asn
 10 15 20
 ctt ttc cag ttc ctg gtg ttc tac ttc ctc atc acc acc atg gct ttg 211
 Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile Thr Thr Met Ala Leu
 25 30 35
 tac gcc atc aag gaa ttt caa gcc tct gaa gta gaa gct ggc ttc gca 259
 Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val Glu Ala Gly Phe Ala
 40 45 50
 tcc agc tca att gtt atc ggc gca gtc ttt tcc agg ttt ttc tcc ggc 307
 Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser Arg Phe Phe Ser Gly
 55 60 65
 tat att att gac cgt ttt ggt cga cgc aag att gtg ctc atc tca gtc 355
 Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile Val Leu Ile Ser Val
 70 75 80 85
 cta gtc act acc att gcg tgt gcc ttg tac ctt ccc atc gaa tca ttg 403
 Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu Pro Ile Glu Ser Leu
 90 95 100
 cca ttg cta tac gca aac agg ttc ctc cac ggt gtt gga tac gct ttt 451
 Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly Val Gly Tyr Ala Phe
 105 110 115
 gct gcc acc gcg atc atg gca atg gtc cag gag ctc att cca gcg tca 499
 Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu Leu Ile Pro Ala Ser
 120 125 130
 cga cgt tcc gaa ggt act ggt tac ctg gca ttg ggc act acc gtt tct 547
 Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu Gly Thr Thr Val Ser
 135 140 145

gca gca ctt gga cca gcc cta gca ctt ttt gtc cta gga aca ttt gat	595
Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val Leu Gly Thr Phe Asp	
150 155 160 165	
tac gac atg ctg ttt atc gtg gtc ttg gca acc tcg gtc atc tct ttg	643
Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr Ser Val Ile Ser Leu	
170 175 180	
atc gcc gtc gtg ttc atg tac ttt aag acc agc gac cct gag cct tct	691
Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser Asp Pro Glu Pro Ser	
185 190 195	
ggg gaa cca gcc aag ttc agc ttc aaa tct att atg aac cca aag atc	739
Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile Met Asn Pro Lys Ile	
200 205 210	
atc ccc atc ggc atc ttt atc ttg ctt att tgc ttt gct tac tct ggc	787
Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys Phe Ala Tyr Ser Gly	
215 220 225	
gtc att gcc tac atc aac gca ttt gct gaa gaa cgc gat ctg att acg	835
Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu Arg Asp Leu Ile Thr	
230 235 240 245	
ggg gct gga ttg ttc ttc att gcc tac gca gta tca atg ttt gtg atg	883
Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val Ser Met Phe Val Met	
250 255 260	
cgc agc ttc ctt ggc aaa ctg cag gac cgt cgc gga gac aac gtc gtt	931
Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg Gly Asp Asn Val Val	
265 270 275	
att tac ttt gga ttg ttc ttc ttc gtt att tcc ttg acg att ttg tcc	979
Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser Leu Thr Ile Leu Ser	
280 285 290	
ttt gcc act tcc aac tgg cac gtt gtg ttg tcc gga gtc att gca ggt	1027
Phe Ala Thr Ser Asn Trp His Val Val Leu Ser Gly Val Ile Ala Gly	
295 300 305	
ctg gga tac ggc act ttg atg cca gca gtg cag tcc atc gct gtt ggt	1075
Leu Gly Tyr Gly Thr Leu Met Pro Ala Val Gln Ser Ile Ala Val Gly	
310 315 320 325	
gta gta gac aaa acc gaa ttc ggt acg gcc ttc tcc act ttg ttc ctg	1123
Val Val Asp Lys Thr Glu Phe Gly Thr Ala Phe Ser Thr Leu Phe Leu	
330 335 340	
ttt gtg gac tta ggt ttt ggc ttt gga cct att atc ctg gga gca gtt	1171
Phe Val Asp Leu Gly Phe Gly Phe Gly Pro Ile Ile Leu Gly Ala Val	
345 350 355	
tct gcg gca att ggt ttc gga cct atg tat gca gca ctg gca ggt gtg	1219
Ser Ala Ala Ile Gly Phe Gly Pro Met Tyr Ala Ala Leu Ala Gly Val	
360 365 370	
ggt gtg att gcc gga atc ttc tac ctg ttc aca cac gct cgc acc gat	1267
Gly Val Ile Ala Gly Ile Phe Tyr Leu Phe Thr His Ala Arg Thr Asp	
375 380 385	

cga gct aag aat ggc ttt gtt aaa cac cca gag cct gtc gct tta gtt 1315
 Arg Ala Lys Asn Gly Phe Val Lys His Pro Glu Pro Val Ala Leu Val
 390 395 400 405

agc tagttctttc agctttccct ccc 1341
 Ser

<210> 182

<211> 406

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 182

Val Ser Val Ala Glu Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met
 1 5 10 15

Gly Trp Phe Ala Asn Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile
 20 25 30

Thr Thr Met Ala Leu Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val
 35 40 45

Glu Ala Gly Phe Ala Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser
 50 55 60

Arg Phe Phe Ser Gly Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile
 65 70 75 80

Val Leu Ile Ser Val Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu
 85 90 95

Pro Ile Glu Ser Leu Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly
 100 105 110

Val Gly Tyr Ala Phe Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu
 115 120 125

Leu Ile Pro Ala Ser Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu
 130 135 140

Gly Thr Thr Val Ser Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val
 145 150 155 160

Leu Gly Thr Phe Asp Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr
 165 170 175

Ser Val Ile Ser Leu Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser
 180 185 190

Asp Pro Glu Pro Ser Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile
 195 200 205

Met Asn Pro Lys Ile Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys
 210 215 220

Phe Ala Tyr Ser Gly Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu
 225 230 235 240

Arg Asp Leu Ile Thr Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val

245										250					255				
Ser	Met	Phe	Val	Met	Arg	Ser	Phe	Leu	Gly	Lys	Leu	Gln	Asp	Arg	Arg				
			260					265					270						
Gly	Asp	Asn	Val	Val	Ile	Tyr	Phe	Gly	Leu	Phe	Phe	Phe	Val	Ile	Ser				
		275					280					285							
Leu	Thr	Ile	Leu	Ser	Phe	Ala	Thr	Ser	Asn	Trp	His	Val	Val	Leu	Ser				
	290					295					300								
Gly	Val	Ile	Ala	Gly	Leu	Gly	Tyr	Gly	Thr	Leu	Met	Pro	Ala	Val	Gln				
305					310					315					320				
Ser	Ile	Ala	Val	Gly	Val	Val	Asp	Lys	Thr	Glu	Phe	Gly	Thr	Ala	Phe				
				325					330					335					
Ser	Thr	Leu	Phe	Leu	Phe	Val	Asp	Leu	Gly	Phe	Gly	Phe	Gly	Pro	Ile				
			340					345					350						
Ile	Leu	Gly	Ala	Val	Ser	Ala	Ala	Ile	Gly	Phe	Gly	Pro	Met	Tyr	Ala				
		355					360					365							
Ala	Leu	Ala	Gly	Val	Gly	Val	Ile	Ala	Gly	Ile	Phe	Tyr	Leu	Phe	Thr				
	370					375					380								
His	Ala	Arg	Thr	Asp	Arg	Ala	Lys	Asn	Gly	Phe	Val	Lys	His	Pro	Glu				
385					390					395					400				
Pro	Val	Ala	Leu	Val	Ser														
				405															

<210> 183

<211> 1006

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1006)

<223> FRXA02116

<400> 183

ttttatatcc tagcaagggt gttgcatgat gcaataaacg tggtagtttg tgttcataac 60

aaaattgcat	gatgcaataa	tttcgattta	aaggagaaca	gtg	tcc	gta	gct	gaa	115
				Val	Ser	Val	Ala	Glu	
				1				5	

gaa	ggg	aaa	ctt	ttt	aca	cca	acg	ttt	gtc	atg	gga	tgg	ttt	gcc	aac	163
Glu	Gly	Lys	Leu	Phe	Thr	Pro	Thr	Phe	Val	Met	Gly	Trp	Phe	Ala	Asn	
			10					15						20		

ctt	ttc	cag	ttc	ctg	gtg	ttc	tac	ttc	ctc	atc	acc	acc	atg	gct	ttg	211
Leu	Phe	Gln	Phe	Leu	Val	Phe	Tyr	Phe	Leu	Ile	Thr	Thr	Met	Ala	Leu	
			25					30					35			

tac	gcc	atc	aag	gaa	ttt	caa	gcc	tct	gaa	gta	gaa	gct	ggc	ttc	gca	259
Tyr	Ala	Ile	Lys	Glu	Phe	Gln	Ala	Ser	Glu	Val	Glu	Ala	Gly	Phe	Ala	
			40				45					50				

tcc agc tca att gtt atc ggc gca gtc ttt tcc agg ttt ttc tcc ggc	307
Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser Arg Phe Phe Ser Gly	
55 60 65	
tat att att gac cgt ttt ggt cga cgc aag att gtg ctc atc tca gtc	355
Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile Val Leu Ile Ser Val	
70 75 80 85	
cta gtc act acc att gcg tgt gcc ttg tac ctt ccc atc gaa tca ttg	403
Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu Pro Ile Glu Ser Leu	
90 95 100	
cca ttg cta tac gca aac agg ttc ctc cac ggt gtt gga tac gct ttt	451
Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly Val Gly Tyr Ala Phe	
105 110 115	
gct gcc acc gcg atc atg gca atg gtc cag gag ctc att cca gcg tca	499
Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu Leu Ile Pro Ala Ser	
120 125 130	
cga cgt tcc gaa ggt act ggt tac ctg gca ttg ggc act acc gtt tct	547
Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu Gly Thr Thr Val Ser	
135 140 145	
gca gca ctt gga cca gcc cta gca ctt ttt gtc cta gga aca ttt gat	595
Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val Leu Gly Thr Phe Asp	
150 155 160 165	
tac gac atg ctg ttt atc gtg gtc ttg gca acc tcg gtc atc tct ttg	643
Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr Ser Val Ile Ser Leu	
170 175 180	
atc gcc gtc gtg ttc atg tac ttt aag acc agc gac cct gag cct tct	691
Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser Asp Pro Glu Pro Ser	
185 190 195	
ggg gaa cca gcc aag ttc agc ttc aaa tct att atg aac cca aag atc	739
Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile Met Asn Pro Lys Ile	
200 205 210	
atc ccc atc ggc atc ttt atc ttg ctt att tgc ttt gct tac tct ggc	787
Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys Phe Ala Tyr Ser Gly	
215 220 225	
gtc att gcc tac atc aac gca ttt gct gaa gaa cgc gat ctg att acg	835
Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu Arg Asp Leu Ile Thr	
230 235 240 245	
ggt gct gga ttg ttc ttc att gcc tac gca gta tca atg ttt gtg atg	883
Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val Ser Met Phe Val Met	
250 255 260	
cgc agc ttc ctt ggc aaa ctg cag gac cgt cgc gga gac aac gtc gtt	931
Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg Gly Asp Asn Val Val	
265 270 275	
att tac ttt gga ttg ttc ttc ttc gtt att tcc ttg acg att ttg tcc	979
Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser Leu Thr Ile Leu Ser	
280 285 290	

1006

ttt gcc act tcc aac tgg cac gtt gtg
 Phe Ala Thr Ser Asn Trp His Val Val
 295 300

<210> 184

<211> 302

<212> PRT

<213> Corynebacterium glutamicum

<400> 184

Val Ser Val Ala Glu Glu Gly Lys Leu Phe Thr Pro Thr Phe Val Met
 1 5 10 15

Gly Trp Phe Ala Asn Leu Phe Gln Phe Leu Val Phe Tyr Phe Leu Ile
 20 25 30

Thr Thr Met Ala Leu Tyr Ala Ile Lys Glu Phe Gln Ala Ser Glu Val
 35 40 45

Glu Ala Gly Phe Ala Ser Ser Ser Ile Val Ile Gly Ala Val Phe Ser
 50 55 60

Arg Phe Phe Ser Gly Tyr Ile Ile Asp Arg Phe Gly Arg Arg Lys Ile
 65 70 75 80

Val Leu Ile Ser Val Leu Val Thr Thr Ile Ala Cys Ala Leu Tyr Leu
 85 90 95

Pro Ile Glu Ser Leu Pro Leu Leu Tyr Ala Asn Arg Phe Leu His Gly
 100 105 110

Val Gly Tyr Ala Phe Ala Ala Thr Ala Ile Met Ala Met Val Gln Glu
 115 120 125

Leu Ile Pro Ala Ser Arg Arg Ser Glu Gly Thr Gly Tyr Leu Ala Leu
 130 135 140

Gly Thr Thr Val Ser Ala Ala Leu Gly Pro Ala Leu Ala Leu Phe Val
 145 150 155 160

Leu Gly Thr Phe Asp Tyr Asp Met Leu Phe Ile Val Val Leu Ala Thr
 165 170 175

Ser Val Ile Ser Leu Ile Ala Val Val Phe Met Tyr Phe Lys Thr Ser
 180 185 190

Asp Pro Glu Pro Ser Gly Glu Pro Ala Lys Phe Ser Phe Lys Ser Ile
 195 200 205

Met Asn Pro Lys Ile Ile Pro Ile Gly Ile Phe Ile Leu Leu Ile Cys
 210 215 220

Phe Ala Tyr Ser Gly Val Ile Ala Tyr Ile Asn Ala Phe Ala Glu Glu
 225 230 235 240

Arg Asp Leu Ile Thr Gly Ala Gly Leu Phe Phe Ile Ala Tyr Ala Val
 245 250 255

Ser Met Phe Val Met Arg Ser Phe Leu Gly Lys Leu Gln Asp Arg Arg
 260 265 270

Gly Asp Asn Val Val Ile Tyr Phe Gly Leu Phe Phe Phe Val Ile Ser
 275 280 285
 Leu Thr Ile Leu Ser Phe Ala Thr Ser Asn Trp His Val Val
 290 295 300

<210> 185
 <211> 568
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(568)
 <223> RXA00858

<400> 185
 ttttgttttt cagatgcatg ttagatgcgt tgagggacaa ggggtggggga gacctccggt 60
 tcttaaattg tctaaccaag aaccggaggt tctttttgtc atg gaa gta aac tta 115
 Met Glu Val Asn Leu
 1 5
 gcc aca tgg cta atc act atc gca gtg att gct ggc ttc ttc att ttc 163
 Ala Thr Trp Leu Ile Thr Ile Ala Val Ile Ala Gly Phe Phe Ile Phe
 10 15 20
 gat ttc tat tcc cac gtc cgc acc cca cac gag ccc act atc aaa gaa 211
 Asp Phe Tyr Ser His Val Arg Thr Pro His Glu Pro Thr Ile Lys Glu
 25 30 35
 tcc gca tgg tgg agc ctc ttc tac gta gcc ctc gcc tgt gtt ttc ggc 259
 Ser Ala Trp Trp Ser Leu Phe Tyr Val Ala Leu Ala Cys Val Phe Gly
 40 45 50
 gtg ttc ctc tgg ttt gct tgg ggc gag cca ggt aac cca cac cag cac 307
 Val Phe Leu Trp Phe Ala Trp Gly Glu Pro Gly Asn Pro His Gln His
 55 60 65
 ggc att gag ttc ttc acc ggt tac gtg aca gag aag gcg ttg agt gtt 355
 Gly Ile Glu Phe Phe Thr Gly Tyr Val Thr Glu Lys Ala Leu Ser Val
 70 75 80 85
 gat aac ctc ttc atc ttc gcg ctg atc atg ggt tct ttc aag att cct 403
 Asp Asn Leu Phe Ile Phe Ala Leu Ile Met Gly Ser Phe Lys Ile Pro
 90 95 100
 cgc aag tac cag cag aag gtt ctg ctc atc ggt atc gcg ctg gca ctg 451
 Arg Lys Tyr Gln Gln Lys Val Leu Leu Ile Gly Ile Ala Leu Ala Leu
 105 110 115
 gtc ttc cgc ctg gca ttc atc ctc gca ggt gct gca gtt atc gaa gcc 499
 Val Phe Arg Leu Ala Phe Ile Leu Ala Gly Ala Ala Val Ile Glu Ala
 120 125 130
 tgg tcc gat gtc ttc tac atc ttc tcc atc tgg ctg atc tac acc gct 547
 Trp Ser Asp Val Phe Tyr Ile Phe Ser Ile Trp Leu Ile Tyr Thr Ala
 135 140 145

568

gtg aag gct cct gtg cac gag
 Val Lys Ala Pro Val His Glu
 150 155

<210> 186
 <211> 156
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 186
 Met Glu Val Asn Leu Ala Thr Trp Leu Ile Thr Ile Ala Val Ile Ala
 1 5 10 15
 Gly Phe Phe Ile Phe Asp Phe Tyr Ser His Val Arg Thr Pro His Glu
 20 25 30
 Pro Thr Ile Lys Glu Ser Ala Trp Trp Ser Leu Phe Tyr Val Ala Leu
 35 40 45
 Ala Cys Val Phe Gly Val Phe Leu Trp Phe Ala Trp Gly Glu Pro Gly
 50 55 60
 Asn Pro His Gln His Gly Ile Glu Phe Phe Thr Gly Tyr Val Thr Glu
 65 70 75 80
 Lys Ala Leu Ser Val Asp Asn Leu Phe Ile Phe Ala Leu Ile Met Gly
 85 90 95
 Ser Phe Lys Ile Pro Arg Lys Tyr Gln Gln Lys Val Leu Leu Ile Gly
 100 105 110
 Ile Ala Leu Ala Leu Val Phe Arg Leu Ala Phe Ile Leu Ala Gly Ala
 115 120 125
 Ala Val Ile Glu Ala Trp Ser Asp Val Phe Tyr Ile Phe Ser Ile Trp
 130 135 140
 Leu Ile Tyr Thr Ala Val Lys Ala Pro Val His Glu
 145 150 155

<210> 187
 <211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(952)
 <223> RXA02305

<400> 187
 tatgcgcgca ggtgtctact ggtgacgcag ccgacgacga ttattttgac gaagccaccg 60
 caaacgatga cttcgatccc gaaaagtgga ggaacatgta atg cca gcc ttt gag 115
 Met Pro Ala Phe Glu
 1 5
 gca atg cca gga atg ccg tat tgg atc gac ctg tcc acc tcg gac att 163
 Ala Met Pro Gly Met Pro Tyr Trp Ile Asp Leu Ser Thr Ser Asp Ile

10							15							20							
gca	aaa	tct	gca	cac	ttc	tac	gaa	aac	gtt	ctc	ggc	tgg	gaa	att	gaa	211					
Ala	Lys	Ser	Ala	His	Phe	Tyr	Glu	Asn	Val	Leu	Gly	Trp	Glu	Ile	Glu						
			25						30					35							
gaa	gtc	aac	gat	ggc	tac	cgc	atg	gct	cgt	ctg	cag	gga	cta	ccc	gtg	259					
Glu	Val	Asn	Asp	Gly	Tyr	Arg	Met	Ala	Arg	Leu	Gln	Gly	Leu	Pro	Val						
		40					45					50									
gca	ggg	ctg	atc	gat	cag	cgc	ggg	gaa	tca	agc	atc	ccg	gat	acc	tgg	307					
Ala	Gly	Leu	Ile	Asp	Gln	Arg	Gly	Glu	Ser	Ser	Ile	Pro	Asp	Thr	Trp						
	55					60					65										
att	acc	tac	ttc	ctc	tcc	tac	gat	ctg	gat	gcc	act	gca	aag	aag	atc	355					
Ile	Thr	Tyr	Phe	Leu	Ser	Tyr	Asp	Leu	Asp	Ala	Thr	Ala	Lys	Lys	Ile						
	70					75				80					85						
gca	gaa	ctg	ggg	gga	cga	att	ctg	gcc	gag	cca	act	gac	gtg	cac	ttg	403					
Ala	Glu	Leu	Gly	Gly	Arg	Ile	Leu	Ala	Glu	Pro	Thr	Asp	Val	His	Leu						
				90					95					100							
gga	cgc	atg	atc	cta	gct	gtt	gat	act	gcc	ggc	gca	ctg	ttc	ggc	gtt	451					
Gly	Arg	Met	Ile	Leu	Ala	Val	Asp	Thr	Ala	Gly	Ala	Leu	Phe	Gly	Val						
			105					110					115								
att	gag	cca	ggc	agc	gag	gaa	tca	ttc	gtc	gct	gct	ggg	gaa	cca	ggc	499					
Ile	Glu	Pro	Gly	Ser	Glu	Glu	Ser	Phe	Val	Ala	Ala	Gly	Glu	Pro	Gly						
		120					125					130									
aca	tcc	gtg	tgg	cat	gaa	ctc	acc	act	gtc	tcc	aaa	tat	tcc	gaa	gct	547					
Thr	Ser	Val	Trp	His	Glu	Leu	Thr	Thr	Val	Ser	Lys	Tyr	Ser	Glu	Ala						
	135					140					145										
atc	gat	ttc	tac	ggg	gag	ctg	ttc	act	tgg	aca	acc	tct	gaa	atg	gct	595					
Ile	Asp	Phe	Tyr	Gly	Glu	Leu	Phe	Thr	Trp	Thr	Thr	Ser	Glu	Met	Ala						
	150					155				160					165						
agt	gct	gaa	gac	gat	agt	ttc	cgc	tac	acc	acc	gca	ttg	gct	gac	ggg	643					
Ser	Ala	Glu	Asp	Asp	Ser	Phe	Arg	Tyr	Thr	Thr	Ala	Leu	Ala	Asp	Gly						
				170					175					180							
tcc	gcc	ttt	gct	gga	att	ttt	gat	gcc	aaa	ggc	cac	ttc	cca	cct	cag	691					
Ser	Ala	Phe	Ala	Gly	Ile	Phe	Asp	Ala	Lys	Gly	His	Phe	Pro	Pro	Gln						
			185					190					195								
gtt	cca	agc	ttc	tgg	cag	tcc	tac	ctt	ggc	gtg	ctc	aac	gcc	gat	gat	739					
Val	Pro	Ser	Phe	Trp	Gln	Ser	Tyr	Leu	Gly	Val	Leu	Asn	Ala	Asp	Asp						
		200					205					210									
gct	gca	gag	aag	gcc	aag	gaa	ttt	ggg	ggc	gat	gtt	att	cgt	aag	cca	787					
Ala	Ala	Ala	Lys	Ala	Lys	Glu	Phe	Gly	Gly	Asp	Val	Ile	Arg	Lys	Pro						
	215					220					225										
tgg	gac	tca	gaa	ttt	ggc	cgc	atg	gtt	ctc	atc	tct	gat	tcc	act	ggg	835					
Trp	Asp	Ser	Glu	Phe	Gly	Arg	Met	Val	Leu	Ile	Ser	Asp	Ser	Thr	Gly						
	230				235					240					245						
gcc	aca	att	acc	ttg	tgt	gaa	gta	gag	gaa	tac	gtc	gag	gaa	gca	gca	883					
Ala	Thr	Ile	Thr	Leu	Cys	Glu	Val	Glu	Glu	Tyr	Val	Glu	Glu	Ala	Ala						
				250					255					260							

gaa ggc gat gat ctc ttc gac atc gat ctc agt gct ttc gaa gag cag 931
 Glu Gly Asp Asp Leu Phe Asp Ile Asp Leu Ser Ala Phe Glu Glu Gln
 265 270 275

ttc cgc aag caa gaa gga cag taatcctaca gcgccatgga gga 975
 Phe Arg Lys Gln Glu Gly Gln
 280

<210> 188

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Met Pro Ala Phe Glu Ala Met Pro Gly Met Pro Tyr Trp Ile Asp Leu
 1 5 10 15

Ser Thr Ser Asp Ile Ala Lys Ser Ala His Phe Tyr Glu Asn Val Leu
 20 25 30

Gly Trp Glu Ile Glu Glu Val Asn Asp Gly Tyr Arg Met Ala Arg Leu
 35 40 45

Gln Gly Leu Pro Val Ala Gly Leu Ile Asp Gln Arg Gly Glu Ser Ser
 50 55 60

Ile Pro Asp Thr Trp Ile Thr Tyr Phe Leu Ser Tyr Asp Leu Asp Ala
 65 70 75 80

Thr Ala Lys Lys Ile Ala Glu Leu Gly Gly Arg Ile Leu Ala Glu Pro
 85 90 95

Thr Asp Val His Leu Gly Arg Met Ile Leu Ala Val Asp Thr Ala Gly
 100 105 110

Ala Leu Phe Gly Val Ile Glu Pro Gly Ser Glu Glu Ser Phe Val Ala
 115 120 125

Ala Gly Glu Pro Gly Thr Ser Val Trp His Glu Leu Thr Thr Val Ser
 130 135 140

Lys Tyr Ser Glu Ala Ile Asp Phe Tyr Gly Glu Leu Phe Thr Trp Thr
 145 150 155 160

Thr Ser Glu Met Ala Ser Ala Glu Asp Asp Ser Phe Arg Tyr Thr Thr
 165 170 175

Ala Leu Ala Asp Gly Ser Ala Phe Ala Gly Ile Phe Asp Ala Lys Gly
 180 185 190

His Phe Pro Pro Gln Val Pro Ser Phe Trp Gln Ser Tyr Leu Gly Val
 195 200 205

Leu Asn Ala Asp Asp Ala Ala Ala Lys Ala Lys Glu Phe Gly Gly Asp
 210 215 220

Val Ile Arg Lys Pro Trp Asp Ser Glu Phe Gly Arg Met Val Leu Ile
 225 230 235 240

<400> 189																
tcacccttgt cgataccagc tactgggtat ctggcgctcgg tccacttggc ggcagcaaag																60
tcttgggaaga catcgatgcc ttcctcgacg cacagcaata atg tcc aca gct ctc																115
Met Ser Thr Ala Leu																5
1																
ccc gat cag ctc aag tgg gaa tac agt gcc ttc ccc gtg cag atc tcg																163
Pro Asp Gln Leu Lys Trp Glu Tyr Ser Ala Phe Pro Val Gln Ile Ser																20
10 15																
cag aag caa cgg ctt agt ccc ggc ttc atg cgg atc acc gtc act ggt																211
Gln Lys Gln Arg Leu Ser Pro Gly Phe Met Arg Ile Thr Val Thr Gly																35
25 30																
gac aag ctc cga ttc ttt ggc cag tgg ggt ttg gac caa cgc atc aaa																259
Asp Lys Leu Arg Phe Phe Gly Gln Trp Gly Leu Asp Gln Arg Ile Lys																50
40 45																
ctg atc att cca agc ccg gct ggg aac atc cca gat ttc gga att ctc																307
Leu Ile Ile Pro Ser Pro Ala Gly Asn Ile Pro Asp Phe Gly Ile Leu																65
55 60																
gac gaa ccc act ccc cca ccg aca acg tgg ctt cct cgt gct aag tct																355
Asp Glu Pro Thr Pro Pro Pro Thr Thr Trp Leu Pro Arg Ala Lys Ser																85
70 75 80																
ttt cca gcg gac caa cga ccg atc ttg cgc acc tac acc cca tct gcg																403
Phe Pro Ala Asp Gln Arg Pro Ile Leu Arg Thr Tyr Thr Pro Ser Ala																100
90 95																
gtc cga ccc gaa cta tgc gaa gta gac att gat atc tat ctt cac aac																451
Val Arg Pro Glu Leu Cys Glu Val Asp Ile Asp Ile Tyr Leu His Asn																115
105 110																
cct tcg gga cca gta tcc aga tgg gca aag aac tgc agt gtt gac gat																499
Pro Ser Gly Pro Val Ser Arg Trp Ala Lys Asn Cys Ser Val Asp Asp																130
120 125 130																
gaa cta atc atc acc ggc cct gac gta cgc gca gga gaa acc ggc tac																547
Glu Leu Ile Ile Thr Gly Pro Asp Val Arg Ala Gly Glu Thr Gly Tyr																

135	140	145	
gga atc acc tat cat ccg act tct gcg atc gat cgc ctc tgt ctc atc			595
Gly Ile Thr Tyr His Pro Thr Ser Ala Ile Asp Arg Leu Cys Leu Ile			
150	155	160	165
ggc gat tgt gca tca gct ccc gcg atc gca aat atc gtc aat caa tca			643
Gly Asp Cys Ala Ser Ala Pro Ala Ile Ala Asn Ile Val Asn Gln Ser			
	170	175	180
aaa gta cct act acg gtt ttc ctc cac gta gac agc cta gaa gat gat			691
Lys Val Pro Thr Thr Val Phe Leu His Val Asp Ser Leu Glu Asp Asp			
	185	190	195
gta ttg atc gcc gat agc tcc acc aag ctc act ttc gaa gac atc gac			739
Val Leu Ile Ala Asp Ser Ser Thr Lys Leu Thr Phe Glu Asp Ile Asp			
	200	205	210
gct tac aaa gca aag gtc ttc caa tgg gct tca gcc aat gca gca gat			787
Ala Tyr Lys Ala Lys Val Phe Gln Trp Ala Ser Ala Asn Ala Ala Asp			
	215	220	225
cct tca gta cac ttc tgg atc gcc ggt gaa act agc atg gtg cgc ttc			835
Pro Ser Val His Phe Trp Ile Ala Gly Glu Thr Ser Met Val Arg Phe			
	230	235	240
att cgc aaa gaa cta atc aac agc tac cga gtt gat tcc tca cga atc			883
Ile Arg Lys Glu Leu Ile Asn Ser Tyr Arg Val Asp Ser Ser Arg Ile			
	250	255	260
act ttc ctc ggc tac tgg aaa tac ggc cga cga acc gta gac			925
Thr Phe Leu Gly Tyr Trp Lys Tyr Gly Arg Arg Thr Val Asp			
	265	270	275
tagctttcag attcagaccc cag			948
<210> 190			
<211> 275			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 190			
Met Ser Thr Ala Leu Pro Asp Gln Leu Lys Trp Glu Tyr Ser Ala Phe			
1	5	10	15
Pro Val Gln Ile Ser Gln Lys Gln Arg Leu Ser Pro Gly Phe Met Arg			
	20	25	30
Ile Thr Val Thr Gly Asp Lys Leu Arg Phe Phe Gly Gln Trp Gly Leu			
	35	40	45
Asp Gln Arg Ile Lys Leu Ile Ile Pro Ser Pro Ala Gly Asn Ile Pro			
	50	55	60
Asp Phe Gly Ile Leu Asp Glu Pro Thr Pro Pro Pro Thr Thr Trp Leu			
	65	70	75
Pro Arg Ala Lys Ser Phe Pro Ala Asp Gln Arg Pro Ile Leu Arg Thr			
	85	90	95

Tyr Thr Pro Ser Ala Val Arg Pro Glu Leu Cys Glu Val Asp Ile Asp
 100 105 110
 Ile Tyr Leu His Asn Pro Ser Gly Pro Val Ser Arg Trp Ala Lys Asn
 115 120 125
 Cys Ser Val Asp Asp Glu Leu Ile Ile Thr Gly Pro Asp Val Arg Ala
 130 135 140
 Gly Glu Thr Gly Tyr Gly Ile Thr Tyr His Pro Thr Ser Ala Ile Asp
 145 150 155 160
 Arg Leu Cys Leu Ile Gly Asp Cys Ala Ser Ala Pro Ala Ile Ala Asn
 165 170 175
 Ile Val Asn Gln Ser Lys Val Pro Thr Thr Val Phe Leu His Val Asp
 180 185 190
 Ser Leu Glu Asp Asp Val Leu Ile Ala Asp Ser Ser Thr Lys Leu Thr
 195 200 205
 Phe Glu Asp Ile Asp Ala Tyr Lys Ala Lys Val Phe Gln Trp Ala Ser
 210 215 220
 Ala Asn Ala Ala Asp Pro Ser Val His Phe Trp Ile Ala Gly Glu Thr
 225 230 235 240
 Ser Met Val Arg Phe Ile Arg Lys Glu Leu Ile Asn Ser Tyr Arg Val
 245 250 255
 Asp Ser Ser Arg Ile Thr Phe Leu Gly Tyr Trp Lys Tyr Gly Arg Arg
 260 265 270
 Thr Val Asp
 275

<210> 191
 <211> 468
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(445)
 <223> RXA00843

<400> 191
 gccctgatgc gaaaccggcg ccaacaatga tgccgacgaa ggcaaagcc actcttagga 60

tttgaataat catggaacaa accttagtag gctcaacgtt atg aaa gtc acg att 115
 Met Lys Val Thr Ile
 1 5

ttc cat aat ccg cgt tgt tcc aca tcc aga aat acc ctc gct tac ctc 163
 Phe His Asn Pro Arg Cys Ser Thr Ser Arg Asn Thr Leu Ala Tyr Leu
 10 15 20

cgc gac aag gac att gag cct gaa att gtt cag tat ctc aaa gac acg 211
 Arg Asp Lys Asp Ile Glu Pro Glu Ile Val Gln Tyr Leu Lys Asp Thr
 25 30 35

```

ccc acc gct tcc gag ctc aaa gaa cta ttc aat acg ctg gga att cca 259
Pro Thr Ala Ser Glu Leu Lys Glu Leu Phe Asn Thr Leu Gly Ile Pro
      40                      45                      50

gtc cac gac ggc atc aga acc cgc gaa gct gag tac aca gaa ctg ggc 307
Val His Asp Gly Ile Arg Thr Arg Glu Ala Glu Tyr Thr Glu Leu Gly
      55                      60                      65

ctg tca cca gaa aca cct gaa act gag ctt atc gac gcc atc gtt gcc 355
Leu Ser Pro Glu Thr Pro Glu Thr Glu Leu Ile Asp Ala Ile Val Ala
      70                      75                      80                      85

cat ccc agg ctc ctt cag cgt ccg atc gtg gtg acg gcc aaa ggc gcg 403
His Pro Arg Leu Leu Gln Arg Pro Ile Val Val Thr Ala Lys Gly Ala
      90                      95                      100

cgc att gcg cgc ccc aaa atc gac gtc att gac agc atc ttg 445
Arg Ile Ala Arg Pro Lys Ile Asp Val Ile Asp Ser Ile Leu
      105                      110                      115

tgacaacatt ttgtagagca acc 468

```

<210> 192
 <211> 115
 <212> PRT
 <213> Corynebacterium glutamicum

```

<400> 192
Met Lys Val Thr Ile Phe His Asn Pro Arg Cys Ser Thr Ser Arg Asn
  1                      5                      10                      15

Thr Leu Ala Tyr Leu Arg Asp Lys Asp Ile Glu Pro Glu Ile Val Gln
  20                      25                      30

Tyr Leu Lys Asp Thr Pro Thr Ala Ser Glu Leu Lys Glu Leu Phe Asn
  35                      40                      45

Thr Leu Gly Ile Pro Val His Asp Gly Ile Arg Thr Arg Glu Ala Glu
  50                      55                      60

Tyr Thr Glu Leu Gly Leu Ser Pro Glu Thr Pro Glu Thr Glu Leu Ile
  65                      70                      75                      80

Asp Ala Ile Val Ala His Pro Arg Leu Leu Gln Arg Pro Ile Val Val
  85                      90                      95

Thr Ala Lys Gly Ala Arg Ile Ala Arg Pro Lys Ile Asp Val Ile Asp
  100                      105                      110

Ser Ile Leu
  115

```

<210> 193
 <211> 432
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>

<221> CDS
 <222> (101)..(409)
 <223> RXA01052

<400> 193

```
tatggccaac cctaggggga tggcctgtgt gttcactgtt aggtttcctc aaaatcttta 60
acgaacaacg aagagcttgc ccgagagtat cttgggtcgc atg gac aca aaa tta 115
                                         Met Asp Thr Lys Leu
                                         1           5

ggc gct gaa ttg ggt act gaa ttt gat ctc att gtt gtt ggt ttc ggc 163
Gly Ala Glu Leu Gly Thr Glu Phe Asp Leu Ile Val Val Gly Phe Gly
                10                15                20

aaa gca ggc aag act atc gcg atg aaa cgc tcg gca gcg ggg gat aag 211
Lys Ala Gly Lys Thr Ile Ala Met Lys Arg Ser Ala Ala Gly Asp Lys
                25                30                35

gtc gca ctg atc gag cag agt cca cag atg tat ggc ggt acc tgc atc 259
Val Ala Leu Ile Glu Gln Ser Pro Gln Met Tyr Gly Gly Thr Cys Ile
                40                45                50

aat gta ggt tgc atc ccc acg aag aag ttg ttg ttt gag act gca acg 307
Asn Val Gly Cys Ile Pro Thr Lys Lys Leu Leu Phe Glu Thr Ala Thr
                55                60                65

ggc aag gat ttc ccg gat gcg gtt gtg gcg cgt gat cag ttg att ggc 355
Gly Lys Asp Phe Pro Asp Ala Val Val Ala Arg Asp Gln Leu Ile Gly
                70                75                80                85

aag ctg aat gcc aag aat ctt gcg atg gcc aca gac aag ggt gtc acc 403
Lys Leu Asn Ala Lys Asn Leu Ala Met Ala Thr Asp Lys Gly Val Thr
                90                95                100

cgt cat tgatggaaaa gctacgttta cag 432
Arg His
```

<210> 194
 <211> 103
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 194

```
Met Asp Thr Lys Leu Gly Ala Glu Leu Gly Thr Glu Phe Asp Leu Ile
  1           5           10           15

Val Val Gly Phe Gly Lys Ala Gly Lys Thr Ile Ala Met Lys Arg Ser
                20                25                30

Ala Ala Gly Asp Lys Val Ala Leu Ile Glu Gln Ser Pro Gln Met Tyr
                35                40                45

Gly Gly Thr Cys Ile Asn Val Gly Cys Ile Pro Thr Lys Lys Leu Leu
  50                55                60

Phe Glu Thr Ala Thr Gly Lys Asp Phe Pro Asp Ala Val Val Ala Arg
  65                70                75                80
```

Asp Gln Leu Ile Gly Lys Leu Asn Ala Lys Asn Leu Ala Met Ala Thr
 85 90 95

Asp Lys Gly Val Thr Arg His
 100

<210> 195

<211> 543

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(520)

<223> RXA01053

<400> 195

```

ttgcatggc cacagacaag ggtgtcacc gtcattgatg gaaaagctac gtttacagct 60
agccacgaaa tcacaagtaa cttcaggtag tgacactctt gtg ctg tat gcg cca 115
                               Val Leu Tyr Ala Pro
                               1 5
acg att gtg atc aac acg ggc tcc acg ccg gtc atc ccc aat gtc cca 163
Thr Ile Val Ile Asn Thr Gly Ser Thr Pro Val Ile Pro Asn Val Pro
                               10 15 20
ggc acc gac aat ccg cat gtt ttt gat tcc act ggc att cag cac att 211
Gly Thr Asp Asn Pro His Val Phe Asp Ser Thr Gly Ile Gln His Ile
                               25 30 35
tcg ccc ctg ccg aag cac ctc gcg atc atc ggc ggt ggc ccc atc ggt 259
Ser Pro Leu Pro Lys His Leu Ala Ile Ile Gly Gly Gly Pro Ile Gly
                               40 45 50
ttg gaa ttt gcc acg ctt ttc agt gga caa ggc tcc aaa gtc acc atc 307
Leu Glu Phe Ala Thr Leu Phe Ser Gly Gln Gly Ser Lys Val Thr Ile
                               55 60 65
atc gac cgt ggt gaa ttg ccg ctg aaa aat ttc gac agg gaa gta gcg 355
Ile Asp Arg Gly Glu Leu Pro Leu Lys Asn Phe Asp Arg Glu Val Ala
                               70 75 80 85
gag ctg gcc aaa acc gac ctg gag gcc cgc gga atc acc ttc ctc aac 403
Glu Leu Ala Lys Thr Asp Leu Glu Ala Arg Gly Ile Thr Phe Leu Asn
                               90 95 100
aac gct gaa ctc acc gga ttc agc ggt gac ctc acc atc gcg ctc aaa 451
Asn Ala Glu Leu Thr Gly Phe Ser Gly Asp Leu Thr Ile Ala Leu Lys
                               105 110 115
gac cac gac ctc ctc gcc gac gcc gca ctt ttt gca tcg gcc gac gcc 499
Asp His Asp Leu Leu Ala Asp Ala Ala Leu Phe Ala Ser Ala Asp Ala
                               120 125 130
cgg cac cga cgg gct cgg cct tgaacaggcg ggcatcaaaa cag 543
Arg His Arg Arg Ala Arg Pro
                               135 140

```

<210> 196
 <211> 140
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 196
 Val Leu Tyr Ala Pro Thr Ile Val Ile Asn Thr Gly Ser Thr Pro Val
 1 5 10 15
 Ile Pro Asn Val Pro Gly Thr Asp Asn Pro His Val Phe Asp Ser Thr
 20 25 30
 Gly Ile Gln His Ile Ser Pro Leu Pro Lys His Leu Ala Ile Ile Gly
 35 40 45
 Gly Gly Pro Ile Gly Leu Glu Phe Ala Thr Leu Phe Ser Gly Gln Gly
 50 55 60
 Ser Lys Val Thr Ile Ile Asp Arg Gly Glu Leu Pro Leu Lys Asn Phe
 65 70 75 80
 Asp Arg Glu Val Ala Glu Leu Ala Lys Thr Asp Leu Glu Ala Arg Gly
 85 90 95
 Ile Thr Phe Leu Asn Asn Ala Glu Leu Thr Gly Phe Ser Gly Asp Leu
 100 105 110
 Thr Ile Ala Leu Lys Asp His Asp Leu Leu Ala Asp Ala Ala Leu Phe
 115 120 125
 Ala Ser Ala Asp Ala Arg His Arg Arg Ala Arg Pro
 130 135 140

<210> 197
 <211> 612
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(589)
 <223> RXA01054

<400> 197
 gacctcctcg cgcagccgc actttttgca tcggccgacg cccggcaccg acgggctcgg 60
 ccttgaacag gcgggcatca aaacaggcac gcgtggggag gtg ctt gtc gac gcc 115
 Val Leu Val Asp Ala
 1 5
 cac ctc cgg acc aac atc gac ggc atc ttc gct gta ggt gat gtc aat 163
 His Leu Arg Thr Asn Ile Asp Gly Ile Phe Ala Val Gly Asp Val Asn
 10 15 20
 ggc ggc ccg cag ttt acc tac gtg tcc tac gat gac cac cgc att gtg 211
 Gly Gly Pro Gln Phe Thr Tyr Val Ser Tyr Asp Asp His Arg Ile Val
 25 30 35
 ctg gat caa cta gcc gga aca ggt aag aaa tcc att gca cac cga ctg 259
 Leu Asp Gln Leu Ala Gly Thr Gly Lys Lys Ser Ile Ala His Arg Leu

40	45	50	
atc ccc acc acc acg ttc atc gaa ccg ccg tta tcc acc atc ggt gac Ile Pro Thr Thr Thr Phe Ile Glu Pro Pro Leu Ser Thr Ile Gly Asp 55 60 65			307
aac act gaa ggg gaa aat gtg gtg gtg aaa aag gcc ttg att gca gat Asn Thr Glu Gly Glu Asn Val Val Val Lys Lys Ala Leu Ile Ala Asp 70 75 80 85			355
atg ccg atc gtt ccc cga cca gag att att aac caa cct cac ggt atg Met Pro Ile Val Pro Arg Pro Glu Ile Ile Asn Gln Pro His Gly Met 90 95 100			403
gtg aag ttt ttc gtc gac aag caa tct gat gcg ctg ctc ggc gcg acc Val Lys Phe Phe Val Asp Lys Gln Ser Asp Ala Leu Leu Gly Ala Thr 105 110 115			451
ttg tac tgc gcc gac tcc cag gag ctc atc aac acc gtg gcg ctt gcc Leu Tyr Cys Ala Asp Ser Gln Glu Leu Ile Asn Thr Val Ala Leu Ala 120 125 130			499
atg cgg cat ggc gtc acc gcc tcc gag ctt ggc gac ggc atc tac acc Met Arg His Gly Val Thr Ala Ser Glu Leu Gly Asp Gly Ile Tyr Thr 135 140 145			547
cac ccc gcc acc tcg gag atc ttc aac caa tta ttg ggc agt His Pro Ala Thr Ser Glu Ile Phe Asn Gln Leu Leu Gly Ser 150 155 160			589
taacgcagcg gatcgaacgg ctt			612

<210> 198

<211> 163

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 198

Val Leu Val Asp Ala His Leu Arg Thr Asn Ile Asp Gly Ile Phe Ala
1 5 10 15

Val Gly Asp Val Asn Gly Gly Pro Gln Phe Thr Tyr Val Ser Tyr Asp
20 25 30

Asp His Arg Ile Val Leu Asp Gln Leu Ala Gly Thr Gly Lys Lys Ser
35 40 45

Ile Ala His Arg Leu Ile Pro Thr Thr Thr Phe Ile Glu Pro Pro Leu
50 55 60

Ser Thr Ile Gly Asp Asn Thr Glu Gly Glu Asn Val Val Val Lys Lys
65 70 75 80

Ala Leu Ile Ala Asp Met Pro Ile Val Pro Arg Pro Glu Ile Ile Asn
85 90 95

Gln Pro His Gly Met Val Lys Phe Phe Val Asp Lys Gln Ser Asp Ala
100 105 110

Leu Leu Gly Ala Thr Leu Tyr Cys Ala Asp Ser Gln Glu Leu Ile Asn

115	120	125
Thr Val Ala Leu Ala Met	Arg His Gly Val Thr	Ala Ser Glu Leu Gly
130	135	140
Asp Gly Ile Tyr Thr His	Pro Ala Thr Ser Glu	Ile Phe Asn Gln Leu
145	150	155
160		
Leu Gly Ser		

<210> 199
 <211> 561
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(538)
 <223> RXN03123

<400> 199
 agctctacca acgcgcctac accttgacca acgtggatgc cgatgccggt acctttgacc 60
 tggcttttgt gctgcacgag ccgctggggc ccgcctcggc gtg ggc gac gcg ctg 115
 Val Gly Asp Ala Leu
 1 5
 cga ggc cgg gga aag cct gaa gtc atg cgc tac cca gga att ccg ttc 163
 Arg Gly Arg Gly Lys Pro Glu Val Met Arg Tyr Pro Gly Ile Pro Phe
 10 15 20
 gcc atc cca gat cca gcg ccg cgt ggc ttc ctt ttc tta ggc gat ctc 211
 Ala Ile Pro Asp Pro Ala Pro Arg Gly Phe Leu Phe Leu Gly Asp Leu
 25 30 35
 acc tct tac cca gcg atc tgc tgc att ctg gag acc ttg gac ggt gaa 259
 Thr Ser Tyr Pro Ala Ile Cys Ser Ile Leu Glu Thr Leu Asp Gly Glu
 40 45 50
 atc cct gcg acc gcg tat ctt atc gcc cac gat cca ctt gat tac acc 307
 Ile Pro Ala Thr Ala Tyr Leu Ile Ala His Asp Pro Leu Asp Tyr Thr
 55 60 65
 ttc gat ttt ccc cag ggc gag cac atc acc gcg cag tgg att tcc aac 355
 Phe Asp Phe Pro Gln Gly Glu His Ile Thr Ala Gln Trp Ile Ser Asn
 70 75 80 85
 gaa caa tcc ttc att gat cac atc gct gac acg gat tac acc gat ttt 403
 Glu Gln Ser Phe Ile Asp His Ile Ala Asp Thr Asp Tyr Thr Asp Phe
 90 95 100
 tat acc tgg atc ggc gcg gaa tcc tcc gaa acc cgt gcg gcc aag aag 451
 Tyr Thr Trp Ile Gly Ala Glu Ser Ser Glu Thr Arg Ala Ala Lys Lys
 105 110 115
 cat ctg cag acc cac gcc ggc atg ccc aag acg cac atg aac gcg caa 499
 His Leu Gln Thr His Ala Gly Met Pro Lys Thr His Met Asn Ala Gln
 120 125 130

ggt tat tgg aac aag ggc aga gcc atg ggt aaa agc aat taaaagattt 548
 Gly Tyr Trp Asn Lys Gly Arg Ala Met Gly Lys Ser Asn
 135 140 145

ttgcttatcg acg 561

<210> 200

<211> 146

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

Val Gly Asp Ala Leu Arg Gly Arg Gly Lys Pro Glu Val Met Arg Tyr
 1 5 10 15

Pro Gly Ile Pro Phe Ala Ile Pro Asp Pro Ala Pro Arg Gly Phe Leu
 20 25 30

Phe Leu Gly Asp Leu Thr Ser Tyr Pro Ala Ile Cys Ser Ile Leu Glu
 35 40 45

Thr Leu Asp Gly Glu Ile Pro Ala Thr Ala Tyr Leu Ile Ala His Asp
 50 55 60

Pro Leu Asp Tyr Thr Phe Asp Phe Pro Gln Gly Glu His Ile Thr Ala
 65 70 75 80

Gln Trp Ile Ser Asn Glu Gln Ser Phe Ile Asp His Ile Ala Asp Thr
 85 90 95

Asp Tyr Thr Asp Phe Tyr Thr Trp Ile Gly Ala Glu Ser Ser Glu Thr
 100 105 110

Arg Ala Ala Lys Lys His Leu Gln Thr His Ala Gly Met Pro Lys Thr
 115 120 125

His Met Asn Ala Gln Gly Tyr Trp Asn Lys Gly Arg Ala Met Gly Lys
 130 135 140

Ser Asn
 145

<210> 201

<211> 736

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(736)

<223> FRXA00993

<400> 201

gctgagctag tgcttttgcg acacacctct tgcgaatggt gattagggtta ggcaagccat 60

atttacaggg tggttgtaaa gcataaggga gcaaggaaac atg ggc aag gga ttt 115
 Met Gly Lys Gly Phe
 1 5

acc ggc gct att ttg acc gtc atg ggc gtg aaa tcg cat atc gcc acc 163
 Thr Gly Ala Ile Leu Thr Val Met Gly Val Lys Ser His Ile Ala Thr
 10 15 20

acc acg gga aaa acc gtg atc aat gac cgc atg gtg acc att cat ttt 211
 Thr Thr Gly Lys Thr Val Ile Asn Asp Arg Met Val Thr Ile His Phe
 25 30 35

cat tcc gag acg ctg ctc aac acg gaa ggt gaa gtc ccc ggc gat tgg 259
 His Ser Glu Thr Leu Leu Asn Thr Glu Gly Glu Val Pro Gly Asp Trp
 40 45 50

ctg cgt ctg tgg ttc ccg cac gag agc cga cct gga aag ctc tac caa 307
 Leu Arg Leu Trp Phe Pro His Glu Ser Arg Pro Gly Lys Leu Tyr Gln
 55 60 65

cgc gcc tac acc ttg acc aac gtg gat gcc gat gcc ggt acc ttt gac 355
 Arg Ala Tyr Thr Leu Thr Asn Val Asp Ala Asp Ala Gly Thr Phe Asp
 70 75 80 85

ctg gct ttt gtg ctg cac gag ccg ctg ggg ccc gcc tcg gcg tgg gcg 403
 Leu Ala Phe Val Leu His Glu Pro Leu Gly Pro Ala Ser Ala Trp Ala
 90 95 100

acg cgc tgc gag gcc ggg gaa agc ctg gaa gtc atg cgc tac cca gga 451
 Thr Arg Cys Glu Ala Gly Glu Ser Leu Glu Val Met Arg Tyr Pro Gly
 105 110 115

att ccg ttc gcc atc cca gat cca gcg ccg cgt ggc ttc ctt ttc cta 499
 Ile Pro Phe Ala Ile Pro Asp Pro Ala Pro Arg Gly Phe Leu Phe Leu
 120 125 130

ggc gat ctc acc tct tac cca gcg atc tgc tcg att ctg gag acc ttg 547
 Gly Asp Leu Thr Ser Tyr Pro Ala Ile Cys Ser Ile Leu Glu Thr Leu
 135 140 145

gac ggt gaa atc cct gcg acc gcg tat ctt atc gcc cac gat cca ctt 595
 Asp Gly Glu Ile Pro Ala Thr Ala Tyr Leu Ile Ala His Asp Pro Leu
 150 155 160 165

gat tac acc ttc gat ttt ccc cag ggc gag cac atc acc gcg cag tgg 643
 Asp Tyr Thr Phe Asp Phe Pro Gln Gly Glu His Ile Thr Ala Gln Trp
 170 175 180

att tcc aac gaa caa tcc ttc att gat cac atc gct gac acg gat tac 691
 Ile Ser Asn Glu Gln Ser Phe Ile Asp His Ile Ala Asp Thr Asp Tyr
 185 190 195

acc gat ttt tat acc tgg atc ggc gcg gaa tcc tcc gaa acc cgt 736
 Thr Asp Phe Tyr Thr Trp Ile Gly Ala Glu Ser Ser Glu Thr Arg
 200 205 210

<210> 202

<211> 212

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 202

Met Gly Lys Gly Phe Thr Gly Ala Ile Leu Thr Val Met Gly Val Lys
 1 5 10 15

```
<210> 203
<211> 732
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(709)
<223> RXA01051
```

```

<400> 203
tgcgacccaa gatactctcg ggcaagctct tcgttggttcg ttaaagattt tgaggaaacc 60

taacagtgaa cacacaggcc atccccctag ggttggccat atg tca acc att cac 115
                                         Met Ser Thr Ile His
                                         . 1                               5

gcc tcc gga atc cag gct cca caa gtg cca cac ggt tcc cac cat gcc 163
Ala Ser Gly Ile Gln Ala Pro Gln Val Pro His Gly Ser His His Ala
          10                      15                      20

```

ccg cca caa aag gac gaa tca gtg aag aag agc ttc aat gcc tct tct 211
 Pro Pro Gln Lys Asp Glu Ser Val Lys Lys Ser Phe Asn Ala Ser Ser
 25 30 35
 tta ctg ttc gcg ttt tcc ttc ggc gtg tac ctg gtg ctg ctt gtg atg 259
 Leu Leu Phe Ala Phe Ser Phe Gly Val Tyr Leu Val Leu Leu Val Met
 40 45 50
 atg aca ctt ctt aaa agt cgc ctt tct tta ggc gga ctg tgg aac aca 307
 Met Thr Leu Leu Lys Ser Arg Leu Ser Leu Gly Gly Leu Trp Asn Thr
 55 60 65
 gaa gca cac caa tac aga tcc atc gac tta gag ctt ttc aac ggc ttt 355
 Glu Ala His Gln Tyr Arg Ser Ile Asp Leu Glu Leu Phe Asn Gly Phe
 70 75 80 85
 gct gat cca cca att tgg tgg ggg cct tgg acc aac act.ttt ggc aac 403
 Ala Asp Pro Pro Ile Trp Trp Gly Pro Trp Thr Asn Thr Phe Gly Asn
 90 95 100
 atc gca ctg ttc atg cca ttt ggg ttt ttc ctg tac aaa atg ctc cgt 451
 Ile Ala Leu Phe Met Pro Phe Gly Phe Phe Leu Tyr Lys Met Leu Arg
 105 110 115
 aga ttc aac cat cga ttc ccc ttc gta gaa acc atc ctg ttt gcc agc 499
 Arg Phe Asn His Arg Phe Pro Phe Val Glu Thr Ile Leu Phe Ala Ser
 120 125 130
 gtc acc agc ctc agt atc gaa gtt ctg caa tgg gtg ttt gct att gga 547
 Val Thr Ser Leu Ser Ile Glu Val Leu Gln Trp Val Phe Ala Ile Gly
 135 140 145
 tat tca gat gtc gat gac ctg ttg ttt aat acg atc ggc gga ctc att 595
 Tyr Ser Asp Val Asp Asp Leu Leu Phe Asn Thr Ile Gly Gly Leu Ile
 150 155 160 165
 gga gca tcc gta gca gcg ctt gtc tcg ctt aaa tcc tcc aag gta gtc 643
 Gly Ala Ser Val Ala Ala Leu Val Ser Leu Lys Ser Ser Lys Val Val
 170 175 180
 agc gga atc atc atg ggc ggt tca cta tct gtg atg gcg atg atg atg 691
 Ser Gly Ile Ile Met Gly Gly Ser Leu Ser Val Met Ala Met Met Met
 185 190 195
 tat tca agt ttt atc gcc tagaagggttt cagcagttcc gct 732
 Tyr Ser Ser Phe Ile Ala
 200

<210> 204

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

Met Ser Thr Ile His Ala Ser Gly Ile Gln Ala Pro Gln Val Pro His
 1 5 10 15

Gly Ser His His Ala Pro Pro Gln Lys Asp Glu Ser Val Lys Lys Ser
 20 25 30

Phe Asn Ala Ser Ser Leu Leu Phe Ala Phe Ser Phe Gly Val Tyr Leu
 35 40 45
 Val Leu Leu Val Met Met Thr Leu Leu Lys Ser Arg Leu Ser Leu Gly
 50 55 60
 Gly Leu Trp Asn Thr Glu Ala His Gln Tyr Arg Ser Ile Asp Leu Glu
 65 70 75 80
 Leu Phe Asn Gly Phe Ala Asp Pro Pro Ile Trp Trp Gly Pro Trp Thr
 85 90 95
 Asn Thr Phe Gly Asn Ile Ala Leu Phe Met Pro Phe Gly Phe Phe Leu
 100 105 110
 Tyr Lys Met Leu Arg Arg Phe Asn His Arg Phe Pro Phe Val Glu Thr
 115 120 125
 Ile Leu Phe Ala Ser Val Thr Ser Leu Ser Ile Glu Val Leu Gln Trp
 130 135 140
 Val Phe Ala Ile Gly Tyr Ser Asp Val Asp Asp Leu Leu Phe Asn Thr
 145 150 155 160
 Ile Gly Gly Leu Ile Gly Ala Ser Val Ala Ala Leu Val Ser Leu Lys
 165 170 175
 Ser Ser Lys Val Val Ser Gly Ile Ile Met Gly Gly Ser Leu Ser Val
 180 185 190
 Met Ala Met Met Met Tyr Ser Ser Phe Ile Ala
 195 200

<210> 205

<211> 1359

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1336)

<223> RXN01873

<400> 205

ccgtcgttgc ccatgggtcac agcctacatg cacaaagtga atcaaaaaca gctattttcta 60

acattttact aatatttgct gttggcgcat gatgaactcc atg agc caa gca ata 115
 Met Ser Gln Ala Ile
 1 5

gat agc aag gtc gag gca cac gaa ggc cac gaa ggc cac gaa ggc atc 163
 Asp Ser Lys Val Glu Ala His Glu Gly His Glu Gly His Glu Gly Ile
 10 15 20

gag cga gga aca cgc aat tac aag cgc gct gtg ttt gcg atg ctg gcc 211
 Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val Phe Ala Met Leu Ala
 25 30 35

gcc ggt ctt gct gct ttc aat ggt ctt tat tgc acg cag gca ttg ctt 259

Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys Thr Gln Ala Leu Leu	
40 45 50	
ccc acc atg acg gaa gag ttg gga att acg ccc act gag tcc gcg ctg	307
Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro Thr Glu Ser Ala Leu	
55 60 65	
acg gtg tcg gct acg act gga atg ttg gcg ctg tgt att gtt ccg gcg	355
Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu Cys Ile Val Pro Ala	
70 75 80 85	
tcg ata ctt tcg gag aaa ttt ggt cgc ggt cgg gtg ctg aca att tca	403
Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg Val Leu Thr Ile Ser	
90 95 100	
ctc acg ttg gcc atc atc gtg gga tta att ttg ccg ctt gtc ccc aat	451
Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu Pro Leu Val Pro Asn	
105 110 115	
att act gct ctc atc ctg ctc aga ggt ctc caa ggt gcg ctg ctt gct	499
Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln Gly Ala Leu Leu Ala	
120 125 130	
ggc act cca gcg gtg gcg atg acc tgg ttg tct gag gaa att cac ccc	547
Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser Glu Glu Ile His Pro	
135 140 145	
aag gat att ggg cat gcg atg gga att tac atc gcg gga aat act gtc	595
Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile Ala Gly Asn Thr Val	
150 155 160 165	
ggc ggg ctc act gga cgt atg att ccg gcg gga cta ctt gaa gta act	643
Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly Leu Leu Glu Val Thr	
170 175 180	
cat tgg caa aac gca ctg ctg gga agt tct atc gct gcg ctg atc ttc	691
His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile Ala Ala Leu Ile Phe	
185 190 195	
ggc gta atc atg gtg gtg ttg ctt ccc aag cag cgg aaa ttc cag ccg	739
Gly Val Ile Met Val Val Leu Leu Pro Lys Gln Arg Lys Phe Gln Pro	
200 205 210	
aag aat atc aat ctg cgc cat gag att tcg gcg atg gct gct cat tgg	787
Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala Met Ala Ala His Trp	
215 220 225	
cgg aat cct cgt ttg gcg ttg ctt ttt ggt act gcg ttt ttg ggc atg	835
Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr Ala Phe Leu Gly Met	
230 235 240 245	
ggg act ttt gtg tcg ctg tac aac tat ttg ggt ttc cgc atg att gat	883
Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly Phe Arg Met Ile Asp	
250 255 260	
cag ttt ggg ctg agt gaa gtg ctg gtt ggt gcg gtg ttc atc atg tat	931
Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala Val Phe Ile Met Tyr	
265 270 275	
ctg gcc ggg acc tgg agt tcc acc cag gcg ggt gcg ttg agg gag aag	979
Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly Ala Leu Arg Glu Lys	

280	285	290	
atc ggc aat ggg tca acg gtt att ttc ttg agt ctg acg atg atc gcg Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser Leu Thr Met Ile Ala 295 300 305			1027
tcg atg gca ctg atg ggg att aat aat ttg tgg gtc acg ttg gtt gcc Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp Val Thr Leu Val Ala 310 315 320 325			1075
ctg ttt gtg ttt acc gcg gca ttt ttc gca ctg cat tcc agt gct tcg Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu His Ser Ser Ala Ser 330 335 340			1123
gga tgg atc gga atc atc gca acg aag gat cgc gcg gaa gcc tcc agc Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg Ala Glu Ala Ser Ser 345 350 355			1171
atg tat ttg ttc tgt tat tac gtg gga tcc tcg gtg att ggt tgg gtt Met Tyr Leu Phe Cys Tyr Tyr Val Gly Ser Ser Val Ile Gly Trp Val 360 365 370			1219
tct gga ttc gcg ttt acg cat ttg ccg tgg ttg gcg ttc att ggc tgg Ser Gly Phe Ala Phe Thr His Leu Pro Trp Leu Ala Phe Ile Gly Trp 375 380 385			1267
ttg att ctg ctt ctt tgc gga gtg ctg gcg att tgt gtg acg ctg gca Leu Ile Leu Leu Leu Cys Gly Val Leu Ala Ile Cys Val Thr Leu Ala 390 395 400 405			1315
agg ctt gcc cgc aac gcc aat taatacagagt ttgtccgtgt tta Arg Leu Ala Arg Asn Ala Asn 410			1359

<210> 206

<211> 412

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 206

Met Ser Gln Ala Ile Asp Ser Lys Val Glu Ala His Glu Gly His Glu
1 5 10 15

Gly His Glu Gly Ile Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val
20 25 30

Phe Ala Met Leu Ala Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys
35 40 45

Thr Gln Ala Leu Leu Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro
50 55 60

Thr Glu Ser Ala Leu Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu
65 70 75 80

Cys Ile Val Pro Ala Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg
85 90 95

Val Leu Thr Ile Ser Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu
100 105 110

Pro Leu Val Pro Asn Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln
 115 120 125
 Gly Ala Leu Leu Ala Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser
 130 135 140
 Glu Glu Ile His Pro Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile
 145 150 155 160
 Ala Gly Asn Thr Val Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly
 165 170 175
 Leu Leu Glu Val Thr His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile
 180 185 190
 Ala Ala Leu Ile Phe Gly Val Ile Met Val Val Leu Leu Pro Lys Gln
 195 200 205
 Arg Lys Phe Gln Pro Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala
 210 215 220
 Met Ala Ala His Trp Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr
 225 230 235 240
 Ala Phe Leu Gly Met Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly
 245 250 255
 Phe Arg Met Ile Asp Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala
 260 265 270
 Val Phe Ile Met Tyr Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly
 275 280 285
 Ala Leu Arg Glu Lys Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser
 290 295 300
 Leu Thr Met Ile Ala Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp
 305 310 315 320
 Val Thr Leu Val Ala Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu
 325 330 335
 His Ser Ser Ala Ser Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg
 340 345 350
 Ala Glu Ala Ser Ser Met Tyr Leu Phe Cys Tyr Tyr Val Gly Ser Ser
 355 360 365
 Val Ile Gly Trp Val Ser Gly Phe Ala Phe Thr His Leu Pro Trp Leu
 370 375 380
 Ala Phe Ile Gly Trp Leu Ile Leu Leu Leu Cys Gly Val Leu Ala Ile
 385 390 395 400
 Cys Val Thr Leu Ala Arg Leu Ala Arg Asn Ala Asn
 405 410

<210> 207

<211> 1215

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1192)

<223> FRXA01873

<400> 207

```

ccgtcgtttgc ccatgggtcac agcctacatg cacaaagtga atcaaaaaca gctattttcta 60

acatttttact aatattttgct gttggcgcat gatgaactcc atg agc caa gca ata 115
                                         Met Ser Gln Ala Ile
                                         1                               5

gat agc aag gtc gag gca cac gaa ggc cac gaa ggc cac gaa ggc atc 163
Asp Ser Lys Val Glu Ala His Glu Gly His Glu Gly His Glu Gly Ile
                        10                        15                        20

gag cga gga aca cgc aat tac aag cgc gct gtg ttt gcg atg ctg gcc 211
Glu Arg Gly Thr Arg Asn Tyr Lys Arg Ala Val Phe Ala Met Leu Ala
                        25                        30                        35

gcc ggt ctt gct gct ttc aat ggt ctt tat tgc acg cag gca ttg ctt 259
Ala Gly Leu Ala Ala Phe Asn Gly Leu Tyr Cys Thr Gln Ala Leu Leu
                        40                        45                        50

ccc acc atg acg gaa gag ttg gga att acg ccc act gag tcc gcg ctg 307
Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro Thr Glu Ser Ala Leu
                        55                        60                        65

acg gtg tcg gct acg act gga atg ttg gcg ctg tgt att gtt ccg gcg 355
Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu Cys Ile Val Pro Ala
                        70                        75                        80                        85

tcg ata ctt tcg gag aaa ttt ggt cgc ggt cgg gtg ctg aca att tca 403
Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg Val Leu Thr Ile Ser
                        90                        95                        100

ctc acg ttg gcc atc atc gtg gga tta att ttg ccg ctt gtc ccc aat 451
Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu Pro Leu Val Pro Asn
                        105                        110                        115

att act gct ctc atc ctg ctc aga ggt ctc caa ggt gcg ctg ctt gct 499
Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln Gly Ala Leu Leu Ala
                        120                        125                        130

ggc act cca gcg gtg gcg atg acc tgg ttg tct gag gaa att cac ccc 547
Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser Glu Glu Ile His Pro
                        135                        140                        145

aag gat att ggg cat gcg atg gga att tac atc gcg gga aat act gtc 595
Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile Ala Gly Asn Thr Val
                        150                        155                        160                        165

ggc ggg ctc act gga cgt atg att ccg gcg gga cta ctt gaa gta act 643
Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly Leu Leu Glu Val Thr
                        170                        175                        180

cat tgg caa aac gca ctg ctg gga agt tct atc gct gcg ctg atc ttc 691
His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile Ala Ala Leu Ile Phe

```

185	190	195	
ggc gta atc atg gtg gtg ttg ctt	ccc aag cag cgg aaa ttc cag ccg	739	
Gly Val Ile Met Val Val Leu Leu	Pro Lys Gln Arg Lys Phe Gln Pro		
200	205 210		
aag aat atc aat ctg cgc cat gag att tcg gcg atg gct gct cat tgg	787		
Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala Met Ala Ala His Trp			
215	220 225		
cgg aat cct cgt ttg gcg ttg ctt ttt ggt act gcg ttt ttg ggc atg	835		
Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr Ala Phe Leu Gly Met			
230	235 240 245		
ggt act ttt gtg tcg ctg tac aac tat ttg ggt ttc cgc atg att gat	883		
Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly Phe Arg Met Ile Asp			
250	255 260		
cag ttt ggg ctg agt gaa gtg ctg gtt ggt gcg gtg ttc atc atg tat	931		
Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala Val Phe Ile Met Tyr			
265	270 275		
ctg gcc ggg acc tgg agt tcc acc cag gcg ggt gcg ttg agg gag aag	979		
Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly Ala Leu Arg Glu Lys			
280	285 290		
atc ggc aat ggg tca acg gtt att ttc ttg agt ctg acg atg atc gcg	1027		
Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser Leu Thr Met Ile Ala			
295	300 305		
tcg atg gca ctg atg ggg att aat aat ttg tgg gtc acg ttg gtt gcc	1075		
Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp Val Thr Leu Val Ala			
310	315 320 325		
ctg ttt gtg ttt acc gcg gca ttt ttc gca ctg cat tcc agt gct tcg	1123		
Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu His Ser Ser Ala Ser			
330	335 340		
gga tgg atc gga atc atc gca acg aag gat cgc gcg gaa gcc tcc agc	1171		
Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg Ala Glu Ala Ser Ser			
345	350 355		
atg tat ttg ttc tgt gaa tac taggatcctc ggtgattggt tgg	1215		
Met Tyr Leu Phe Cys Glu Tyr			
360			

<210> 208

<211> 364

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

Met	Ser	Gln	Ala	Ile	Asp	Ser	Lys	Val	Glu	Ala	His	Glu	Gly	His	Glu
1				5					10					15	

Gly	His	Glu	Gly	Ile	Glu	Arg	Gly	Thr	Arg	Asn	Tyr	Lys	Arg	Ala	Val
		20					25						30		

Phe	Ala	Met	Leu	Ala	Ala	Gly	Leu	Ala	Ala	Phe	Asn	Gly	Leu	Tyr	Cys
		35					40					45			

Thr Gln Ala Leu Leu Pro Thr Met Thr Glu Glu Leu Gly Ile Thr Pro
 50 55 60
 Thr Glu Ser Ala Leu Thr Val Ser Ala Thr Thr Gly Met Leu Ala Leu
 65 70 75 80
 Cys Ile Val Pro Ala Ser Ile Leu Ser Glu Lys Phe Gly Arg Gly Arg
 85 90 95
 Val Leu Thr Ile Ser Leu Thr Leu Ala Ile Ile Val Gly Leu Ile Leu
 100 105 110
 Pro Leu Val Pro Asn Ile Thr Ala Leu Ile Leu Leu Arg Gly Leu Gln
 115 120 125
 Gly Ala Leu Leu Ala Gly Thr Pro Ala Val Ala Met Thr Trp Leu Ser
 130 135 140
 Glu Glu Ile His Pro Lys Asp Ile Gly His Ala Met Gly Ile Tyr Ile
 145 150 155 160
 Ala Gly Asn Thr Val Gly Gly Leu Thr Gly Arg Met Ile Pro Ala Gly
 165 170 175
 Leu Leu Glu Val Thr His Trp Gln Asn Ala Leu Leu Gly Ser Ser Ile
 180 185 190
 Ala Ala Leu Ile Phe Gly Val Ile Met Val Val Leu Leu Pro Lys Gln
 195 200 205
 Arg Lys Phe Gln Pro Lys Asn Ile Asn Leu Arg His Glu Ile Ser Ala
 210 215 220
 Met Ala Ala His Trp Arg Asn Pro Arg Leu Ala Leu Leu Phe Gly Thr
 225 230 235 240
 Ala Phe Leu Gly Met Gly Thr Phe Val Ser Leu Tyr Asn Tyr Leu Gly
 245 250 255
 Phe Arg Met Ile Asp Gln Phe Gly Leu Ser Glu Val Leu Val Gly Ala
 260 265 270
 Val Phe Ile Met Tyr Leu Ala Gly Thr Trp Ser Ser Thr Gln Ala Gly
 275 280 285
 Ala Leu Arg Glu Lys Ile Gly Asn Gly Ser Thr Val Ile Phe Leu Ser
 290 295 300
 Leu Thr Met Ile Ala Ser Met Ala Leu Met Gly Ile Asn Asn Leu Trp
 305 310 315 320
 Val Thr Leu Val Ala Leu Phe Val Phe Thr Ala Ala Phe Phe Ala Leu
 325 330 335
 His Ser Ser Ala Ser Gly Trp Ile Gly Ile Ile Ala Thr Lys Asp Arg
 340 345 350
 Ala Glu Ala Ser Ser Met Tyr Leu Phe Cys Glu Tyr
 355 360

```
<220>
<221> CDS
<222> (101) .. (1549)
<223> RXN00034
```

<400> 209																
taaattttgt	ggcactcccc	acattttctat	caatcttatag	aaagtatgac	ttaaagtcga	60										
ttttgcaagt	ttctatagat	tgatagaaaa	gggagtttag	atg	tct	tac	aca	tct							115	
				Met	Ser	Tyr	Thr	Ser							5	
				1												
ttt	aaa	ggc	gat	gat	aaa	gcc	ctc	atc	ggc	ata	gtt	tta	tca	gtt	ctc	163
Phe	Lys	Gly	Asp	Asp	Lys	Ala	Leu	Ile	Gly	Ile	Val	Leu	Ser	Val	Leu	20
				10					15							
aca	ttt	tgg	ctt	ttt	gct	cag	tca	acc	cta	aat	atc	ggc	cca	gat	atg	211
Thr	Phe	Trp	Leu	Phe	Ala	Gln	Ser	Thr	Leu	Asn	Ile	Gly	Pro	Asp	Met	35
			25					30								
gca	act	gat	tta	ggg	atg	agc	gat	ggc	acc	atg	aac	ata	gct	gtc	gtg	259
Ala	Thr	Asp	Leu	Gly	Met	Ser	Asp	Gly	Thr	Met	Asn	Ile	Ala	Val	Val	50
		40					45					50				
gcc	gcc	gcg	tta	ttc	tgt	gga	aca	ttt	atc	gtc	gca	gcc	ggc	ggc	atc	307
Ala	Ala	Ala	Leu	Phe	Cys	Gly	Thr	Phe	Ile	Val	Ala	Ala	Gly	Gly	Ile	65
		55				60										
gca	gat	gtc	ttt	ggc	cga	gta	cga	atc	atg	atg	att	ggc	aac	atc	ctt	355
Ala	Asp	Val	Phe	Gly	Arg	Val	Arg	Ile	Met	Met	Ile	Gly	Asn	Ile	Leu	85
	70				75				80							
aac	atc	ctg	gga	tct	ctc	ctc	atc	gcc	acg	gca	acg	act	tct	tta	gcc	403
Asn	Ile	Leu	Gly	Ser	Leu	Leu	Ile	Ala	Thr	Ala	Thr	Thr	Ser	Leu	Ala	100
				90					95							
acc	caa	atg	gtg	atc	acc	ggc	cga	gtt	ctc	caa	gga	ctg	gca	gca	gcg	451
Thr	Gln	Met	Val	Ile	Thr	Gly	Arg	Val	Leu	Gln	Gly	Leu	Ala	Ala	Ala	115
			105					110								
gcc	atc	atg	tct	gca	tcc	cta	gca	tta	gtt	aag	aca	tat	tgg	tta	ggc	499
Ala	Ile	Met	Ser	Ala	Ser	Leu	Ala	Leu	Val	Lys	Thr	Tyr	Trp	Leu	Gly	120
							125					130				
act	gac	cgc	caa	cga	gca	gtc	tcc	att	tgg	tcc	att	ggc	tca	tgg	ggc	547
Thr	Asp	Arg	Gln	Arg	Ala	Val	Ser	Ile	Trp	Ser	Ile	Gly	Ser	Trp	Gly	145
	135					140										
ggc	acc	gga	ttc	tgc	gcg	ctt	ttc	gcg	ggt	ctt	gtt	gta	gca	agc	ccc	595
Gly	Thr	Gly	Phe	Cys	Ala	Leu	Phe	Ala	Gly	Leu	Val	Val	Ala	Ser	Pro	165
					155				160							
ttt	ggc	tgg	aga	gga	atc	ttc	gcc	ctc	tgc	gcg	atc	gtc	tcc	atc	gtt	643
Phe	Gly	Trp	Arg	Gly	Ile	Phe	Ala	Leu	Cys	Ala	Ile	Val	Ser	Ile	Val	170
				175					175					180		

gct att gcc ctt acc cgc cac atc ccg gaa tcc cgt ccg gct caa tcc	691
Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser Arg Pro Ala Gln Ser	
185 190 195	
att ggc atg cat ttg gat tgg agt ggc atc atc gtt ctt gcc ctc agt	739
Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile Val Leu Ala Leu Ser	
200 205 210	
gtt cta tct ctt gaa ttg ttt att acc caa ggt gaa tca ctt ggc tgg	787
Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly Glu Ser Leu Gly Trp	
215 220 225	
acg cac tgg atg acc tgg act ctc ctt gcc gtt tct ttg aca ttt ctt	835
Thr His Trp Met Thr Trp Thr Leu Leu Ala Val Ser Leu Thr Phe Leu	
230 235 240 245	
gca gtt ttc gtc ttc att gaa cgc atc gcc agc tgg cca gtt ctc gac	883
Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser Trp Pro Val Leu Asp	
250 255 260	
ttc aac ctt ttc aaa gac cac gcc ttc agc ggt gcg acc atc acc aac	931
Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly Ala Thr Ile Thr Asn	
265 270 275	
ttc att atg agc gct act ggc gga gta gtt gcc gtt gtc atg tgg gtt	979
Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala Val Val Met Trp Val	
280 285 290	
cag caa atg gga tgg ggt gtc tcc cca aca atc tcg gga ctc acc agc	1027
Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile Ser Gly Leu Thr Ser	
295 300 305	
atc ggc ttc gca gcc ttt gtc atc ctt ttc att cga gtt gga gaa aag	1075
Ile Gly Phe Ala Ala Phe Val Ile Leu Phe Ile Arg Val Gly Glu Lys	
310 315 320 325	
gcc atg cag aaa gtt ggc gcc cga gca gtg atc atc acc gct ggc atc	1123
Ala Met Gln Lys Val Gly Ala Arg Ala Val Ile Ile Thr Ala Gly Ile	
330 335 340	
ttg gta gcg acc gcg acc gcc ctc cta atg atc acc gcg gtc agc gag	1171
Leu Val Ala Thr Ala Thr Ala Leu Leu Met Ile Thr Ala Val Ser Glu	
345 350 355	
tca acg tac atc gtc atc tcc ctc gcc ggc ttc tcc ctt tat ggc ctt	1219
Ser Thr Tyr Ile Val Ile Ser Leu Ala Gly Phe Ser Leu Tyr Gly Leu	
360 365 370	
ggc ctc gga ctc ttc gcc acc cca gtc acc gat act gcg ctt gga aca	1267
Gly Leu Gly Leu Phe Ala Thr Pro Val Thr Asp Thr Ala Leu Gly Thr	
375 380 385	
ctt ccc aaa gac cgt acc ggc gct ggt gca ggt gta ttc aag atg tcc	1315
Leu Pro Lys Asp Arg Thr Gly Ala Gly Ala Gly Val Phe Lys Met Ser	
390 395 400 405	
tct tcc ctc ggc gca gca ctc ggc atc gca atc tcc act tca gtg ttc	1363
Ser Ser Leu Gly Ala Ala Leu Gly Ile Ala Ile Ser Thr Ser Val Phe	
410 415 420	

```

ctc gca ctt cgc gac ggc acc tcc atc aac tcc gac gtc gca ctc gcc 1411
Leu Ala Leu Arg Asp Gly Thr Ser Ile Asn Ser Asp Val Ala Leu Ala
      425                      430                      435

gga aca gtt tca ctt ggc atc aac gtt gta ttc gca gca aca gcc acc 1459
Gly Thr Val Ser Leu Gly Ile Asn Val Val Phe Ala Ala Thr Ala Thr
      440                      445                      450

atc acc gca gca gtc ctt att cca aaa gcc gct ggc aaa gtc tca caa 1507
Ile Thr Ala Ala Val Leu Ile Pro Lys Ala Ala Gly Lys Val Ser Gln
      455                      460                      465

acc agc atc acc ctt cct gag cca gct atc gct gta aaa atc 1549
Thr Ser Ile Thr Leu Pro Glu Pro Ala Ile Ala Val Lys Ile
470                      475                      480

taaaacttca ccaggacaga taa 1572

```

<210> 210

<211> 483

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

```

Met Ser Tyr Thr Ser Phe Lys Gly Asp Asp Lys Ala Leu Ile Gly Ile
  1                      5                      10                      15

Val Leu Ser Val Leu Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn
      20                      25                      30

Ile Gly Pro Asp Met Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met
      35                      40                      45

Asn Ile Ala Val Val Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val
      50                      55                      60

Ala Ala Gly Gly Ile Ala Asp Val Phe Gly Arg Val Arg Ile Met Met
      65                      70                      75                      80

Ile Gly Asn Ile Leu Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala
      85                      90                      95

Thr Thr Ser Leu Ala Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln
      100                      105                      110

Gly Leu Ala Ala Ala Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys
      115                      120                      125

Thr Tyr Trp Leu Gly Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser
      130                      135                      140

Ile Gly Ser Trp Gly Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu
      145                      150                      155                      160

Val Val Ala Ser Pro Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala
      165                      170                      175

Ile Val Ser Ile Val Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser
      180                      185                      190

```

Arg Pro Ala Gln Ser Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile
 195 200 205
 Val Leu Ala Leu Ser Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly
 210 215 220
 Glu Ser Leu Gly Trp Thr His Trp Met Thr Trp Thr Leu Leu Ala Val
 225 230 235 240
 Ser Leu Thr Phe Leu Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser
 245 250 255
 Trp Pro Val Leu Asp Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly
 260 265 270
 Ala Thr Ile Thr Asn Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala
 275 280 285
 Val Val Met Trp Val Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile
 290 295 300
 Ser Gly Leu Thr Ser Ile Gly Phe Ala Ala Phe Val Ile Leu Phe Ile
 305 310 315 320
 Arg Val Gly Glu Lys Ala Met Gln Lys Val Gly Ala Arg Ala Val Ile
 325 330 335
 Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu Leu Met Ile
 340 345 350
 Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu Ala Gly Phe
 355 360 365
 Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro Val Thr Asp
 370 375 380
 Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala Gly Ala Gly
 385 390 395 400
 Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly Ile Ala Ile
 405 410 415
 Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser Ile Asn Ser
 420 425 430
 Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn Val Val Phe
 435 440 445
 Ala Ala Thr Ala Thr Ile Thr Ala Ala Val Leu Ile Pro Lys Ala Ala
 450 455 460
 Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro Ala Ile Ala
 465 470 475 480
 Val Lys Ile

<210> 211
 <211> 1045
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1045)

<223> FRXA02273

<400> 211

```

taaattttgt ggcactcccc acatttctat caatctatag aaagtatgac ttaaagtcga 60

ttttgcaagt ttctatagat tgatagaaaa gggagtttag atg tct tac aca tct 115
                                         Met Ser Tyr Thr Ser
                                         1           5

ttt aaa ggc gat gat aaa gcc ctc atc ggc ata gtt tta tca gtt ctc 163
Phe Lys Gly Asp Asp Lys Ala Leu Ile Gly Ile Val Leu Ser Val Leu
                        10                15                20

aca ttt tgg ctt ttt gct cag tca acc cta aat atc ggc cca gat atg 211
Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn Ile Gly Pro Asp Met
                        25                30                35

gca act gat tta ggg atg agc gat ggc acc atg aac ata gct gtc gtg 259
Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met Asn Ile Ala Val Val
                        40                45                50

gcc gcc gcg tta ttc tgt gga aca ttt atc gtc gca gcc ggc ggc atc 307
Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val Ala Ala Gly Gly Ile
                        55                60                65

gca gat gtc ttt ggc cga gta cga atc atg atg att ggc aac atc ctt 355
Ala Asp Val Phe Gly Arg Val Arg Ile Met Met Ile Gly Asn Ile Leu
                        70                75                80                85

aac atc ctg gga tct ctc ctc atc gcc acg gca acg act tct tta gcc 403
Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala Thr Thr Ser Leu Ala
                        90                95                100

acc caa atg gtg atc acc ggc cga gtt ctc caa gga ctg gca gca gcg 451
Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln Gly Leu Ala Ala Ala
                        105                110                115

gcc atc atg tct gca tcc cta gca tta gtt aag aca tat tgg tta ggt 499
Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys Thr Tyr Trp Leu Gly
                        120                125                130

act gac cgc caa cga gca gtc tcc att tgg tcc att ggt tca tgg ggt 547
Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser Ile Gly Ser Trp Gly
                        135                140                145

ggc acc gga ttc tgc gcg ctt ttc gcg ggt ctt gtt gta gca agc ccc 595
Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu Val Val Ala Ser Pro
                        150                155                160                165

ttt ggt tgg aga gga atc ttc gcc ctc tgc gcg atc gtc tcc atc gtt 643
Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala Ile Val Ser Ile Val
                        170                175                180

gct att gcc ctt acc cgc cac atc ccg gaa tcc cgt ccg gct caa tcc 691
Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser Arg Pro Ala Gln Ser
                        185                190                195

```



```

att ggc atg cat ttg gat tgg agt ggc atc atc gtt ctt gcc ctc agt 739
Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile Val Leu Ala Leu Ser
      200                      205                      210

gtt cta tct ctt gaa ttg ttt att acc caa ggt gaa tca ctt ggc tgg 787
Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly Glu Ser Leu Gly Trp
      215                      220                      225

acg cac tgg atg acc tgg act ctc ctt gcc gtt tct ttg aca ttt ctt 835
Thr His Trp Met Thr Trp Thr Leu Leu Ala Val Ser Leu Thr Phe Leu
      230                      235                      240                      245

gca gtt ttc gtc ttc att gaa cgc atc gcc agc tgg cca gtt ctc gac 883
Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser Trp Pro Val Leu Asp
      250                      255                      260

ttc aac ctt ttc aaa gac cac gcc ttc agc ggt gcg acc atc acc aac 931
Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly Ala Thr Ile Thr Asn
      265                      270                      275

ttc att atg agc gct act ggc gga gta gtt gcc gtt gtc atg tgg gtt 979
Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala Val Val Met Trp Val
      280                      285                      290

cag caa atg gga tgg ggt gtc tcc cca aca atc tcg gga ctc acc agc 1027
Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile Ser Gly Leu Thr Ser
      295                      300                      305

atc ggc ttc gca gcc ttt
Ile Gly Phe Ala Ala Phe
310                      315

```

<210> 212

<211> 315

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 212

```

Met Ser Tyr Thr Ser Phe Lys Gly Asp Asp Lys Ala Leu Ile Gly Ile
  1                      5                      10                      15

Val Leu Ser Val Leu Thr Phe Trp Leu Phe Ala Gln Ser Thr Leu Asn
      20                      25                      30

Ile Gly Pro Asp Met Ala Thr Asp Leu Gly Met Ser Asp Gly Thr Met
      35                      40                      45

Asn Ile Ala Val Val Ala Ala Ala Leu Phe Cys Gly Thr Phe Ile Val
      50                      55                      60

Ala Ala Gly Gly Ile Ala Asp Val Phe Gly Arg Val Arg Ile Met Met
      65                      70                      75                      80

Ile Gly Asn Ile Leu Asn Ile Leu Gly Ser Leu Leu Ile Ala Thr Ala
      85                      90                      95

Thr Thr Ser Leu Ala Thr Gln Met Val Ile Thr Gly Arg Val Leu Gln
      100                      105                      110

```

Gly Leu Ala Ala Ala Ala Ile Met Ser Ala Ser Leu Ala Leu Val Lys
 115 120 125
 Thr Tyr Trp Leu Gly Thr Asp Arg Gln Arg Ala Val Ser Ile Trp Ser
 130 135 140
 Ile Gly Ser Trp Gly Gly Thr Gly Phe Cys Ala Leu Phe Ala Gly Leu
 145 150 155 160
 Val Val Ala Ser Pro Phe Gly Trp Arg Gly Ile Phe Ala Leu Cys Ala
 165 170 175
 Ile Val Ser Ile Val Ala Ile Ala Leu Thr Arg His Ile Pro Glu Ser
 180 185 190
 Arg Pro Ala Gln Ser Ile Gly Met His Leu Asp Trp Ser Gly Ile Ile
 195 200 205
 Val Leu Ala Leu Ser Val Leu Ser Leu Glu Leu Phe Ile Thr Gln Gly
 210 215 220
 Glu Ser Leu Gly Trp Thr His Trp Met Thr Trp Thr Leu Leu Ala Val
 225 230 235 240
 Ser Leu Thr Phe Leu Ala Val Phe Val Phe Ile Glu Arg Ile Ala Ser
 245 250 255
 Trp Pro Val Leu Asp Phe Asn Leu Phe Lys Asp His Ala Phe Ser Gly
 260 265 270
 Ala Thr Ile Thr Asn Phe Ile Met Ser Ala Thr Gly Gly Val Val Ala
 275 280 285
 Val Val Met Trp Val Gln Gln Met Gly Trp Gly Val Ser Pro Thr Ile
 290 295 300
 Ser Gly Leu Thr Ser Ile Gly Phe Ala Ala Phe
 305 310 315

<210> 213
 <211> 826
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(826)
 <223> RXN03075

<400> 213
 tgtgcaaaat tgcattcagg ctgaaaaatt cctaaaggga ctccgtccga ataattggaa 60

agcccagaag aacagtcaac tcctagatta aaggataatc gtg gcg aaa ttc ctg 115
 Val Ala Lys Phe Leu
 1 5

tat aag tta ggc tcc acg gcc tat caa aag aaa tgg ccg ttt ctt gcg 163
 Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys Trp Pro Phe Leu Ala
 10 15 20

gtc tgg ctc gtg att ctc ata ggt atc acg acg ctg gcg ggg ctg tat 211
 Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr Leu Ala Gly Leu Tyr
 25 30 35

gcc aag cca acg tcg agt agc ttc tct atc cct ggt ctt gat tct gtc 259
 Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val
 40 45 50

acg acc atg gag aag atg cag gag cgt ttc cct ggt tcg gat gat gca 307
 Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala
 55 60 65

aca tcg gct ccc act ggt tct gtc gtc att cag gca ccg gaa ggc aag 355
 Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln Ala Pro Glu Gly Lys
 70 75 80 85

acc ctc act gat cct gag gtt ggg gct gaa gta aac cag atg ctt gat 403
 Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp
 90 95 100

gag gtt cgg gcg act ggt gtg ctg aag gat gct gat tcc gtt gtg gat 451
 Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala Asp Ser Val Val Asp
 105 110 115

cct gtg ttg gct gcg cag ggt gtg gct gct cag atg acc cca gcc ctg 499
 Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln Met Thr Pro Ala Leu
 120 125 130

gag gct cag ggt gta cct gcg gag aag atc gcc gca gat att gag tcg 547
 Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala Ala Asp Ile Glu Ser
 135 140 145

att agt cca ctg agt gca gat gag act acc ggc atc atc tcg atg act 595
 Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly Ile Ile Ser Met Thr
 150 155 160 165

ttt gat gca gat tct gcc atg gat ata tcc gca gag gat cgt gag aag 643
 Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys
 170 175 180

gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc 691
 Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val
 185 190 195

tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc 739
 Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr Ser Leu Asp Met Thr
 200 205 210

tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc 787
 Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr
 215 220 225

ttc ggt tcg ttc atc gct gcc ggt atg ccg ctg atc tct 826
 Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser
 230 235 240

<210> 214

<211> 242

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 214

Val Ala Lys Phe Leu Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys
 1 5 10 15
 Trp Pro Phe Leu Ala Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr
 20 25 30
 Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro
 35 40 45
 Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro
 50 55 60
 Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
 65 70 75 80
 Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
 85 90 95
 Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
 100 105 110
 Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
 115 120 125
 Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
 130 135 140
 Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
 145 150 155 160
 Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala
 165 170 175
 Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
 180 185 190
 Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr
 195 200 205
 Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
 210 215 220
 Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu
 225 230 235 240
 Ile Ser

<210> 215

<211> 826

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(826)

<223> FRXA02907

<400> 215

```

tgtgcaaaat tgcattcagg ctgaaaaatt cctaaaggga ctccgtccga ataattggaa 60

agcccagaag aacagtcaac tcctagatta aaggataatc gtg gcg aaa ttc ctg 115
Val Ala Lys Phe Leu
1 5

tat aag tta ggc tcc acg gcc tat caa aag aaa tgg ccg ttt ctt gcg 163
Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys Trp Pro Phe Leu Ala
10 15 20

gtc tgg ctc gtg att ctc ata ggt atc acg acg ctg gcg ggg ctg tat 211
Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr Leu Ala Gly Leu Tyr
25 30 35

gcc aag cca acg tcg agt agc ttc tct atc cct ggt ctt gat tct gtc 259
Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro Gly Leu Asp Ser Val
40 45 50

acg acc atg gag aag atg cag gag cgt ttc cct ggt tcg gat gat gca 307
Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro Gly Ser Asp Asp Ala
55 60 65

aca tcg gct ccc act ggt tct gtc gtc att cag gca ccg gaa ggc aag 355
Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln Ala Pro Glu Gly Lys
70 75 80 85

acc ctc act gat cct gag gtt ggg gct gaa gta aac cag atg ctt gat 403
Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val Asn Gln Met Leu Asp
90 95 100

gag gtt cgg gcg act ggt gtg ctg aag gat gct gat tcc gtt gtg gat 451
Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala Asp Ser Val Val Asp
105 110 115

cct gtg ttg gct gcg cag ggt gtg gct gct cag atg acc cca gcc ctg 499
Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln Met Thr Pro Ala Leu
120 125 130

gag gct cag ggt gta cct gcg gag aag atc gcc gca gat att gag tcg 547
Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala Ala Asp Ile Glu Ser
135 140 145

att agt cca ctg agt gca gat gag act acc ggc atc atc tcg atg act 595
Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly Ile Ile Ser Met Thr
150 155 160 165

ttt gat gca gat tct gcc atg gat ata tcc gca gag gat cgt gag aag 643
Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala Glu Asp Arg Glu Lys
170 175 180

gtc acc aat att ctt gat gaa tac gat gac ggc gat ctg act gtt gtc 691
Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly Asp Leu Thr Val Val
185 190 195

tac aac ggc aac gtg ttt ggc gca gct gca acc agc ttg gac atg acc 739
Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr Ser Leu Asp Met Thr
200 205 210

tct gag ctc atc ggc ctg ctg gtg gct gcg gtc gtt ctt atc gtg acc 787
Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val Val Leu Ile Val Thr

```

215 220 225
 ttc ggt tcg ttc atc gct gcc ggt atg ccg ctg atc tct 826
 Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu Ile Ser
 230 235 240

 <210> 216
 <211> 242
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 216
 Val Ala Lys Phe Leu Tyr Lys Leu Gly Ser Thr Ala Tyr Gln Lys Lys
 1 5 10 15
 Trp Pro Phe Leu Ala Val Trp Leu Val Ile Leu Ile Gly Ile Thr Thr
 20 25 30
 Leu Ala Gly Leu Tyr Ala Lys Pro Thr Ser Ser Ser Phe Ser Ile Pro
 35 40 45
 Gly Leu Asp Ser Val Thr Thr Met Glu Lys Met Gln Glu Arg Phe Pro
 50 55 60
 Gly Ser Asp Asp Ala Thr Ser Ala Pro Thr Gly Ser Val Val Ile Gln
 65 70 75 80
 Ala Pro Glu Gly Lys Thr Leu Thr Asp Pro Glu Val Gly Ala Glu Val
 85 90 95
 Asn Gln Met Leu Asp Glu Val Arg Ala Thr Gly Val Leu Lys Asp Ala
 100 105 110
 Asp Ser Val Val Asp Pro Val Leu Ala Ala Gln Gly Val Ala Ala Gln
 115 120 125
 Met Thr Pro Ala Leu Glu Ala Gln Gly Val Pro Ala Glu Lys Ile Ala
 130 135 140
 Ala Asp Ile Glu Ser Ile Ser Pro Leu Ser Ala Asp Glu Thr Thr Gly
 145 150 155 160
 Ile Ile Ser Met Thr Phe Asp Ala Asp Ser Ala Met Asp Ile Ser Ala
 165 170 175
 Glu Asp Arg Glu Lys Val Thr Asn Ile Leu Asp Glu Tyr Asp Asp Gly
 180 185 190
 Asp Leu Thr Val Val Tyr Asn Gly Asn Val Phe Gly Ala Ala Ala Thr
 195 200 205
 Ser Leu Asp Met Thr Ser Glu Leu Ile Gly Leu Leu Val Ala Ala Val
 210 215 220
 Val Leu Ile Val Thr Phe Gly Ser Phe Ile Ala Ala Gly Met Pro Leu
 225 230 235 240
 Ile Ser

```
<220>
<221> CDS
<222> (101) .. (2290)
<223> RXA00479
```

<400> 217															60
tagatcccaa ggctcaaaat ttattactta aacaagttga gcaactagcc agccgcaaat															
cttagaacta accttttacgc ctttaacgga agtgaatttg atg tct act agc atc															115
Met Ser Thr Ser Ile															5
1															
aca aca gag aac aag aag aaa tct ggt cct cct cgc ttg atg aga atc															163
Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro Arg Leu Met Arg Ile															20
10 15															
ttt ctg ccc gcc ttg cta att tta gtt tgg ctt gta gga gct gga gtc															211
Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu Val Gly Ala Gly Val															35
25 30															
ggc ggt cct tat ttt ggc aag gtt agt gag gtc tcc tcc aac agc cag															259
Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val Ser Ser Asn Ser Gln															50
40 45															
acc aca tat ctg cca gaa tct gcc gat gcc act caa gta cag gaa cag															307
Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr Gln Val Gln Glu Gln															65
55 60															
ttg gga gat ttt act gat tct gaa tcc atc cca gcc att gtc gta atg															355
Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro Ala Ile Val Val Met															85
70 75															
gtc agc gat gaa ccc tta aca cag caa gac atc aca caa ctc aat gaa															403
Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile Thr Gln Leu Asn Glu															100
90 95															
gtt gtt gct ggg ctt tca gaa tta gac ata gtt tcc gat gaa gtc tcc															451
Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val Ser Asp Glu Val Ser															115
105 110															
cct gct att cca tcc gag gac ggc aga gct gtc caa gtg ttt gtc ccc															499
Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val Gln Val Phe Val Pro															130
120 125															
ctc aat cca tca gcg gag ctg acg gaa agc gtc gag aag ctc tct gag															547
Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val Glu Lys Leu Ser Glu															145
135 140															
acc ttg acc cag caa acg ccg gac tat gtg agc acc tat gtg acc gga															595
Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser Thr Tyr Val Thr Gly															165
150 155															
ccg gct ggg ttt acc gct gat ctc agc gca gct ttc gcg ggt att gat															643
Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala Phe Ala Gly Ile Asp															180
170 175															

ggg Gly	cta Leu	ctc Leu	cta Leu 185	gca Ala	gtc Val	gcc Ala	ttg Leu 190	gct Ala	gcc Ala	gtc Val	ctt Leu	gtc Val 195	att Ile	ctt Leu	gtc Val	691
atc Ile	gtc Val	tat Tyr 200	cgc Arg	tcc Ser	ttc Phe	att Ile	ctg Leu 205	ccc Pro	atc Ile	gcc Ala	gtg Val	ctt Leu 210	gcc Ala	acc Thr	agt Ser	739
ttg Leu	ttt Phe 215	gcg Ala	ctg Leu	act Thr	gta Val	gct Ala 220	cta Leu	ttg Leu	gtg Val	gtg Val	tgg Trp 225	tgg Trp	cta Leu	gct Ala	aag Lys	787
tgg Trp 230	gac Asp	atc Ile	ctg Leu	ctg Leu	ctt Leu 235	tcg Ser	ggg Gly	cag Gln	act Thr	caa Gln 240	ggc Gly	atc Ile	ctc Leu	ttc Phe	att Ile 245	835
ctg Leu	gtc Val	att Ile	ggc Gly 250	gcc Ala	gcc Ala	acc Thr	gac Asp	tac Tyr 255	tca Ser	ttg Leu	cta Leu	tac Tyr	gtt Val	gct Ala 260	cgt Arg	883
ttc Phe	cgt Arg	gaa Glu 265	gag Glu	tta Leu	cgc Arg	gtt Val	caa Gln 270	caa Gln	gat Asp	aaa Lys	ggg Gly	ata Ile 275	gcc Ala	aca Thr	ggg Gly	931
aaa Lys	gcc Ala 280	atc Ile	cgg Arg	gca Ala	tcg Ser	gtg Val	gaa Glu 285	ccc Pro	att Ile	ctt Leu	gcc Ala	tcg Ser 290	ggc Gly	agc Ser	act Thr	979
gtt Val	att Ile 295	gcg Ala	ggc Gly	ctc Leu	ctt Leu	tgt Cys 300	ttg Leu	cta Leu	ttt Phe	agt Ser	gat Asp 305	ttg Leu	aaa Lys	tct Ser	aac Asn	1027
tcc Ser 310	acg Thr	cta Leu	ggg Gly	cca Pro	gta Val 315	gct Ala	tcg Ser	gtg Val	ggc Gly	att Ile 320	att Ile	ttt Phe	gca Ala	atg Met	ctt Leu 325	1075
tct Ser	gct Ala	ctt Leu	act Thr 330	ctg Leu	cta Leu	cca Pro	gcc Ala	ctg Leu	ctg Leu	ttt Phe 335	gta Val	ttc Phe	ggg Gly	cgg Arg 340	gtg Val	1123
gcc Ala	ttt Phe	tgg Trp 345	ccc Pro	aag Lys	cga Arg	cca Pro	aaa Lys	tac Tyr 350	gaa Glu	cct Pro	gaa Glu	aaa Lys 355	gcc Ala	cgt Arg	gcg Ala	1171
aaa Lys	aac Asn 360	gac Asp	atc Ile	ccc Pro	gcc Ala	agc Ser	ggg Gly 365	atc Ile	tgg Trp	tca Ser	aaa Lys	gtg Val 370	gct Ala	gat Asp	tta Leu	1219
gtg Val	gag Glu 375	cag Gln	cat His	cct Pro	cgt Arg	gca Ala 380	atc Ile	tgg Trp	gta Val	tct Ser	aca Thr 385	ctt Leu	att Ile	gtg Val	ctt Leu	1267
ctc Leu 390	ttg Leu	ggg Gly	gcg Ala	gct Ala	ttc Phe 395	gtt Val	ccc Pro	aca Thr	cta Leu	aaa Lys 400	gcg Ala	gac Asp	ggg Gly	gtg Val	tcc Ser 405	1315
caa Gln	tcc Ser	gac Asp	cta Leu 410	gtt Val	ctg Leu	ggg Gly	tcc Ser	tct Ser	gaa Glu 415	gca Ala	cgt Arg	gat Asp	ggc Gly	cag Gln 420	cag Gln	1363

gct tta ggc gaa cac ttc ccc ggt gga tcc ggc agt cct gct tat att	1411
Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly Ser Pro Ala Tyr Ile	
425 430 435	
atc gtt gat gaa aca cag gca gca cag gct gct gac gta gtc ctt aac	1459
Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala Asp Val Val Leu Asn	
440 445 450	
aac gac aat ttc gag act gta act gta act agt gct gac tcc ccc tct	1507
Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser Ala Asp Ser Pro Ser	
455 460 465	
ggc tca gcc cca atc acc gct gac ggt att gtg ccg tta ggt tct ggt	1555
Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val Pro Leu Gly Ser Gly	
470 475 480 485	
aca gct cca ggc ccg gta gtt gta gaa ggg caa gtc ctt tta caa gca	1603
Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln Val Leu Leu Gln Ala	
490 495 500	
aca ctt gtc gaa gca cca gat tcc gaa gaa gct caa aaa gct att cgc	1651
Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala Gln Lys Ala Ile Arg	
505 510 515	
agt atc cgc caa act ttt gca gat gaa aat ata tca gcg gta gta ggc	1699
Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile Ser Ala Val Val Gly	
520 525 530	
ggt gtc act gca act tcc gta gac act aac gat gcc tcc atc cat gac	1747
Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp Ala Ser Ile His Asp	
535 540 545	
cgc aac ctg atc atc cca att gta ttg ctg gtc att ttg gtt att ctc	1795
Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val Ile Leu Val Ile Leu	
550 555 560 565	
atg ctg ttg ctg cgg tct att gtc gca cca ctc ctg cta gta gtc acc	1843
Met Leu Leu Leu Arg Ser Ile Val Ala Pro Leu Leu Leu Val Val Thr	
570 575 580	
acc gtg gtg tct ttt gct act gct tta ggc gtg gct gct tta ctt ttc	1891
Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val Ala Ala Leu Leu Phe	
585 590 595	
aat cac gtt ttc agt ttc cca gga gca gac ccc gca gta cct ctc tac	1939
Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro Ala Val Pro Leu Tyr	
600 605 610	
gga ttt gta ttt tta gta gcc ttg ggc atc gac tac aac att ttc tta	1987
Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp Tyr Asn Ile Phe Leu	
615 620 625	
gtc acc cga atc cgt gaa gaa acc aaa acc cac ggc aca aga ctt gga	2035
Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His Gly Thr Arg Leu Gly	
630 635 640 645	
att ctt cga ggc ctg aca gta acc ggc gga gta att acc tca gct gga	2083
Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val Ile Thr Ser Ala Gly	
650 655 660	
gta gtt ctc gcc gca acg ttc gca gca ctc tat gtc atc cca att cta	2131

Val Val Leu Ala Ala Thr Phe Ala Ala Leu Tyr Val Ile Pro Ile Leu
665 670 675

ttc ctg gca caa att gcc ttc att gtc gct ttt gga gtt ctt att gat 2179
Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe Gly Val Leu Ile Asp
680 685 690

acc ctg ctc gtt cgc gcc ttc ttg gtg cct gct ttg ttc tac gac atc 2227
Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala Leu Phe Tyr Asp Ile
695 700 705

gga ccg aaa atc tgg tgg ccg tca aaa ttg tcc aat cag aaa tac cag 2275
Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser Asn Gln Lys Tyr Gln
710 715 720 725

aag cag cct cag cta tgacacacca aaattcgcct ctc 2313
Lys Gln Pro Gln Leu
730

<210> 218

<211> 730

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met Ser Thr Ser Ile Thr Thr Glu Asn Lys Lys Lys Ser Gly Pro Pro
1 5 10 15

Arg Leu Met Arg Ile Phe Leu Pro Ala Leu Leu Ile Leu Val Trp Leu
20 25 30

Val Gly Ala Gly Val Gly Gly Pro Tyr Phe Gly Lys Val Ser Glu Val
35 40 45

Ser Ser Asn Ser Gln Thr Thr Tyr Leu Pro Glu Ser Ala Asp Ala Thr
50 55 60

Gln Val Gln Glu Gln Leu Gly Asp Phe Thr Asp Ser Glu Ser Ile Pro
65 70 75 80

Ala Ile Val Val Met Val Ser Asp Glu Pro Leu Thr Gln Gln Asp Ile
85 90 95

Thr Gln Leu Asn Glu Val Val Ala Gly Leu Ser Glu Leu Asp Ile Val
100 105 110

Ser Asp Glu Val Ser Pro Ala Ile Pro Ser Glu Asp Gly Arg Ala Val
115 120 125

Gln Val Phe Val Pro Leu Asn Pro Ser Ala Glu Leu Thr Glu Ser Val
130 135 140

Glu Lys Leu Ser Glu Thr Leu Thr Gln Gln Thr Pro Asp Tyr Val Ser
145 150 155 160

Thr Tyr Val Thr Gly Pro Ala Gly Phe Thr Ala Asp Leu Ser Ala Ala
165 170 175

Phe Ala Gly Ile Asp Gly Leu Leu Leu Ala Val Ala Leu Ala Ala Val
180 185 190

Leu Val Ile Leu Val Ile Val Tyr Arg Ser Phe Ile Leu Pro Ile Ala
 195 200 205
 Val Leu Ala Thr Ser Leu Phe Ala Leu Thr Val Ala Leu Leu Val Val
 210 215 220
 Trp Trp Leu Ala Lys Trp Asp Ile Leu Leu Leu Ser Gly Gln Thr Gln
 225 230 235 240
 Gly Ile Leu Phe Ile Leu Val Ile Gly Ala Ala Thr Asp Tyr Ser Leu
 245 250 255
 Leu Tyr Val Ala Arg Phe Arg Glu Glu Leu Arg Val Gln Gln Asp Lys
 260 265 270
 Gly Ile Ala Thr Gly Lys Ala Ile Arg Ala Ser Val Glu Pro Ile Leu
 275 280 285
 Ala Ser Gly Ser Thr Val Ile Ala Gly Leu Leu Cys Leu Leu Phe Ser
 290 295 300
 Asp Leu Lys Ser Asn Ser Thr Leu Gly Pro Val Ala Ser Val Gly Ile
 305 310 315 320
 Ile Phe Ala Met Leu Ser Ala Leu Thr Leu Leu Pro Ala Leu Leu Phe
 325 330 335
 Val Phe Gly Arg Val Ala Phe Trp Pro Lys Arg Pro Lys Tyr Glu Pro
 340 345 350
 Glu Lys Ala Arg Ala Lys Asn Asp Ile Pro Ala Ser Gly Ile Trp Ser
 355 360 365
 Lys Val Ala Asp Leu Val Glu Gln His Pro Arg Ala Ile Trp Val Ser
 370 375 380
 Thr Leu Ile Val Leu Leu Leu Gly Ala Ala Phe Val Pro Thr Leu Lys
 385 390 395 400
 Ala Asp Gly Val Ser Gln Ser Asp Leu Val Leu Gly Ser Ser Glu Ala
 405 410 415
 Arg Asp Gly Gln Gln Ala Leu Gly Glu His Phe Pro Gly Gly Ser Gly
 420 425 430
 Ser Pro Ala Tyr Ile Ile Val Asp Glu Thr Gln Ala Ala Gln Ala Ala
 435 440 445
 Asp Val Val Leu Asn Asn Asp Asn Phe Glu Thr Val Thr Val Thr Ser
 450 455 460
 Ala Asp Ser Pro Ser Gly Ser Ala Pro Ile Thr Ala Asp Gly Ile Val
 465 470 475 480
 Pro Leu Gly Ser Gly Thr Ala Pro Gly Pro Val Val Val Glu Gly Gln
 485 490 495
 Val Leu Leu Gln Ala Thr Leu Val Glu Ala Pro Asp Ser Glu Glu Ala
 500 505 510

Gln Lys Ala Ile Arg Ser Ile Arg Gln Thr Phe Ala Asp Glu Asn Ile
 515 520 525
 Ser Ala Val Val Gly Gly Val Thr Ala Thr Ser Val Asp Thr Asn Asp
 530 535 540
 Ala Ser Ile His Asp Arg Asn Leu Ile Ile Pro Ile Val Leu Leu Val
 545 550 555 560
 Ile Leu Val Ile Leu Met Leu Leu Leu Arg Ser Ile Val Ala Pro Leu
 565 570 575
 Leu Leu Val Val Thr Thr Val Val Ser Phe Ala Thr Ala Leu Gly Val
 580 585 590
 Ala Ala Leu Leu Phe Asn His Val Phe Ser Phe Pro Gly Ala Asp Pro
 595 600 605
 Ala Val Pro Leu Tyr Gly Phe Val Phe Leu Val Ala Leu Gly Ile Asp
 610 615 620
 Tyr Asn Ile Phe Leu Val Thr Arg Ile Arg Glu Glu Thr Lys Thr His
 625 630 635 640
 Gly Thr Arg Leu Gly Ile Leu Arg Gly Leu Thr Val Thr Gly Gly Val
 645 650 655
 Ile Thr Ser Ala Gly Val Val Leu Ala Ala Thr Phe Ala Ala Leu Tyr
 660 665 670
 Val Ile Pro Ile Leu Phe Leu Ala Gln Ile Ala Phe Ile Val Ala Phe
 675 680 685
 Gly Val Leu Ile Asp Thr Leu Leu Val Arg Ala Phe Leu Val Pro Ala
 690 695 700
 Leu Phe Tyr Asp Ile Gly Pro Lys Ile Trp Trp Pro Ser Lys Leu Ser
 705 710 715 720
 Asn Gln Lys Tyr Gln Lys Gln Pro Gln Leu
 725 730

<210> 219

<211> 983

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(960)

<223> RXN03124

<400> 219

atg act cct acc ctg gcg tcg atg att ggt ctg gct gtc ggt atc gac 48
 Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
 1 5 10 15

tac gcg cta ttt atc gtg tcc cgt ttc cgc aat gag ttg att tct cag 96
 Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
 20 25 30

act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc	144
Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg	
35 40 45	
acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc	192
Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly	
50 55 60	
act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct	240
Thr Ala Gly Ser Ala Val Phe Ala Gly Thr Thr Val Leu Ile Ala	
65 70 75 80	
ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc	288
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala	
85 90 95	
att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc	336
Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser	
100 105 110	
ttc ctc cca gct ctg ctt ggc ctg ctt ggc act cgc atc ttc gca gca	384
Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala	
115 120 125	
cgc gtg cct gga cct aag gtt ccg gat cct gag gac gag aag cca acg	432
Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr	
130 135 140	
atg ggt ctg aag tgg gtc cgc ctt gtg cgc aag atg ccg gtg gct tac	480
Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr	
145 150 155 160	
ctg ctg gtt ggc gtc gtt ttg ctt ggt gca atc gca att cct gcg acc	528
Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr	
165 170 175	
aat atg cgc ctg gcc atg ccg act gat ggc acc tcc acg ctg ggc acc	576
Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr	
180 185 190	
gcg ccg cgc acg ggg tat gac atg acg gca gat gcg ttc ggc ccg ggc	624
Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly	
195 200 205	
cgc aac gcg ccc atg att gcg ctt atc gac gca acc gac gtc cct gag	672
Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu	
210 215 220	
gaa gaa cgc cca ttg gtg ttt gga cag gcg gtg gag caa ttc ttg aac	720
Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn	
225 230 235 240	
act gat ggt gtg aag aat gct cag atc act cag acc acg gag aat ttc	768
Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe	
245 250 255	
gat acc gcg cag atc ctg tta ccc cag aat ttg atg cga tcg atg agc	816
Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser	
260 265 270	

```

gca cct ctg aga ctc tcg caa ctc ttc gtg cag atg ctg aga cct tcg      864
Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser
      275                                280                                285

ctg atg aca ccg gcg cga cgt atg gca tta ctg gcg tca ccc caa ttt      912
Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe
      290                                295                                300

acg atg aca tct ctg ctc gcc tcg gcg acg tcc tgg ttc ctt acg ttc      960
Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe
      305                                310                                315                                320

tgatcgtttt gggtctagcg ttc                                          983

```

<210> 220

<211> 320

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 220

```

Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp
  1              5              10              15

Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln
      20              25              30

Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg
      35              40              45

Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly
      50              55              60

Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala
      65              70              75              80

Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala
      85              90              95

Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser
      100             105             110

Phe Leu Pro Ala Leu Leu Gly Leu Leu Gly Thr Arg Ile Phe Ala Ala
      115             120             125

Arg Val Pro Gly Pro Lys Val Pro Asp Pro Glu Asp Glu Lys Pro Thr
      130             135             140

Met Gly Leu Lys Trp Val Arg Leu Val Arg Lys Met Pro Val Ala Tyr
      145             150             155             160

Leu Leu Val Gly Val Val Leu Leu Gly Ala Ile Ala Ile Pro Ala Thr
      165             170             175

Asn Met Arg Leu Ala Met Pro Thr Asp Gly Thr Ser Thr Leu Gly Thr
      180             185             190

Ala Pro Arg Thr Gly Tyr Asp Met Thr Ala Asp Ala Phe Gly Pro Gly
      195             200             205

Arg Asn Ala Pro Met Ile Ala Leu Ile Asp Ala Thr Asp Val Pro Glu

```

210	215	220
Glu Glu Arg Pro Leu Val Phe Gly Gln Ala Val Glu Gln Phe Leu Asn 225 230 235 240		
Thr Asp Gly Val Lys Asn Ala Gln Ile Thr Gln Thr Thr Glu Asn Phe 245 250 255		
Asp Thr Ala Gln Ile Leu Leu Pro Gln Asn Leu Met Arg Ser Met Ser 260 265 270		
Ala Pro Leu Arg Leu Ser Gln Leu Phe Val Gln Met Leu Arg Pro Ser 275 280 285		
Leu Met Thr Pro Ala Arg Arg Met Ala Leu Leu Ala Ser Pro Gln Phe 290 295 300		
Thr Met Thr Ser Leu Leu Ala Ser Ala Thr Ser Trp Phe Leu Thr Phe 305 310 315 320		

<210> 221
 <211> 762
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(762)
 <223> FRXA01180

<400> 221	
atg act cct acc ctg gcg tcg atg att ggt ctg gct gtc ggt atc gac Met Thr Pro Thr Leu Ala Ser Met Ile Gly Leu Ala Val Gly Ile Asp 1 5 10 15	48
tac gcg cta ttt atc gtg tcc cgt ttc cgc aat gag ttg att tct cag Tyr Ala Leu Phe Ile Val Ser Arg Phe Arg Asn Glu Leu Ile Ser Gln 20 25 30	96
act ggc gct aat gat ctg gag cca aag gaa ttg gct gag cgt ctg cgc Thr Gly Ala Asn Asp Leu Glu Pro Lys Glu Leu Ala Glu Arg Leu Arg 35 40 45	144
acc atg ccg ttg gct gct cgt gcg cat gcg atg gga atg gct gtg ggc Thr Met Pro Leu Ala Ala Arg Ala His Ala Met Gly Met Ala Val Gly 50 55 60	192
act gcg ggt tct gcg gtt gta ttc gcg ggt acc acg gtg ctg atc gct Thr Ala Gly Ser Ala Val Val Phe Ala Gly Thr Thr Val Leu Ile Ala 65 70 75 80	240
ctg gtt gct ctg tcg atc att aat att cca ttt cta acc gtg atg gcc Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala 85 90 95	288
att gct gcc gca atc acc gtt gcc atc gca gtt ctg gtt gct ctg tcc Ile Ala Ala Ala Ile Thr Val Ala Ile Ala Val Leu Val Ala Leu Ser	336

100										105										110										
ttc	ctc	cca	gct	ctg	ctt	ggc	ctg	ctt	ggc	act	cgc	atc	ttc	gca	gca		384													
Phe	Leu	Pro	Ala	Leu	Leu	Gly	Leu	Leu	Gly	Thr	Arg	Ile	Phe	Ala	Ala															
115						120						125																		
cgc	gtg	cct	gga	cct	aag	gtt	ccg	gat	cct	gag	gac	gag	aag	cca	acg		432													
Arg	Val	Pro	Gly	Pro	Lys	Val	Pro	Asp	Pro	Glu	Asp	Glu	Lys	Pro	Thr															
130						135						140																		
atg	ggc	ctg	aag	tgg	gtc	cgc	ctt	gtg	cgc	aag	atg	ccg	gtg	gct	tac		480													
Met	Gly	Leu	Lys	Trp	Val	Arg	Leu	Val	Arg	Lys	Met	Pro	Val	Ala	Tyr															
145						150						155				160														
ctg	ctg	gtt	ggc	gtc	gtt	ttg	ctt	ggc	gca	atc	gca	att	cct	gcg	acc		528													
Leu	Leu	Val	Gly	Val	Val	Leu	Leu	Gly	Ala	Ile	Ala	Ile	Pro	Ala	Thr															
			165						170						175															
aat	atg	cgc	ctg	gcc	atg	ccg	act	gat	ggc	acc	tcc	acg	ctg	ggc	acc		576													
Asn	Met	Arg	Leu	Ala	Met	Pro	Thr	Asp	Gly	Thr	Ser	Thr	Leu	Gly	Thr															
			180						185						190															
gcg	ccg	cgc	acg	ggg	tat	gac	atg	acg	gca	gat	gcg	ttc	ggc	ccg	ggc		624													
Ala	Pro	Arg	Thr	Gly	Tyr	Asp	Met	Thr	Ala	Asp	Ala	Phe	Gly	Pro	Gly															
195						200						205																		
cgc	aac	gcg	ccc	atg	att	gcg	ctt	atc	gac	gca	acc	gac	gtc	cct	gag		672													
Arg	Asn	Ala	Pro	Met	Ile	Ala	Leu	Ile	Asp	Ala	Thr	Asp	Val	Pro	Glu															
210						215						220																		
gaa	gaa	cgc	cca	ttg	gtg	ttt	gga	cag	gcg	gtg	gag	caa	ttc	ttg	aac		720													
Glu	Glu	Arg	Pro	Leu	Val	Phe	Gly	Gln	Ala	Val	Glu	Gln	Phe	Leu	Asn															
225				230						235				240																
act	gat	ggc	gtg	aag	aat	gct	cag	atc	act	cag	acc	acg	gag				762													
Thr	Asp	Gly	Val	Lys	Asn	Ala	Gln	Ile	Thr	Gln	Thr	Thr	Glu																	
			245						250																					
<210> 222																														
<211> 254																														
<212> PRT																														
<213> Corynebacterium glutamicum																														
<400> 222																														
Met	Thr	Pro	Thr	Leu	Ala	Ser	Met	Ile	Gly	Leu	Ala	Val	Gly	Ile	Asp															
1				5					10					15																
Tyr	Ala	Leu	Phe	Ile	Val	Ser	Arg	Phe	Arg	Asn	Glu	Leu	Ile	Ser	Gln															
			20						25						30															
Thr	Gly	Ala	Asn	Asp	Leu	Glu	Pro	Lys	Glu	Leu	Ala	Glu	Arg	Leu	Arg															
			35						40						45															
Thr	Met	Pro	Leu	Ala	Ala	Arg	Ala	His	Ala	Met	Gly	Met	Ala	Val	Gly															
50						55						60																		
Thr	Ala	Gly	Ser	Ala	Val	Val	Phe	Ala	Gly	Thr	Thr	Val	Leu	Ile	Ala															
65				70						75				80																
Leu Val Ala Leu Ser Ile Ile Asn Ile Pro Phe Leu Thr Val Met Ala																														


```
<210> 223
<211> 393
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(370)  
<223> RXA02586
```

```

<400> 223
ttctctgaga tcgtcatgat gaagtacatc gcgttcggca tgatecgcagc gctgattctg 60

gatgccacca tcatccgcgat gctgcttgtc ccccgccgtg atg cac ctg ctt cgc 115
Met His Leu Leu Arg
1 5

gac gac aac tgg tgg gca ccc ggc ttc gtt aaa aag gcc tac acc gtc 163
Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys Lys Ala Tyr Thr Val
10 15 20

atg ggt cac ggc tct gag gtg gag gaa gca cct cgc cca acc acc cgt 211
Met Gly His Gly Ser Glu Val Glu Glu Ala Pro Arg Pro Thr Thr Arg
25 30 35

cgc ctc aac gac gat gag gaa gtc acc gtg cat gaa gca gtt gtc gct 259
Arg Leu Asn Asp Asp Glu Glu Val Thr Val His Glu Ala Val Val Ala
40 45 50

```

ggc gat acc gtg gca tct cgc ggt ggt ttg agc acg cag gaa aac cgt 307
 Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser Thr Gln Glu Asn Arg
 55 60 65
 gat ctg gtg tcc ttc gtg gaa ctt aag gct cgt ttg gaa aag cgc agg 355
 Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg Leu Glu Lys Arg Arg
 70 75 80 85
 ctt gag gat cta gat taaatctatg cgaggatttt tca 393
 Leu Glu Asp Leu Asp
 90

<210> 224
 <211> 90
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 224
 Met His Leu Leu Arg Asp Asp Asn Trp Trp Ala Pro Gly Phe Val Lys
 1 5 10 15
 Lys Ala Tyr Thr Val Met Gly His Gly Ser Glu Val Glu Glu Ala Pro
 20 25 30
 Arg Pro Thr Thr Arg Arg Leu Asn Asp Asp Glu Glu Val Thr Val His
 35 40 45
 Glu Ala Val Val Ala Gly Asp Thr Val Ala Ser Arg Gly Gly Leu Ser
 50 55 60
 Thr Gln Glu Asn Arg Asp Leu Val Ser Phe Val Glu Leu Lys Ala Arg
 65 70 75 80
 Leu Glu Lys Arg Arg Leu Glu Asp Leu Asp
 85 90

<210> 225
 <211> 2214
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2191)
 <223> RXA02587

<400> 225
 agcctggata acctgccaga cgggtggcgca tggctgcagc cgttccgccc tctgactgcc 60
 ttgttatcca accgccacaa ttcccaggag taatccaccc gtg ttt tct aaa tgg 115
 Val Phe Ser Lys Trp
 1 5
 ggc cac ttt gct tac aga ttt agg cgc att gtt ccg tta gtc gtc atc 163
 Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val Pro Leu Val Val Ile
 10 15 20
 gcc gcg att ttg gct ttg ttt gtc att ttc ggc acc aag ctg ggc gac 211

Ala	Ala	Ile	Leu	Ala	Leu	Phe	Val	Ile	Phe	Gly	Thr	Lys	Leu	Gly	Asp		
			25					30					35				
cgc	atg	agc	cag	gaa	gga	tgg	gat	gat	cct	ggc	tct	tcc	tcg	acc	gct	259	
Arg	Met	Ser	Gln	Glu	Gly	Trp	Asp	Asp	Pro	Gly	Ser	Ser	Ser	Thr	Ala		
		40					45					50					
gcg	gcg	cgc	atc	gag	ttg	gag	acc	ttt	ggg	cgt	gac	aat	gac	ggc	gat	307	
Ala	Ala	Arg	Ile	Glu	Leu	Glu	Thr	Phe	Gly	Arg	Asp	Asn	Asp	Gly	Asp		
		55				60					65						
gtc	gtg	ttg	ctg	ttt	act	gcg	cct	gaa	ggc	act	tct	ttc	gat	gat	gca	355	
Val	Val	Leu	Leu	Phe	Thr	Ala	Pro	Glu	Gly	Thr	Ser	Phe	Asp	Asp	Ala		
	70				75					80					85		
gag	gtg	ttc	tcc	agc	atc	tct	ggc	tac	tta	gat	ggg	cta	atc	gag	aac	403	
Glu	Val	Phe	Ser	Ser	Ile	Ser	Gly	Tyr	Leu	Asp	Gly	Leu	Ile	Glu	Asn		
			90					95						100			
aac	cct	gat	gaa	gtc	agc	cac	atc	aac	agc	tac	ttt	gac	act	cgt	aat	451	
Asn	Pro	Asp	Glu	Val	Ser	His	Ile	Asn	Ser	Tyr	Phe	Asp	Thr	Arg	Asn		
			105					110					115				
caa	aat	ctc	ctc	agc	aaa	gac	ggc	acc	caa	acc	ttt	gca	gct	ctc	ggg	499	
Gln	Asn	Leu	Leu	Ser	Lys	Asp	Gly	Thr	Gln	Thr	Phe	Ala	Ala	Leu	Gly		
		120					125					130					
ctc	aaa	ggc	gac	ggc	gag	caa	acg	ctg	aag	gac	ttc	cgg	gag	att	gaa	547	
Leu	Lys	Gly	Asp	Gly	Glu	Gln	Thr	Leu	Lys	Asp	Phe	Arg	Glu	Ile	Glu		
	135					140					145						
gat	cag	ctc	cat	ccg	gac	aac	ctt	gcc	ggc	ggc	gtc	acc	act	gag	gtc	595	
Asp	Gln	Leu	His	Pro	Asp	Asn	Leu	Ala	Gly	Gly	Val	Thr	Thr	Glu	Val		
	150				155					160					165		
gcg	ggc	gcc	acc	gct	gta	gcc	gac	gca	ctc	gat	gag	ggc	atg	gct	ggc	643	
Ala	Gly	Ala	Thr	Ala	Val	Ala	Asp	Ala	Leu	Asp	Glu	Gly	Met	Ala	Gly		
				170				175						180			
gat	att	tca	cgc	gcc	gaa	gtt	ttt	gcg	ctg	cct	ttc	gtg	gct	atc	ttg	691	
Asp	Ile	Ser	Arg	Ala	Glu	Val	Phe	Ala	Leu	Pro	Phe	Val	Ala	Ile	Leu		
			185					190					195				
ctg	ctc	atc	gtg	ttt	ggc	tca	gtt	gtt	gcc	gcg	gcg	atg	cca	ttg	atc	739	
Leu	Leu	Ile	Val	Phe	Gly	Ser	Val	Val	Ala	Ala	Ala	Met	Pro	Leu	Ile		
		200					205					210					
gtg	ggc	att	ttg	tcc	atc	ttg	ggc	tcg	ctg	ggc	atc	ttg	gca	att	ttg	787	
Val	Gly	Ile	Leu	Ser	Ile	Leu	Gly	Ser	Leu	Gly	Ile	Leu	Ala	Ile	Leu		
	215					220					225						
gct	gga	ttc	ttc	cag	gtc	aac	gta	ttt	gca	caa	tct	gtt	gtg	acc	ctt	835	
Ala	Gly	Phe	Phe	Gln	Val	Asn	Val	Phe	Ala	Gln	Ser	Val	Val	Thr	Leu		
	230				235					240					245		
ctg	ggc	ttg	ggc	ctt	gcc	att	gac	tat	ggc	tta	ttc	atg	gtc	tct	cgt	883	
Leu	Gly	Leu	Gly	Leu	Ala	Ile	Asp	Tyr	Gly	Leu	Phe	Met	Val	Ser	Arg		
				250					255					260			
ttc	cgt	gag	gaa	atg	gat	aag	ggc	acc	ccg	gtt	gaa	cag	gct	gtt	gcc	931	
Phe	Arg	Glu	Glu	Met	Asp	Lys	Gly	Thr	Pro	Val	Glu	Gln	Ala	Val	Ala		

265							270					275						
acc	act	acg	gcg	acc	gcg	ggt	aag	act	gtg	gtg	ttc	tct	gca	gcg	atg	979		
Thr	Thr	Thr	Ala	Thr	Ala	Gly	Lys	Thr	Val	Val	Phe	Ser	Ala	Ala	Met			
280							285					290						
gtg	gct	gtg	gcg	ctg	tcc	ggg	ttg	ttt	gtt	ttc	cca	cag	gct	ttc	ttg	1027		
Val	Ala	Val	Ala	Leu	Ser	Gly	Leu	Phe	Val	Phe	Pro	Gln	Ala	Phe	Leu			
295							300					305						
aag	tcg	gtg	gca	ttc	ggt	gcg	att	tcc	gcg	gtt	ggc	ctt	gct	gct	ttg	1075		
Lys	Ser	Val	Ala	Phe	Gly	Ala	Ile	Ser	Ala	Val	Gly	Leu	Ala	Ala	Leu			
310							315					320					325	
atg	tcg	gtg	acg	gtg	ttg	ccg	tcg	ctg	ttc	agc	atg	ttg	ggt	aag	aat	1123		
Met	Ser	Val	Thr	Val	Leu	Pro	Ser	Leu	Phe	Ser	Met	Leu	Gly	Lys	Asn			
330							335					340						
atc	gat	aag	tgg	agt	ttg	cgt	cgc	act	gct	cga	aca	gcg	cgc	cgt	ttg	1171		
Ile	Asp	Lys	Trp	Ser	Leu	Arg	Arg	Thr	Ala	Arg	Thr	Ala	Arg	Arg	Leu			
345							350					355						
gaa	gac	acc	att	tgg	tac	cgc	gtg	ccg	gca	tgg	gca	atg	cgc	cat	gcc	1219		
Glu	Asp	Thr	Ile	Trp	Tyr	Arg	Val	Pro	Ala	Trp	Ala	Met	Arg	His	Ala			
360							365					370						
aag	gca	gtg	acc	gtg	ggc	gtc	gta	ttg	ctc	ttg	ctt	gct	ctt	aca	gtg	1267		
Lys	Ala	Val	Thr	Val	Gly	Val	Val	Leu	Leu	Leu	Leu	Ala	Leu	Thr	Val			
375							380					385						
ccg	ttg	acg	ggc	gtg	aaa	ttc	ggc	ggc	atc	aat	gaa	acg	tat	ctg	cca	1315		
Pro	Leu	Thr	Gly	Val	Lys	Phe	Gly	Gly	Ile	Asn	Glu	Thr	Tyr	Leu	Pro			
390							395					400					405	
cca	gct	aac	gac	acc	cgc	gtc	gcc	caa	gag	cgt	ttc	gac	gag	gcg	ttt	1363		
Pro	Ala	Asn	Asp	Thr	Arg	Val	Ala	Gln	Glu	Arg	Phe	Asp	Glu	Ala	Phe			
410							415					420						
ccc	gcc	ttc	cgc	acc	gag	ccg	gtc	aag	ctt	gtg	gtc	acc	ggg	gcg	gac	1411		
Pro	Ala	Phe	Arg	Thr	Glu	Pro	Val	Lys	Leu	Val	Val	Thr	Gly	Ala	Asp			
425							430					435						
aac	aac	cag	ctg	atc	gat	atc	tat	gtt	cag	gcc	aac	gaa	gtt	gag	gga	1459		
Asn	Asn	Gln	Leu	Ile	Asp	Ile	Tyr	Val	Gln	Ala	Asn	Glu	Val	Glu	Gly			
440							445					450						
ctg	aca	gat	cgt	ttc	acc	gca	ggt	gcg	act	acc	gat	gat	ggc	acc	acg	1507		
Leu	Thr	Asp	Arg	Phe	Thr	Ala	Gly	Ala	Thr	Thr	Asp	Asp	Gly	Thr	Thr			
455							460					465						
gtg	ttg	tct	act	ggt	att	cag	gat	cgt	tcc	ctc	aat	gag	cag	gta	gtg	1555		
Val	Leu	Ser	Thr	Gly	Ile	Gln	Asp	Arg	Ser	Leu	Asn	Glu	Gln	Val	Val			
470							475					480					485	
gag	cag	ctt	cgc	gct	att	tcc	gtc	cct	gag	ggc	gtt	gag	gtg	cag	atc	1603		
Glu	Gln	Leu	Arg	Ala	Ile	Ser	Val	Pro	Glu	Gly	Val	Glu	Val	Gln	Ile			
490							495					500						
ggt	ggc	act	cca	gcc	atg	gag	atc	gaa	tcc	att	gag	gcg	ctc	ttt	gaa	1651		
Gly	Gly	Thr	Pro	Ala	Met	Glu	Ile	Glu	Ser	Ile	Glu	Ala	Leu	Phe	Glu			
505							510					515						

aag ctc ctc tgg atg gct ctc tac att gtg ctg gcc act ttc atc ctc 1699
Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu Ala Thr Phe Ile Leu
520 525 530

atg gca ttg gta ttt ggt tgc gtg att ttg ccg gcg aag gcc atc atc 1747
Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro Ala Lys Ala Ile Ile
535 540 545

atg acc att ctg ggt atg ggt gcc acc ttg ggt att ctc acc ttg atg 1795
Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly Ile Leu Thr Leu Met
550 555 560 565

ttc gtc gat ggc gtg ggt gcc agc gca ttg aac ttc tcc cct ggc cca 1843
Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn Phe Ser Pro Gly Pro
570 575 580

ctg atg agt cca gtg ctg gtg ctg atc atg gct att att tac gga ctt 1891
Leu Met Ser Pro Val Leu Val Leu Ile Met Ala Ile Ile Tyr Gly Leu
585 590 595

tcc acc gac tat gag gtg ttc ctg gta tct cgc atg gtg gag gcc cgc 1939
Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg Met Val Glu Ala Arg
600 605 610

gat aaa ggc gaa tcc acc gac gac gcc atc aga tac ggc act gca cac 1987
Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg Tyr Gly Thr Ala His
615 620 625

acc gga tct atc atc acc gcg gcc gca ctg atc atg att gtg gtc tgt 2035
Thr Gly Ser Ile Ile Thr Ala Ala Leu Ile Met Ile Val Val Cys
630 635 640 645

gga gcg ttt ggt ttc tct gag atc gtc atg atg aag tac atc gcg ttc 2083
Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met Lys Tyr Ile Ala Phe
650 655 660

ggc atg atc gca gcg ctg att ctg gat gcc acc atc atc cgc atg ctg 2131
Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr Ile Ile Arg Met Leu
665 670 675

ctt gtc ccc cgc cgt gat gca cct gct tgc cga cga caa ctg gtg ggc 2179
Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg Arg Gln Leu Val Gly
680 685 690

acc cgg ctt cgt taaaaaggcc tacaccgtca tgg 2214
Thr Arg Leu Arg
695

<210> 226

<211> 697

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 226

Val Phe Ser Lys Trp Gly His Phe Ala Tyr Arg Phe Arg Arg Ile Val
1 5 10 15

Pro Leu Val Val Ile Ala Ala Ile Leu Ala Leu Phe Val Ile Phe Gly
20 25 30

Thr Lys Leu Gly Asp Arg Met Ser Gln Glu Gly Trp Asp Asp Pro Gly
 35 40 45
 Ser Ser Ser Thr Ala Ala Ala Arg Ile Glu Leu Glu Thr Phe Gly Arg
 50 55 60
 Asp Asn Asp Gly Asp Val Val Leu Leu Phe Thr Ala Pro Glu Gly Thr
 65 70 75 80
 Ser Phe Asp Asp Ala Glu Val Phe Ser Ser Ile Ser Gly Tyr Leu Asp
 85 90 95
 Gly Leu Ile Glu Asn Asn Pro Asp Glu Val Ser His Ile Asn Ser Tyr
 100 105 110
 Phe Asp Thr Arg Asn Gln Asn Leu Leu Ser Lys Asp Gly Thr Gln Thr
 115 120 125
 Phe Ala Ala Leu Gly Leu Lys Gly Asp Gly Glu Gln Thr Leu Lys Asp
 130 135 140
 Phe Arg Glu Ile Glu Asp Gln Leu His Pro Asp Asn Leu Ala Gly Gly
 145 150 155 160
 Val Thr Thr Glu Val Ala Gly Ala Thr Ala Val Ala Asp Ala Leu Asp
 165 170 175
 Glu Gly Met Ala Gly Asp Ile Ser Arg Ala Glu Val Phe Ala Leu Pro
 180 185 190
 Phe Val Ala Ile Leu Leu Leu Ile Val Phe Gly Ser Val Val Ala Ala
 195 200 205
 Ala Met Pro Leu Ile Val Gly Ile Leu Ser Ile Leu Gly Ser Leu Gly
 210 215 220
 Ile Leu Ala Ile Leu Ala Gly Phe Phe Gln Val Asn Val Phe Ala Gln
 225 230 235 240
 Ser Val Val Thr Leu Leu Gly Leu Gly Leu Ala Ile Asp Tyr Gly Leu
 245 250 255
 Phe Met Val Ser Arg Phe Arg Glu Glu Met Asp Lys Gly Thr Pro Val
 260 265 270
 Glu Gln Ala Val Ala Thr Thr Thr Ala Thr Ala Gly Lys Thr Val Val
 275 280 285
 Phe Ser Ala Ala Met Val Ala Val Ala Leu Ser Gly Leu Phe Val Phe
 290 295 300
 Pro Gln Ala Phe Leu Lys Ser Val Ala Phe Gly Ala Ile Ser Ala Val
 305 310 315 320
 Gly Leu Ala Ala Leu Met Ser Val Thr Val Leu Pro Ser Leu Phe Ser
 325 330 335
 Met Leu Gly Lys Asn Ile Asp Lys Trp Ser Leu Arg Arg Thr Ala Arg
 340 345 350

Thr Ala Arg Arg Leu Glu Asp Thr Ile Trp Tyr Arg Val Pro Ala Trp
 355 360 365
 Ala Met Arg His Ala Lys Ala Val Thr Val Gly Val Val Leu Leu Leu
 370 375 380
 Leu Ala Leu Thr Val Pro Leu Thr Gly Val Lys Phe Gly Gly Ile Asn
 385 390 395 400
 Glu Thr Tyr Leu Pro Pro Ala Asn Asp Thr Arg Val Ala Gln Glu Arg
 405 410 415
 Phe Asp Glu Ala Phe Pro Ala Phe Arg Thr Glu Pro Val Lys Leu Val
 420 425 430
 Val Thr Gly Ala Asp Asn Asn Gln Leu Ile Asp Ile Tyr Val Gln Ala
 435 440 445
 Asn Glu Val Glu Gly Leu Thr Asp Arg Phe Thr Ala Gly Ala Thr Thr
 450 455 460
 Asp Asp Gly Thr Thr Val Leu Ser Thr Gly Ile Gln Asp Arg Ser Leu
 465 470 475 480
 Asn Glu Gln Val Val Glu Gln Leu Arg Ala Ile Ser Val Pro Glu Gly
 485 490 495
 Val Glu Val Gln Ile Gly Gly Thr Pro Ala Met Glu Ile Glu Ser Ile
 500 505 510
 Glu Ala Leu Phe Glu Lys Leu Leu Trp Met Ala Leu Tyr Ile Val Leu
 515 520 525
 Ala Thr Phe Ile Leu Met Ala Leu Val Phe Gly Ser Val Ile Leu Pro
 530 535 540
 Ala Lys Ala Ile Ile Met Thr Ile Leu Gly Met Gly Ala Thr Leu Gly
 545 550 555 560
 Ile Leu Thr Leu Met Phe Val Asp Gly Val Gly Ala Ser Ala Leu Asn
 565 570 575
 Phe Ser Pro Gly Pro Leu Met Ser Pro Val Leu Val Leu Ile Met Ala
 580 585 590
 Ile Ile Tyr Gly Leu Ser Thr Asp Tyr Glu Val Phe Leu Val Ser Arg
 595 600 605
 Met Val Glu Ala Arg Asp Lys Gly Glu Ser Thr Asp Asp Ala Ile Arg
 610 615 620
 Tyr Gly Thr Ala His Thr Gly Ser Ile Ile Thr Ala Ala Ala Leu Ile
 625 630 635 640
 Met Ile Val Val Cys Gly Ala Phe Gly Phe Ser Glu Ile Val Met Met
 645 650 655
 Lys Tyr Ile Ala Phe Gly Met Ile Ala Ala Leu Ile Leu Asp Ala Thr
 660 665 670
 Ile Ile Arg Met Leu Leu Val Pro Arg Arg Asp Ala Pro Ala Ser Arg

```

        675                680                685
Arg Gln Leu Val Gly Thr Arg Leu Arg
   690                695

<210> 227
<211> 729
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(706)
<223> RXN03042

<400> 227
atgacaccgg cgcgacgtat ggcattactg gcgtaccca atttacgatg acatctctgc 60

tcgcctcggc gacgtcctgg ttccttacgt tctgatcggt ttg gtt cta gcg ttc 115
                        Leu Val Leu Ala Phe
                        1                5

ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163
Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
                        10                15                20

gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211
Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
                        25                30                35

gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259
Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
                        40                45                50

ctg ctg tcc ttc ttg ccg atc atg ctc atc ggc ctg gta ttt ggt ctg 307
Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly Leu Val Phe Gly Leu
                        55                60                65

gcc atg gat tac cag atc ttc ctc gtt act cgt atg cgt gag ggc ttc 355
Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg Met Arg Glu Gly Phe
                        70                75                80                85

acc aag ggc aag act gcg ggc aac gca acg tcg aat ggt ttc aag cac 403
Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser Asn Gly Phe Lys His
                        90                95                100

ggt gcc cgc gtg gtc act gct gcg gcg ctg atc atg gtg tct gtg ttc 451
Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile Met Val Ser Val Phe
                        105                110                115

gcg gca ttc ata gcg cag gac atg gcg ttt att aag acc atg ggc ttt 499
Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile Lys Thr Met Gly Phe
                        120                125                130

gct ctg gcc gtt gct gtg ttc ttc gat gcc ttc gtt gtt cgc atg atg 547
Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe Val Val Arg Met Met
                        135                140                145

att atc cct gca aca atg ttc ctg ctt gat gac aag gct tgg tgg cta 595
Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp Lys Ala Trp Trp Leu

```


150	155								160				165				
cct aag tgg ttg gat aag att ctt ccc aac gtt gat gtt gaa ggt gag																	643
Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val Asp Val Glu Gly Glu																	
	170								175				180				
ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat																	691
Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn																	
	185								190				195				
gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta																	729
Val Gly Val Gly Ala																	
	200																

```
<210> 228
<211> 202
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 228															
Leu	Val	Leu	Ala	Phe	Leu	Val	Leu	Leu	Leu	Val	Phe	Arg	Ser	Ile	Trp
1				5					10					15	
Val	Pro	Leu	Ile	Ala	Ala	Leu	Gly	Phe	Gly	Leu	Ser	Val	Leu	Ala	Thr
			20					25					30		
Phe	Gly	Ala	Thr	Val	Ala	Ile	Phe	Gln	Glu	Gly	Ala	Phe	Gly	Ile	Ile
		35					40					45			
Asp	Asp	Pro	Gln	Pro	Leu	Leu	Ser	Phe	Leu	Pro	Ile	Met	Leu	Ile	Gly
	50					55					60				
Leu	Val	Phe	Gly	Leu	Ala	Met	Asp	Tyr	Gln	Ile	Phe	Leu	Val	Thr	Arg
65					70					75					80
Met	Arg	Glu	Gly	Phe	Thr	Lys	Gly	Lys	Thr	Ala	Gly	Asn	Ala	Thr	Ser
				85					90					95	
Asn	Gly	Phe	Lys	His	Gly	Ala	Arg	Val	Val	Thr	Ala	Ala	Ala	Leu	Ile
			100					105					110		
Met	Val	Ser	Val	Phe	Ala	Ala	Phe	Ile	Ala	Gln	Asp	Met	Ala	Phe	Ile
		115					120					125			
Lys	Thr	Met	Gly	Phe	Ala	Leu	Ala	Val	Ala	Val	Phe	Phe	Asp	Ala	Phe
	130					135					140				
Val	Val	Arg	Met	Met	Ile	Ile	Pro	Ala	Thr	Met	Phe	Leu	Leu	Asp	Asp
145					150					155					160
Lys	Ala	Trp	Trp	Leu	Pro	Lys	Trp	Leu	Asp	Lys	Ile	Leu	Pro	Asn	Val
				165					170					175	
Asp	Val	Glu	Gly	Glu	Gly	Leu	Ser	Glu	Leu	His	Glu	Ala	Arg	Thr	Glu
			180					185					190		
Glu	Leu	Lys	Glu	Asn	Val	Gly	Val	Gly	Ala						
		195					200								

```
<220>
<221> CDS
<222> (101)..(706)
<223> FRXA02893
```

<400> 229																	
atgacaccgg	cgcgacgtat	ggcattactg	gcgtacccca	atttacgatg	acatctctgc	60											
tcgcctcggc	gacgtcctgg	ttccttacgt	tctgatcggt	ttg	ggt	cta	gcg	ttc	115								
				Leu	Val	Leu	Ala	Phe	5								
									1								
ctc	gtg	ctg	ttg	ctc	gtg	ttc	cgg	tcc	att	tgg	gtc	cca	ttg	atc	gcg	163	
Leu	Val	Leu	Leu	Leu	Val	Phe	Arg	Ser	Ile	Trp	Val	Pro	Leu	Ile	Ala		
				10					15							20	
gct	ctg	ggc	ttt	ggc	ttg	tca	ggt	ctg	gct	acc	ttt	ggt	gct	acc	gtg	211	
Ala	Leu	Gly	Phe	Gly	Leu	Ser	Val	Leu	Ala	Thr	Phe	Gly	Ala	Thr	Val		
			25					30							35		
gcg	atc	ttc	caa	gaa	ggg	gct	ttc	ggc	atc	atc	gac	gat	cct	cag	cca	259	
Ala	Ile	Phe	Gln	Glu	Gly	Ala	Phe	Gly	Ile	Ile	Asp	Asp	Pro	Gln	Pro		
		40					45							50			
ctg	ctg	tcc	ttc	ttg	ccg	atc	atg	ctc	atc	ggc	ctg	gta	ttt	ggt	ctg	307	
Leu	Leu	Ser	Phe	Leu	Pro	Ile	Met	Leu	Ile	Gly	Leu	Val	Phe	Gly	Leu		
	55					60							65				
gcc	atg	gat	tac	cag	atc	ttc	ctc	ggt	act	cgt	atg	cgt	gag	ggc	ttc	355	
Ala	Met	Asp	Tyr	Gln	Ile	Phe	Leu	Val	Thr	Arg	Met	Arg	Glu	Gly	Phe		
70					75							80	85				
acc	aag	ggc	aag	act	gcg	ggc	aac	gca	acg	tcg	aat	ggg	ttc	aag	cac	403	
Thr	Lys	Gly	Lys	Thr	Ala	Gly	Asn	Ala	Thr	Ser	Asn	Gly	Phe	Lys	His		
				90							95	100					
ggg	gcc	cg	gtg	gtc	act	gct	gcg	gcg	ctg	atc	atg	gtg	tct	gtg	ttc	451	
Gly	Ala	Arg	Val	Val	Thr	Ala	Ala	Ala	Leu	Ile	Met	Val	Ser	Val	Phe		
			105				110							115			
gcg	gca	ttc	ata	gcg	cag	gac	atg	gcg	ttt	att	aag	acc	atg	ggc	ttt	499	
Ala	Ala	Phe	Ile	Ala	Gln	Asp	Met	Ala	Phe	Ile	Lys	Thr	Met	Gly	Phe		
		120					125							130			
gct	ctg	gcc	ggt	gct	gtg	ttc	ttc	gat	gcc	ttc	ggt	ggt	cg	atg	atg	547	
Ala	Leu	Ala	Val	Ala	Val	Phe	Phe	Asp	Ala	Phe	Val	Val	Arg	Met	Met		
	135					140							145				
att	atc	cct	gca	aca	atg	ttc	ctg	ctt	gat	gac	aag	gct	tgg	tgg	cta	595	
Ile	Ile	Pro	Ala	Thr	Met	Phe	Leu	Leu	Asp	Asp	Lys	Ala	Trp	Trp	Leu		
150					155							160	165				
cct	aag	tgg	ttg	gat	aag	att	ctt	ccc	aac	ggt	gat	ggt	gaa	ggg	gag	643	
Pro	Lys	Trp	Leu	Asp	Lys	Ile	Leu	Pro	Asn	Val	Asp	Val	Glu	Gly	Glu		
				170							175	180					

ggt ctt agt gaa cta cat gag gct cgc acc gag gaa ctg aag gaa aat 691
 Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu Glu Leu Lys Glu Asn
 185 190 195

gta ggt gtc ggg gct tagagaaaca aaaaaggctg cta 729
 Val Gly Val Gly Ala
 200

<210> 230

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 230

Leu Val Leu Ala Phe Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp
 1 5 10 15

Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
 20 25 30

Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
 35 40 45

Asp Asp Pro Gln Pro Leu Leu Ser Phe Leu Pro Ile Met Leu Ile Gly
 50 55 60

Leu Val Phe Gly Leu Ala Met Asp Tyr Gln Ile Phe Leu Val Thr Arg
 65 70 75 80

Met Arg Glu Gly Phe Thr Lys Gly Lys Thr Ala Gly Asn Ala Thr Ser
 85 90 95

Asn Gly Phe Lys His Gly Ala Arg Val Val Thr Ala Ala Ala Leu Ile
 100 105 110

Met Val Ser Val Phe Ala Ala Phe Ile Ala Gln Asp Met Ala Phe Ile
 115 120 125

Lys Thr Met Gly Phe Ala Leu Ala Val Ala Val Phe Phe Asp Ala Phe
 130 135 140

Val Val Arg Met Met Ile Ile Pro Ala Thr Met Phe Leu Leu Asp Asp
 145 150 155 160

Lys Ala Trp Trp Leu Pro Lys Trp Leu Asp Lys Ile Leu Pro Asn Val
 165 170 175

Asp Val Glu Gly Glu Gly Leu Ser Glu Leu His Glu Ala Arg Thr Glu
 180 185 190

Glu Leu Lys Glu Asn Val Gly Val Gly Ala
 195 200

<210> 231

<211> 1605

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1582)

<223> RXA01616

<400> 231

```

cctacgattt ccgacgtctt aaatcgccac acagcgccgt ggtctaaaac accaacaaaa 60

gagttgtaac tgtaccgacc attcgttaca gttacgatcc atg act tca gaa acc 115
              Met Thr Ser Glu Thr
              1                      5

tta cag gcg caa gcg cct acg aaa acc caa cgt tgg gct ttc ctc gcc 163
Leu Gln Ala Gln Ala Pro Thr Lys Thr Gln Arg Trp Ala Phe Leu Ala
              10                      15                      20

gtt atc agc ggt ggt ctc ttt ctg atc ggt gta gac aac tcg att ctc 211
Val Ile Ser Gly Gly Leu Phe Leu Ile Gly Val Asp Asn Ser Ile Leu
              25                      30                      35

tac acc gca ctc cct ctg ctg cgt gaa cag ctc gca gcc tcc gaa acc 259
Tyr Thr Ala Leu Pro Leu Leu Arg Glu Gln Leu Ala Ala Ser Glu Thr
              40                      45                      50

caa gcg ttg tgg atc atc aac gca tat ccc ctg ctc atg gcg ggc ctt 307
Gln Ala Leu Trp Ile Ile Asn Ala Tyr Pro Leu Leu Met Ala Gly Leu
              55                      60                      65

cgt ttg ggt gcc ggc act ttg ggt gac aaa aac ggc cac cgc cgg atg 355
Arg Leu Gly Ala Gly Thr Leu Gly Asp Lys Asn Gly His Arg Arg Met
              70                      75                      80                      85

ttc ctc atg ggc ttg agc att ttc gga atc gct tca ctt ggt gct gcg 403
Phe Leu Met Gly Leu Ser Ile Phe Gly Ile Ala Ser Leu Gly Ala Ala
              90                      95                      100

ttt gct cca act gcg tgg gct ctt gtt gct gcg aga gct ttc ctt ggc 451
Phe Ala Pro Thr Ala Trp Ala Leu Val Ala Ala Arg Ala Phe Leu Gly
              105                      110                      115

atc ggt gcg gca acg atg atg cct gca acc ttg gct ctg atc cgc att 499
Ile Gly Ala Ala Thr Met Met Pro Ala Thr Leu Ala Leu Ile Arg Ile
              120                      125                      130

acg ttt gag gat gag cgt gag cgc aac act gca att ggt att tgg ggt 547
Thr Phe Glu Asp Glu Arg Glu Arg Asn Thr Ala Ile Gly Ile Trp Gly
              135                      140                      145

tcc gtg gca att ctt ggc gct gcg gca ggc ccg atc att ggt ggt gcg 595
Ser Val Ala Ile Leu Gly Ala Ala Ala Gly Pro Ile Ile Gly Gly Ala
              150                      155                      160                      165

ctg ttg gaa ttc ttc tgg tgg ggt tcg gtt ttc ctc att aac gtt ccg 643
Leu Leu Glu Phe Phe Trp Trp Gly Ser Val Phe Leu Ile Asn Val Pro
              170                      175                      180

gtg gct gtt atc gcg ttg atc gct acg ctt ttt gtg gcg ccg gcc aat 691
Val Ala Val Ile Ala Leu Ile Ala Thr Leu Phe Val Ala Pro Ala Asn
              185                      190                      195

atc gcg aat ccg tct aag cat tgg gat ttc ttg tcg tcg ttc tat gcg 739
Ile Ala Asn Pro Ser Lys His Trp Asp Phe Leu Ser Ser Phe Tyr Ala

```

200					205					210						
ctg	ctc	aca	ctt	gct	ggg	ttg	atc	atc	acg	atc	aag	gaa	tct	gtg	aat	787
Leu	Leu	Thr	Leu	Ala	Gly	Leu	Ile	Ile	Thr	Ile	Lys	Glu	Ser	Val	Asn	
	215					220					225					
act	gca	cgc	cat	atg	cct	ctt	ctt	ttg	ggg	gca	gtc	atc	atg	ttg	atc	835
Thr	Ala	Arg	His	Met	Pro	Leu	Leu	Leu	Gly	Ala	Val	Ile	Met	Leu	Ile	
230					235					240					245	
att	ggg	gcg	gtg	ttg	ttt	agc	agt	cgt	cag	aag	aag	atc	gag	gag	cca	883
Ile	Gly	Ala	Val	Leu	Phe	Ser	Ser	Arg	Gln	Lys	Lys	Ile	Glu	Glu	Pro	
				250					255						260	
ctt	cta	gat	ctg	tcg	ttg	ttc	cgt	aat	cgc	ctt	ttc	tta	ggc	ggg	gtg	931
Leu	Leu	Asp	Leu	Ser	Leu	Phe	Arg	Asn	Arg	Leu	Phe	Leu	Gly	Gly	Val	
			265					270					275			
gtt	gct	gcg	ggc	atg	gcg	atg	ttt	act	gtg	tcc	ggg	ttg	gaa	atg	act	979
Val	Ala	Ala	Gly	Met	Ala	Met	Phe	Thr	Val	Ser	Gly	Leu	Glu	Met	Thr	
	280						285					290				
acc	tcg	cag	cgt	ttc	cag	ttg	tct	gtg	ggg	ttc	act	cca	ctt	gag	gct	1027
Thr	Ser	Gln	Arg	Phe	Gln	Leu	Ser	Val	Gly	Phe	Thr	Pro	Leu	Glu	Ala	
	295					300					305					
ggg	ttg	ctc	atg	atc	cca	gct	gca	ttg	ggg	agc	ttc	ccg	atg	tct	att	1075
Gly	Leu	Leu	Met	Ile	Pro	Ala	Ala	Leu	Gly	Ser	Phe	Pro	Met	Ser	Ile	
310					315					320					325	
atc	ggg	ggg	gca	aac	ctg	cat	cgt	tgg	ggc	ttc	aaa	ccg	ctg	atc	agt	1123
Ile	Gly	Gly	Ala	Asn	Leu	His	Arg	Trp	Gly	Phe	Lys	Pro	Leu	Ile	Ser	
				330					335						340	
ggg	ggg	ttt	gct	gcc	act	gcc	gtt	ggc	atc	gcc	ctg	tgt	att	tgg	ggc	1171
Gly	Gly	Phe	Ala	Ala	Thr	Ala	Val	Gly	Ile	Ala	Leu	Cys	Ile	Trp	Gly	
			345					350					355			
gcg	act	cat	act	gat	ggg	ttg	ccg	ttt	ttc	atc	gcg	ggg	cta	ttc	ttc	1219
Ala	Thr	His	Thr	Asp	Gly	Leu	Pro	Phe	Phe	Ile	Ala	Gly	Leu	Phe	Phe	
			360				365					370				
atg	ggc	gcg	ggg	gct	ggg	tcg	gta	atg	tct	gtg	tct	tcc	act	gcg	att	1267
Met	Gly	Ala	Gly	Ala	Gly	Ser	Val	Met	Ser	Val	Ser	Ser	Thr	Ala	Ile	
	375					380					385					
atc	ggg	tcc	gcg	ccg	gtg	cgt	aag	gct	ggc	atg	gcg	tcg	tcg	atc	gaa	1315
Ile	Gly	Ser	Ala	Pro	Val	Arg	Lys	Ala	Gly	Met	Ala	Ser	Ser	Ile	Glu	
390					395					400					405	
gag	gtc	tct	tat	gag	ttc	ggc	acg	ctg	ttg	tct	gtc	gcg	att	ttg	ggg	1363
Glu	Val	Ser	Tyr	Glu	Phe	Gly	Thr	Leu	Leu	Ser	Val	Ala	Ile	Leu	Gly	
				410					415					420		
agc	ttg	ttc	cca	ttc	ttc	tac	tcg	ctg	cat	gcc	ccg	gca	gag	gtt	gcg	1411
Ser	Leu	Phe	Pro	Phe	Phe	Tyr	Ser	Leu	His	Ala	Pro	Ala	Glu	Val	Ala	
			425					430					435			
gat	aac	ttc	tcg	gcg	ggg	gtt	cac	cac	gcg	att	gat	ggc	gat	gcg	gcg	1459
Asp	Asn	Phe	Ser	Ala	Gly	Val	His	His	Ala	Ile	Asp	Gly	Asp	Ala	Ala	
		440					445					450				

cgt gca tct ttg gac acc gca tac att aac gtg ttg atc att gcc cta 1507
 Arg Ala Ser Leu Asp Thr Ala Tyr Ile Asn Val Leu Ile Ile Ala Leu
 455 460 465

gta tgc gca gta gcg gct gct ctg atc agc agt tac ctt ttc cgc gga 1555
 Val Cys Ala Val Ala Ala Ala Leu Ile Ser Ser Tyr Leu Phe Arg Gly
 470 475 480 485

aat ccg aag gga gcc aat aat gcg cac tagtaaaaaa gagatgattc 1602
 Asn Pro Lys Gly Ala Asn Asn Ala His
 490

tgc 1605

<210> 232

<211> 494

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Met Thr Ser Glu Thr Leu Gln Ala Gln Ala Pro Thr Lys Thr Gln Arg
 1 5 10 15

Trp Ala Phe Leu Ala Val Ile Ser Gly Gly Leu Phe Leu Ile Gly Val
 20 25 30

Asp Asn Ser Ile Leu Tyr Thr Ala Leu Pro Leu Leu Arg Glu Gln Leu
 35 40 45

Ala Ala Ser Glu Thr Gln Ala Leu Trp Ile Ile Asn Ala Tyr Pro Leu
 50 55 60

Leu Met Ala Gly Leu Arg Leu Gly Ala Gly Thr Leu Gly Asp Lys Asn
 65 70 75 80

Gly His Arg Arg Met Phe Leu Met Gly Leu Ser Ile Phe Gly Ile Ala
 85 90 95

Ser Leu Gly Ala Ala Phe Ala Pro Thr Ala Trp Ala Leu Val Ala Ala
 100 105 110

Arg Ala Phe Leu Gly Ile Gly Ala Ala Thr Met Met Pro Ala Thr Leu
 115 120 125

Ala Leu Ile Arg Ile Thr Phe Glu Asp Glu Arg Glu Arg Asn Thr Ala
 130 135 140

Ile Gly Ile Trp Gly Ser Val Ala Ile Leu Gly Ala Ala Ala Gly Pro
 145 150 155 160

Ile Ile Gly Gly Ala Leu Leu Glu Phe Phe Trp Trp Gly Ser Val Phe
 165 170 175

Leu Ile Asn Val Pro Val Ala Val Ile Ala Leu Ile Ala Thr Leu Phe
 180 185 190

Val Ala Pro Ala Asn Ile Ala Asn Pro Ser Lys His Trp Asp Phe Leu
 195 200 205

Ser Ser Phe Tyr Ala Leu Leu Thr Leu Ala Gly Leu Ile Ile Thr Ile
 210 215 220
 Lys Glu Ser Val Asn Thr Ala Arg His Met Pro Leu Leu Leu Gly Ala
 225 230 235 240
 Val Ile Met Leu Ile Ile Gly Ala Val Leu Phe Ser Ser Arg Gln Lys
 245 250 255
 Lys Ile Glu Glu Pro Leu Leu Asp Leu Ser Leu Phe Arg Asn Arg Leu
 260 265 270
 Phe Leu Gly Gly Val Val Ala Ala Gly Met Ala Met Phe Thr Val Ser
 275 280 285
 Gly Leu Glu Met Thr Thr Ser Gln Arg Phe Gln Leu Ser Val Gly Phe
 290 295 300
 Thr Pro Leu Glu Ala Gly Leu Leu Met Ile Pro Ala Ala Leu Gly Ser
 305 310 315 320
 Phe Pro Met Ser Ile Ile Gly Gly Ala Asn Leu His Arg Trp Gly Phe
 325 330 335
 Lys Pro Leu Ile Ser Gly Gly Phe Ala Ala Thr Ala Val Gly Ile Ala
 340 345 350
 Leu Cys Ile Trp Gly Ala Thr His Thr Asp Gly Leu Pro Phe Phe Ile
 355 360 365
 Ala Gly Leu Phe Phe Met Gly Ala Gly Ala Gly Ser Val Met Ser Val
 370 375 380
 Ser Ser Thr Ala Ile Ile Gly Ser Ala Pro Val Arg Lys Ala Gly Met
 385 390 395 400
 Ala Ser Ser Ile Glu Glu Val Ser Tyr Glu Phe Gly Thr Leu Leu Ser
 405 410 415
 Val Ala Ile Leu Gly Ser Leu Phe Pro Phe Phe Tyr Ser Leu His Ala
 420 425 430
 Pro Ala Glu Val Ala Asp Asn Phe Ser Ala Gly Val His His Ala Ile
 435 440 445
 Asp Gly Asp Ala Ala Arg Ala Ser Leu Asp Thr Ala Tyr Ile Asn Val
 450 455 460
 Leu Ile Ile Ala Leu Val Cys Ala Val Ala Ala Ala Leu Ile Ser Ser
 465 470 475 480
 Tyr Leu Phe Arg Gly Asn Pro Lys Gly Ala Asn Asn Ala His
 485 490

<210> 233

<211> 1500

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1477)

<223> RXA01666

<400> 233

```

cgacgcgcc ctccaccttt tcagtagcgt cacgggcgcc aatcctgtat ttttagcagc 60
agtttgaggg tttttgctcc ccattcttag gagacacccc gtg tcc acg ttt cat 115
                                   Val Ser Thr Phe His
                                   1 5

aaa gtt ttg atc aac acc atg atc tcc aac gtc acc act gga ttt ctg 163
Lys Val Leu Ile Asn Thr Met Ile Ser Asn Val Thr Thr Gly Phe Leu
                                   10 15 20

ttc ttt gcc gtg gtg ttt tgg atg tat ctt tcc act ggc aac gtc gca 211
Phe Phe Ala Val Val Phe Trp Met Tyr Leu Ser Thr Gly Asn Val Ala
                                   25 30 35

ctg acc ggc atc gtc agt gga att tac atg ggt ttg atc gcc gtt tgt 259
Leu Thr Gly Ile Val Ser Gly Ile Tyr Met Gly Leu Ile Ala Val Cys
                                   40 45 50

tcc atc ttt ttc gga acc gtt gtt gat cac aat cgc aag aag tcc gtc 307
Ser Ile Phe Phe Gly Thr Val Val Asp His Asn Arg Lys Lys Ser Val
                                   55 60 65

atg ctg ttt tcc agc gtc acc aca ctc gtg ttt tat tgt ctc agt gcc 355
Met Leu Phe Ser Ser Val Thr Thr Leu Val Phe Tyr Cys Leu Ser Ala
                                   70 75 80 85

ctg gtg tgg gtg ttt tgg ctg gag gaa gac ggc ctg agc atc gga aat 403
Leu Val Trp Val Phe Trp Leu Glu Glu Asp Gly Leu Ser Ile Gly Asn
                                   90 95 100

acc gcc ctg tgg gtg ttc gtt tct ttc atc ctc atc gga tca atc gtg 451
Thr Ala Leu Trp Val Phe Val Ser Phe Ile Leu Ile Gly Ser Ile Val
                                   105 110 115

gaa cac atg cgc aac atc gca ctg tcc acc gtg gtc acg ctg ttg gtt 499
Glu His Met Arg Asn Ile Ala Leu Ser Thr Val Val Thr Leu Leu Val
                                   120 125 130

cct gaa gct gaa cgc gac aaa gca aac ggc ctg gta gga gcc gtg caa 547
Pro Glu Ala Glu Arg Asp Lys Ala Asn Gly Leu Val Gly Ala Val Gln
                                   135 140 145

ggt gtt gga ttt tta gtc acc agc gtc att gct ggt tcc gcc atc ggg 595
Gly Val Gly Phe Leu Val Thr Ser Val Ile Ala Gly Ser Ala Ile Gly
                                   150 155 160 165

ttc ttg ggc atg gaa atc acc ctg tgg atc tgc ctt ggg ctc tca ctt 643
Phe Leu Gly Met Glu Ile Thr Leu Trp Ile Cys Leu Gly Leu Ser Leu
                                   170 175 180

gtc gcg ctg ctg cac ctg ctg ccg att cgc gtc gac gaa ccg gaa atc 691
Val Ala Leu Leu His Leu Leu Pro Ile Arg Val Asp Glu Pro Glu Ile
                                   185 190 195

atc acc caa gaa gac gca cag cct act gtt tct gac gat tca gtt ccc 739
Ile Thr Gln Glu Asp Ala Gln Pro Thr Val Ser Asp Asp Ser Val Pro

```


200	205	210	
aca cct acc tcc gat ttg gcg atc gtg tcc aaa ggc atc gac cta aaa Thr Pro Thr Ser Asp Leu Ala Ile Val Ser Lys Gly Ile Asp Leu Lys 215 220 225			787
gga tca atg aaa atc atc ctg agt gtt ccg gga ctg ctc gcg ctt gtg Gly Ser Met Lys Ile Ile Leu Ser Val Pro Gly Leu Leu Ala Leu Val 230 235 240 245			835
ttg ttt gcg tcc ttc aac aac ctc atc ggc ggc gtg tac tcc gca ctc Leu Phe Ala Ser Phe Asn Asn Leu Ile Gly Gly Val Tyr Ser Ala Leu 250 255 260			883
atg gac cct tac ggc ctg gaa ctt ttc agc cca cag ctg tgg ggg cta Met Asp Pro Tyr Gly Leu Glu Leu Phe Ser Pro Gln Leu Trp Gly Leu 265 270 275			931
ctg ctt gga ctc acc agc ctc ggc ttc atc gtt ggt ggt gct gtg atc Leu Leu Gly Leu Thr Ser Leu Gly Phe Ile Val Gly Gly Ala Val Ile 280 285 290			979
tcc aaa act ggc ttg ggc aaa aac cct gtg cgc acc ttg ctg ctg gtt Ser Lys Thr Gly Leu Gly Lys Asn Pro Val Arg Thr Leu Leu Leu Val 295 300 305			1027
aat gtt ggt gtg gct ttt gtt ggc atg tta ttt gcc att cgc gaa tgg Asn Val Gly Val Ala Phe Val Gly Met Leu Phe Ala Ile Arg Glu Trp 310 315 320 325			1075
tgg tgg ctc tac atc ctg ggc att ttc atc ttc atg gct atc acc cca Trp Trp Leu Tyr Ile Leu Gly Ile Phe Ile Phe Met Ala Ile Thr Pro 330 335 340			1123
gct gcc gaa gcc gca gaa caa acc atc ctt caa cga gtc gtc cca ttc Ala Ala Glu Ala Ala Glu Gln Thr Ile Leu Gln Arg Val Val Pro Phe 345 350 355			1171
cgc caa caa ggc cgc gta ttt gga cta gcc atg gca gtg gaa atg gca Arg Gln Gln Gly Arg Val Phe Gly Leu Ala Met Ala Val Glu Met Ala 360 365 370			1219
gcc aac ccg ctc tcc aca gtg atc gtg gcg att ttg gcc gaa gcc tac Ala Asn Pro Leu Ser Thr Val Ile Val Ala Ile Leu Ala Glu Ala Tyr 375 380 385			1267
ctc att cca tgg atg gct ggc ccc ggc gcg gac acc atc tgg ggc gtg Leu Ile Pro Trp Met Ala Gly Pro Gly Ala Asp Thr Ile Trp Gly Val 390 395 400 405			1315
atc ctc ggc gag ggt aaa gct cgc ggc atg gca ctg atg ttc ctc gca Ile Leu Gly Glu Gly Lys Ala Arg Gly Met Ala Leu Met Phe Leu Ala 410 415 420			1363
tca ggt gcc atc atg ttg gtt gtc gtg ctg ttg gca ttc atg tcg agg Ser Gly Ala Ile Met Leu Val Val Val Leu Leu Ala Phe Met Ser Arg 425 430 435			1411
tcc tac cgg aaa ctc agc cag tac tac gcc acc acc agc caa gac att Ser Tyr Arg Lys Leu Ser Gln Tyr Tyr Ala Thr Thr Ser Gln Asp Ile 440 445 450			1459

gcg gga gct gct gag aag taagtgtct agaccgttgt ttg
 Ala Gly Ala Ala Glu Lys
 455

1500

<210> 234
 <211> 459
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 234
 Val Ser Thr Phe His Lys Val Leu Ile Asn Thr Met Ile Ser Asn Val
 1 5 10 15
 Thr Thr Gly Phe Leu Phe Phe Ala Val Val Phe Trp Met Tyr Leu Ser
 20 25 30
 Thr Gly Asn Val Ala Leu Thr Gly Ile Val Ser Gly Ile Tyr Met Gly
 35 40 45
 Leu Ile Ala Val Cys Ser Ile Phe Phe Gly Thr Val Val Asp His Asn
 50 55 60
 Arg Lys Lys Ser Val Met Leu Phe Ser Ser Val Thr Thr Leu Val Phe
 65 70 75 80
 Tyr Cys Leu Ser Ala Leu Val Trp Val Phe Trp Leu Glu Glu Asp Gly
 85 90 95
 Leu Ser Ile Gly Asn Thr Ala Leu Trp Val Phe Val Ser Phe Ile Leu
 100 105 110
 Ile Gly Ser Ile Val Glu His Met Arg Asn Ile Ala Leu Ser Thr Val
 115 120 125
 Val Thr Leu Leu Val Pro Glu Ala Glu Arg Asp Lys Ala Asn Gly Leu
 130 135 140
 Val Gly Ala Val Gln Gly Val Gly Phe Leu Val Thr Ser Val Ile Ala
 145 150 155 160
 Gly Ser Ala Ile Gly Phe Leu Gly Met Glu Ile Thr Leu Trp Ile Cys
 165 170 175
 Leu Gly Leu Ser Leu Val Ala Leu Leu His Leu Leu Pro Ile Arg Val
 180 185 190
 Asp Glu Pro Glu Ile Ile Thr Gln Glu Asp Ala Gln Pro Thr Val Ser
 195 200 205
 Asp Asp Ser Val Pro Thr Pro Thr Ser Asp Leu Ala Ile Val Ser Lys
 210 215 220
 Gly Ile Asp Leu Lys Gly Ser Met Lys Ile Ile Leu Ser Val Pro Gly
 225 230 235 240
 Leu Leu Ala Leu Val Leu Phe Ala Ser Phe Asn Asn Leu Ile Gly Gly
 245 250 255
 Val Tyr Ser Ala Leu Met Asp Pro Tyr Gly Leu Glu Leu Phe Ser Pro

260										265										270										
Gln	Leu	Trp	Gly	Leu	Leu	Leu	Gly	Leu	Thr	Ser	Leu	Gly	Phe	Ile	Val															
		275					280					285																		
Gly	Gly	Ala	Val	Ile	Ser	Lys	Thr	Gly	Leu	Gly	Lys	Asn	Pro	Val	Arg															
	290					295					300																			
Thr	Leu	Leu	Leu	Val	Asn	Val	Gly	Val	Ala	Phe	Val	Gly	Met	Leu	Phe															
305					310					315					320															
Ala	Ile	Arg	Glu	Trp	Trp	Trp	Leu	Tyr	Ile	Leu	Gly	Ile	Phe	Ile	Phe															
				325				330						335																
Met	Ala	Ile	Thr	Pro	Ala	Ala	Glu	Ala	Ala	Glu	Gln	Thr	Ile	Leu	Gln															
			340				345						350																	
Arg	Val	Val	Pro	Phe	Arg	Gln	Gln	Gly	Arg	Val	Phe	Gly	Leu	Ala	Met															
		355				360						365																		
Ala	Val	Glu	Met	Ala	Ala	Asn	Pro	Leu	Ser	Thr	Val	Ile	Val	Ala	Ile															
	370					375					380																			
Leu	Ala	Glu	Ala	Tyr	Leu	Ile	Pro	Trp	Met	Ala	Gly	Pro	Gly	Ala	Asp															
385					390					395					400															
Thr	Ile	Trp	Gly	Val	Ile	Leu	Gly	Glu	Gly	Lys	Ala	Arg	Gly	Met	Ala															
			405					410					415																	
Leu	Met	Phe	Leu	Ala	Ser	Gly	Ala	Ile	Met	Leu	Val	Val	Val	Leu	Leu															
			420				425						430																	
Ala	Phe	Met	Ser	Arg	Ser	Tyr	Arg	Lys	Leu	Ser	Gln	Tyr	Tyr	Ala	Thr															
		435				440						445																		
Thr	Ser	Gln	Asp	Ile	Ala	Gly	Ala	Ala	Glu	Lys																				
		450				455																								

<210> 235

<211> 1521

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1498)

<223> RXA00062

<400> 235

cttcaacata ggcgttgggg ctgactttta aacaggtacc agtagtaccg gcataagcga 60

tcactgttgc	gttttcttgc	tgccatcaaa	aattagtcac	atg	att	tta	agc	atc	115
				Met	Ile	Leu	Ser	Ile	
				1				5	

gtc	ctt	ttg	ggc	tac	ttc	atg	att	ctg	ctt	gac	acc	tcc	atc	gtc	att	163
Val	Leu	Leu	Gly	Tyr	Phe	Met	Ile	Leu	Leu	Asp	Thr	Ser	Ile	Val	Ile	
			10					15						20		

acg	ggt	cta	cct	gcc	atc	ggc	agt	gaa	ctt	ggc	atc	gat	ccc	gtg	cac	211
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Thr	Gly	Leu	Pro	Ala	Ile	Gly	Ser	Glu	Leu	Gly	Ile	Asp	Pro	Val	His		
			25					30					35				
ctg	tca	tg	gtg	cag	agt	tcc	tac	aca	tta	gtc	ttc	ggc	gca	ctt	ctt	259	
Leu	Ser	Trp	Val	Gln	Ser	Ser	Tyr	Thr	Leu	Val	Phe	Gly	Ala	Leu	Leu		
		40					45					50					
ctg	ctg	gga	gct	cgt	gcc	ggt	gat	atc	ttc	ggc	cga	aag	aaa	gtg	ctc	307	
Leu	Leu	Gly	Ala	Arg	Ala	Gly	Asp	Ile	Phe	Gly	Arg	Lys	Lys	Val	Leu		
		55				60					65						
tac	att	ggt	ctc	gcg	ttg	ttt	gcg	gct	tca	tcg	ttg	gca	att	gcg	ctt	355	
Tyr	Ile	Gly	Leu	Ala	Leu	Phe	Ala	Ala	Ser	Ser	Leu	Ala	Ile	Ala	Leu		
		70				75				80					85		
tct	cca	aat	gct	gcg	gtc	ctc	att	gga	gca	cgc	gta	ggt	caa	ggc	gcg	403	
Ser	Pro	Asn	Ala	Ala	Val	Leu	Ile	Gly	Ala	Arg	Val	Val	Gln	Gly	Ala		
				90					95					100			
gga	gct	gcg	att	atc	gct	cca	gcg	aca	ctt	gcg	ttg	att	act	gag	ttc	451	
Gly	Ala	Ala	Ile	Ile	Ala	Pro	Ala	Thr	Leu	Ala	Leu	Ile	Thr	Glu	Phe		
			105					110					115				
ttc	ccc	gaa	ggc	cca	gct	cgc	ctt	cgt	gct	acc	tct	gct	tat	ggt	gct	499	
Phe	Pro	Glu	Gly	Pro	Ala	Arg	Leu	Arg	Ala	Thr	Ser	Ala	Tyr	Gly	Ala		
		120					125					130					
ggt	gcc	ggc	atc	ggt	gtg	gca	gca	ggc	cta	gtg	atc	ggc	ggc	gta	ttt	547	
Val	Ala	Gly	Ile	Gly	Val	Ala	Ala	Gly	Leu	Val	Ile	Gly	Gly	Val	Phe		
		135				140					145						
gct	gat	ctt	ttg	tcg	tg	cgc	atc	ggc	ttc	ttt	atc	aac	gtc	ccc	atc	595	
Ala	Asp	Leu	Leu	Ser	Trp	Arg	Ile	Gly	Phe	Phe	Ile	Asn	Val	Pro	Ile		
					155					160					165		
gcc	gca	gtg	ttg	gcc	tac	ata	gtg	cac	aaa	gcc	att	ccc	gca	acc	ttc	643	
Ala	Ala	Val	Leu	Ala	Tyr	Ile	Val	His	Lys	Ala	Ile	Pro	Ala	Thr	Phe		
				170					175					180			
agc	agg	cct	gga	tca	ctc	gac	atc	ttc	gga	gca	att	acc	tcc	acg	gca	691	
Ser	Arg	Pro	Gly	Ser	Leu	Asp	Ile	Phe	Gly	Ala	Ile	Thr	Ser	Thr	Ala		
			185					190					195				
ggt	atc	gcc	gcg	gtg	ctc	tac	gca	att	gtc	cgc	agc	gcc	gat	tac	agc	739	
Gly	Ile	Ala	Ala	Val	Leu	Tyr	Ala	Ile	Val	Arg	Ser	Ala	Asp	Tyr	Ser		
		200					205					210					
tg	aca	gat	ccg	ttt	gtg	ttg	att	tcc	ctc	gtg	ctg	ggc	atc	gca	gtg	787	
Trp	Thr	Asp	Pro	Phe	Val	Leu	Ile	Ser	Leu	Val	Leu	Gly	Ile	Ala	Val		
		215				220					225						
ttc	atc	tg	ttc	ctg	cgc	cat	gaa	tcc	tca	gcc	aaa	gaa	cca	ctt	ctg	835	
Phe	Ile	Trp	Phe	Leu	Arg	His	Glu	Ser	Ser	Ala	Lys	Glu	Pro	Leu	Leu		
		230				235				240					245		
ccc	ctg	ggg	ctc	ttt	aaa	aac	cgc	agg	cga	aac	acc	atc	ttg	gcc	agc	883	
Pro	Leu	Gly	Leu	Phe	Lys	Asn	Arg	Arg	Arg	Asn	Thr	Ile	Leu	Ala	Ser		
				250					255					260			
cgc	tft	ctt	ctg	gtt	ggc	tcc	gtg	atg	tca	ttc	ttc	ttc	ttt	gcc	acc	931	
Arg	Phe	Leu	Leu	Val	Gly	Ser	Val	Met	Ser	Phe	Phe	Phe	Phe	Ala	Thr		

265										270										275										
cag	ctg	ttc	cag	gac	acc	atg	gga	atg	aat	gct	ctc	cag	gca	ggc	ctt	979														
Gln	Leu	Phe	Gln	Asp	Thr	Met	Gly	Met	Asn	Ala	Leu	Gln	Ala	Gly	Leu															
280						285						290																		
gcg	ttc	atg	ccg	cta	tct	ctg	ctg	cag	ttt	gcc	agc	gcc	gcg	atg	gtg	1027														
Ala	Phe	Met	Pro	Leu	Ser	Leu	Leu	Gln	Phe	Ala	Ser	Ala	Ala	Met	Val															
295						300						305																		
cca	cgg	ctt	tcc	cga	gca	ggc	gta	tct	gat	tcc	atg	ctc	acc	gtc	atc	1075														
Pro	Arg	Leu	Ser	Arg	Ala	Gly	Val	Ser	Asp	Ser	Met	Leu	Thr	Val	Ile															
310			315						320			325																		
ggc	ttc	gcc	atc	atg	gtc	atc	ggc	atg	gca	ggc	ctc	gca	ttt	gta	cca	1123														
Gly	Phe	Ala	Ile	Met	Val	Ile	Gly	Met	Ala	Gly	Leu	Ala	Phe	Val	Pro															
			330						335			340																		
aac	acg	atg	atc	gcg	ctg	atc	cta	cca	ata	gtt	ttg	gtg	gga	ttt	ggc	1171														
Asn	Thr	Met	Ile	Ala	Leu	Ile	Leu	Pro	Ile	Val	Leu	Val	Gly	Phe	Gly															
			345			350						355																		
caa	ggc	ttc	gct	ttc	gga	cca	atg	aca	gct	ctg	gca	gtt	caa	ggc	gca	1219														
Gln	Gly	Phe	Ala	Phe	Gly	Pro	Met	Thr	Ala	Leu	Ala	Val	Gln	Gly	Ala															
360						365						370																		
ccg	aag	gac	caa	tcc	ggc	gcc	gtt	tct	ggc	ctg	gtg	aat	tcc	ctt	cac	1267														
Pro	Lys	Asp	Gln	Ser	Gly	Ala	Val	Ser	Gly	Leu	Val	Asn	Ser	Leu	His															
375						380						385																		
caa	atc	ggc	ggc	acc	ttc	ggc	ttg	ggc	gtg	ttc	tcc	tcc	ttg	gct	gtc	1315														
Gln	Ile	Gly	Gly	Thr	Phe	Gly	Leu	Gly	Val	Phe	Ser	Ser	Leu	Ala	Val															
390			395						400			405																		
gct	gtc	atc	gga	cat	gat	gca	aca	tca	gag	atg	atc	agc	gac	cgc	gca	1363														
Ala	Val	Ile	Gly	His	Asp	Ala	Thr	Ser	Glu	Met	Ile	Ser	Asp	Arg	Ala															
			410						415			420																		
cac	ttc	gga	ttc	ttg	ctc	tcc	acc	gtg	acg	ctg	acg	ctg	gcc	acc	atc	1411														
His	Phe	Gly	Phe	Leu	Leu	Ser	Thr	Val	Thr	Leu	Thr	Leu	Ala	Thr	Ile															
			425			430						435																		
ttt	gcg	gtc	aca	ctg	ctg	aag	cgc	cac	gaa	acc	cga	aag	agt	agc	gag	1459														
Phe	Ala	Val	Thr	Leu	Leu	Lys	Arg	His	Glu	Thr	Arg	Lys	Ser	Ser	Glu															
440						445						450																		
cgc	cca	acc	cag	ctc	gtc	gac	gaa	aag	gca	gtt	acc	tct	tagtg	cgc	ctg	1508														
Arg	Pro	Thr	Gln	Leu	Val	Asp	Glu	Lys	Ala	Val	Thr	Ser																		
455			460						465																					
cagcatccca gtt															1521															

<210> 236

<211> 466

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

Met	Ile	Leu	Ser	Ile	Val	Leu	Leu	Gly	Tyr	Phe	Met	Ile	Leu	Leu	Asp
1				5					10					15	

Thr Ser Ile Val Ile Thr Gly Leu Pro Ala Ile Gly Ser Glu Leu Gly
 20 25 30
 Ile Asp Pro Val His Leu Ser Trp Val Gln Ser Ser Tyr Thr Leu Val
 35 40 45
 Phe Gly Ala Leu Leu Leu Leu Gly Ala Arg Ala Gly Asp Ile Phe Gly
 50 55 60
 Arg Lys Lys Val Leu Tyr Ile Gly Leu Ala Leu Phe Ala Ala Ser Ser
 65 70 75 80
 Leu Ala Ile Ala Leu Ser Pro Asn Ala Ala Val Leu Ile Gly Ala Arg
 85 90 95
 Val Val Gln Gly Ala Gly Ala Ala Ile Ile Ala Pro Ala Thr Leu Ala
 100 105 110
 Leu Ile Thr Glu Phe Phe Pro Glu Gly Pro Ala Arg Leu Arg Ala Thr
 115 120 125
 Ser Ala Tyr Gly Ala Val Ala Gly Ile Gly Val Ala Ala Gly Leu Val
 130 135 140
 Ile Gly Gly Val Phe Ala Asp Leu Leu Ser Trp Arg Ile Gly Phe Phe
 145 150 155 160
 Ile Asn Val Pro Ile Ala Ala Val Leu Ala Tyr Ile Val His Lys Ala
 165 170 175
 Ile Pro Ala Thr Phe Ser Arg Pro Gly Ser Leu Asp Ile Phe Gly Ala
 180 185 190
 Ile Thr Ser Thr Ala Gly Ile Ala Ala Val Leu Tyr Ala Ile Val Arg
 195 200 205
 Ser Ala Asp Tyr Ser Trp Thr Asp Pro Phe Val Leu Ile Ser Leu Val
 210 215 220
 Leu Gly Ile Ala Val Phe Ile Trp Phe Leu Arg His Glu Ser Ser Ala
 225 230 235 240
 Lys Glu Pro Leu Leu Pro Leu Gly Leu Phe Lys Asn Arg Arg Arg Asn
 245 250 255
 Thr Ile Leu Ala Ser Arg Phe Leu Leu Val Gly Ser Val Met Ser Phe
 260 265 270
 Phe Phe Phe Ala Thr Gln Leu Phe Gln Asp Thr Met Gly Met Asn Ala
 275 280 285
 Leu Gln Ala Gly Leu Ala Phe Met Pro Leu Ser Leu Leu Gln Phe Ala
 290 295 300
 Ser Ala Ala Met Val Pro Arg Leu Ser Arg Ala Gly Val Ser Asp Ser
 305 310 315 320
 Met Leu Thr Val Ile Gly Phe Ala Ile Met Val Ile Gly Met Ala Gly
 325 330 335

Leu Ala Phe Val Pro Asn Thr Met Ile Ala Leu Ile Leu Pro Ile Val
 340 345 350
 Leu Val Gly Phe Gly Gln Gly Phe Ala Phe Gly Pro Met Thr Ala Leu
 355 360 365
 Ala Val Gln Gly Ala Pro Lys Asp Gln Ser Gly Ala Val Ser Gly Leu
 370 375 380
 Val Asn Ser Leu His Gln Ile Gly Gly Thr Phe Gly Leu Gly Val Phe
 385 390 395 400
 Ser Ser Leu Ala Val Ala Val Ile Gly His Asp Ala Thr Ser Glu Met
 405 410 415
 Ile Ser Asp Arg Ala His Phe Gly Phe Leu Leu Ser Thr Val Thr Leu
 420 425 430
 Thr Leu Ala Thr Ile Phe Ala Val Thr Leu Leu Lys Arg His Glu Thr
 435 440 445
 Arg Lys Ser Ser Glu Arg Pro Thr Gln Leu Val Asp Glu Lys Ala Val
 450 455 460
 Thr Ser
 465

<210> 237
 <211> 1584
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1561)
 <223> RXA00215

<400> 237
 cagtgcacaaac tgacccccgca tcctaaaccg cgccagattt ctacctcaaa gaattgaagg 60

ccttttccag gcgcccctcgt gcgtgaaaga ataactcaac gtg tct gac aaa aag 115
 Val Ser Asp Lys Lys
 1 5

cag gat cta aca tcc tcc gca gca ggt agt gct gca ccc caa acc aag 163
 Gln Asp Leu Thr Ser Ser Ala Ala Gly Ser Ala Ala Pro Gln Thr Lys
 10 15 20

gcc tac ccc gcc atg ccc ttg cct gaa aag caa gct tgg cca gct cta 211
 Ala Tyr Pro Ala Met Pro Leu Pro Glu Lys Gln Ala Trp Pro Ala Leu
 25 30 35

att gcc ttg tgc att ggg ttt ttc atg atc ctg ttg gat caa acc atc 259
 Ile Ala Leu Cys Ile Gly Phe Phe Met Ile Leu Leu Asp Gln Thr Ile
 40 45 50

gtg gcc gtc tct acc cca gcg tta cag gca gac atg ggc gcg tcc tac 307
 Val Ala Val Ser Thr Pro Ala Leu Gln Ala Asp Met Gly Ala Ser Tyr
 55 60 65

aac gag gtc atc tgg gta acc tcg gtg tat ctc ctc act ttc gcg gtg	355
Asn Glu Val Ile Trp Val Thr Ser Val Tyr Leu Leu Thr Phe Ala Val	
70 75 80 85	
cca ctg ctt gtt act ggc cgt ttg ggc gac aag tac ggt ccg aaa aat	403
Pro Leu Leu Val Thr Gly Arg Leu Gly Asp Lys Tyr Gly Pro Lys Asn	
90 95 100	
gtc tat gtc gca ggc atg gtt atc ttc aca gtg agc tct ttg gcc tgt	451
Val Tyr Val Ala Gly Met Val Ile Phe Thr Val Ser Ser Leu Ala Cys	
105 110 115	
ggg ttg gcc cca gac atg ttc acg ttg att atc gct cgt ggc gtt caa	499
Gly Leu Ala Pro Asp Met Phe Thr Leu Ile Ile Ala Arg Gly Val Gln	
120 125 130	
ggg ttg ggc gca gcc ctt ttg act cca caa acc atg gca aca atc aac	547
Gly Leu Gly Ala Ala Leu Leu Thr Pro Gln Thr Met Ala Thr Ile Asn	
135 140 145	
cgc atc ttt gct ttt gag cgc cgc ggt gca gct ctt gga gtg tgg ggt	595
Arg Ile Phe Ala Phe Glu Arg Arg Gly Ala Ala Leu Gly Val Trp Gly	
150 155 160 165	
tct aca gct ggc ctt gca tcc cta gca gga ccg atc ctg ggt ggt gtc	643
Ser Thr Ala Gly Leu Ala Ser Leu Ala Gly Pro Ile Leu Gly Gly Val	
170 175 180	
atc acc gaa aac tgg ggt tgg caa tgg gtc ttc tac atc aac gtg ccc	691
Ile Thr Glu Asn Trp Gly Trp Gln Trp Val Phe Tyr Ile Asn Val Pro	
185 190 195	
atc ggc gtg atc tcg gtg atc gca gta atg aag tac gtt cct gaa ttc	739
Ile Gly Val Ile Ser Val Ile Ala Val Met Lys Tyr Val Pro Glu Phe	
200 205 210	
cca ccg ctg acc cga ccg ctt gat ccg ctt tct atc gtg ttg tcc atc	787
Pro Pro Leu Thr Arg Pro Leu Asp Pro Leu Ser Ile Val Leu Ser Ile	
215 220 225	
gtg gcc gtg ttc ttc ctg gtg ttt gct ttc cag gaa ggc gaa ggc gct	835
Val Ala Val Phe Phe Leu Val Phe Ala Phe Gln Glu Gly Glu Gly Ala	
230 235 240 245	
ggc tgg gcg gca tgg gtg tgg atc atg atc gta gcc gcc ttt gcg ctc	883
Gly Trp Ala Ala Trp Val Trp Ile Met Ile Val Ala Ala Phe Ala Leu	
250 255 260	
ttt gcg tgg ttt atc tac caa caa agc agg gcc gag aaa tcc gga aac	931
Phe Ala Trp Phe Ile Tyr Gln Gln Ser Arg Ala Glu Lys Ser Gly Asn	
265 270 275	
gat cct ctc gtc cca ctg gag att ttc aag ttt aga aac ttc agc ctc	979
Asp Pro Leu Val Pro Leu Glu Ile Phe Lys Phe Arg Asn Phe Ser Leu	
280 285 290	
ggc aat atc tgc atc atg gcc atg gga ttc acc gtg gct ggt act cct	1027
Gly Asn Ile Cys Ile Met Ala Met Gly Phe Thr Val Ala Gly Thr Pro	
295 300 305	
ctg ccc atc atg ttg tac ttc cag caa gca cac gga atg aac gcc atg	1075

Leu Pro Ile Met Leu Tyr Phe Gln Gln Ala His Gly Met Asn Ala Met
 310 315 320 325
 gaa gcg ggt ttc atg atg gtg cct caa gct ctc atg gca gca gta ctg 1123
 Glu Ala Gly Phe Met Met Val Pro Gln Ala Leu Met Ala Ala Val Leu
 330 335 340
 tca cca ttt gtt gga aag ctg gtt gat cga tcc aac cct gga ctc atg 1171
 Ser Pro Phe Val Gly Lys Leu Val Asp Arg Ser Asn Pro Gly Leu Met
 345 350 355
 gca gcc ctc ggt ttt agc aca gtg gct gtg tcc att gta ctg ctg tca 1219
 Ala Ala Leu Gly Phe Ser Thr Val Ala Val Ser Ile Val Leu Leu Ser
 360 365 370
 atg gta atg att ttc gat acg ggt cta gtc tgg gca ctt gtt tcg atg 1267
 Met Val Met Ile Phe Asp Thr Gly Leu Val Trp Ala Leu Val Ser Met
 375 380 385
 act ttg ctc ggc atc gga aac gcc ttt gtg tgg gca ccg aac tcg acc 1315
 Thr Leu Leu Gly Ile Gly Asn Ala Phe Val Trp Ala Pro Asn Ser Thr
 390 395 400 405
 tcc act atg cgc gac ctg cca cac aag ttc atg gga gcg ggc tct ggc 1363
 Ser Thr Met Arg Asp Leu Pro His Lys Phe Met Gly Ala Gly Ser Gly
 410 415 420
 gtg ttc aat aca acc cgc caa tta ggt tca gtc atc ggc gcc gct gcc 1411
 Val Phe Asn Thr Thr Arg Gln Leu Gly Ser Val Ile Gly Ala Ala Ala
 425 430 435
 atc ggc gcg gta atg cag att cga ctg gca gca ggc gat gag ggc gca 1459
 Ile Gly Ala Val Met Gln Ile Arg Leu Ala Ala Gly Asp Glu Gly Ala
 440 445 450
 gct ttt ggt caa gca ctt cta ctt gcc gct gcg gtg ctg gtt atc ggc 1507
 Ala Phe Gly Gln Ala Leu Leu Leu Ala Ala Val Leu Val Ile Gly
 455 460 465
 att gtg gca tca acg atg gca gga aaa aat gca cac cca gcg ccg gta 1555
 Ile Val Ala Ser Thr Met Ala Gly Lys Asn Ala His Pro Ala Pro Val
 470 475 480 485
 aag cct taaaggtcgc atgaatcctt cga 1584
 Lys Pro

<210> 238

<211> 487

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

Val Ser Asp Lys Lys Gln Asp Leu Thr Ser Ser Ala Ala Gly Ser Ala
 1 5 10 15

Ala Pro Gln Thr Lys Ala Tyr Pro Ala Met Pro Leu Pro Glu Lys Gln
 20 25 30

Ala Trp Pro Ala Leu Ile Ala Leu Cys Ile Gly Phe Phe Met Ile Leu

35					40					45						
Leu	Asp	Gln	Thr	Ile	Val	Ala	Val	Ser	Thr	Pro	Ala	Leu	Gln	Ala	Asp	
50					55					60						
Met	Gly	Ala	Ser	Tyr	Asn	Glu	Val	Ile	Trp	Val	Thr	Ser	Val	Tyr	Leu	
65					70					75					80	
Leu	Thr	Phe	Ala	Val	Pro	Leu	Leu	Val	Thr	Gly	Arg	Leu	Gly	Asp	Lys	
85					90					95						
Tyr	Gly	Pro	Lys	Asn	Val	Tyr	Val	Ala	Gly	Met	Val	Ile	Phe	Thr	Val	
100					105					110						
Ser	Ser	Leu	Ala	Cys	Gly	Leu	Ala	Pro	Asp	Met	Phe	Thr	Leu	Ile	Ile	
115					120					125						
Ala	Arg	Gly	Val	Gln	Gly	Leu	Gly	Ala	Ala	Leu	Leu	Thr	Pro	Gln	Thr	
130					135					140						
Met	Ala	Thr	Ile	Asn	Arg	Ile	Phe	Ala	Phe	Glu	Arg	Arg	Gly	Ala	Ala	
145					150					155					160	
Leu	Gly	Val	Trp	Gly	Ser	Thr	Ala	Gly	Leu	Ala	Ser	Leu	Ala	Gly	Pro	
165					170					175						
Ile	Leu	Gly	Gly	Val	Ile	Thr	Glu	Asn	Trp	Gly	Trp	Gln	Trp	Val	Phe	
180					185					190						
Tyr	Ile	Asn	Val	Pro	Ile	Gly	Val	Ile	Ser	Val	Ile	Ala	Val	Met	Lys	
195					200					205						
Tyr	Val	Pro	Glu	Phe	Pro	Leu	Thr	Arg	Pro	Leu	Asp	Pro	Leu	Ser		
210					215					220						
Ile	Val	Leu	Ser	Ile	Val	Ala	Val	Phe	Phe	Leu	Val	Phe	Ala	Phe	Gln	
225					230					235					240	
Glu	Gly	Glu	Gly	Ala	Gly	Trp	Ala	Ala	Trp	Val	Trp	Ile	Met	Ile	Val	
245					250					255						
Ala	Ala	Phe	Ala	Leu	Phe	Ala	Trp	Phe	Ile	Tyr	Gln	Gln	Ser	Arg	Ala	
260					265					270						
Glu	Lys	Ser	Gly	Asn	Asp	Pro	Leu	Val	Pro	Leu	Glu	Ile	Phe	Lys	Phe	
275					280					285						
Arg	Asn	Phe	Ser	Leu	Gly	Asn	Ile	Cys	Ile	Met	Ala	Met	Gly	Phe	Thr	
290					295					300						
Val	Ala	Gly	Thr	Pro	Leu	Pro	Ile	Met	Leu	Tyr	Phe	Gln	Gln	Ala	His	
305					310					315					320	
Gly	Met	Asn	Ala	Met	Glu	Ala	Gly	Phe	Met	Met	Val	Pro	Gln	Ala	Leu	
325					330					335						
Met	Ala	Ala	Val	Leu	Ser	Pro	Phe	Val	Gly	Lys	Leu	Val	Asp	Arg	Ser	
340					345					350						
Asn	Pro	Gly	Leu	Met	Ala	Ala	Leu	Gly	Phe	Ser	Thr	Val	Ala	Val	Ser	
355					360					365						

Ile Val Leu Leu Ser Met Val Met Ile Phe Asp Thr Gly Leu Val Trp
 370 375 380
 Ala Leu Val Ser Met Thr Leu Leu Gly Ile Gly Asn Ala Phe Val Trp
 385 390 395 400
 Ala Pro Asn Ser Thr Ser Thr Met Arg Asp Leu Pro His Lys Phe Met
 405 410 415
 Gly Ala Gly Ser Gly Val Phe Asn Thr Thr Arg Gln Leu Gly Ser Val
 420 425 430
 Ile Gly Ala Ala Ala Ile Gly Ala Val Met Gln Ile Arg Leu Ala Ala
 435 440 445
 Gly Asp Glu Gly Ala Ala Phe Gly Gln Ala Leu Leu Leu Ala Ala Ala
 450 455 460
 Val Leu Val Ile Gly Ile Val Ala Ser Thr Met Ala Gly Lys Asn Ala
 465 470 475 480
 His Pro Ala Pro Val Lys Pro
 485

<210> 239
 <211> 1455
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1432)
 <223> RXN03064

<400> 239
 tggagccttg tcttcctcca gcaatccac aacggagcag gttgggatcc cgagaaatgt 60
 tgatcatcatc ttggctgtat tagttttttac agcctttgtc atg atg ttg aat gag 115
 Met Met Leu Asn Glu
 1 5
 act act ctg gca gtc gcg ttg ccg tgc atc atg gcg gac ttt gac att 163
 Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met Ala Asp Phe Asp Ile
 10 15 20
 gag gcg aat act gcg cag tgg ttg ctc act ggt ttt atg ttg acc atg 211
 Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly Phe Met Leu Thr Met
 25 30 35
 gct gtg gtt ctt cca gct act ggt tgg atg ttg gaa cgt ttt acc act 259
 Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu Glu Arg Phe Thr Thr
 40 45 50
 cgt agt gtg ttt att ttc gcc acg gtg gtc ttc ctg atc ggt act gtg 307
 Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe Leu Ile Gly Thr Val
 55 60 65
 acg gct gcg ttg tct cct act ttt gcg att atg ctt gca gcc cgc gtc 355
 Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met Leu Ala Ala Arg Val

70	75	80	85	
gct cag gcg att ggt acc gct gtg atc atg ccg ctg ctg atg act gtc				403
Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro Leu Leu Met Thr Val	90	95	100	
gcg atg acc gtt gtt cct cca gag cgc cgt ggc gcc gtc atg ggt ttg				451
Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly Ala Val Met Gly Leu	105	110	115	
att gcg gtc gtg atg gcc gtt ggt cct gct ctt gga cct agt gtg gct				499
Ile Ala Val Val Met Ala Val Gly Pro Ala Leu Gly Pro Ser Val Ala	120	125	130	
ggg ttc gta ctc agc ttg tct tcg tgg cac gcg att ttc tgg gtc atg				547
Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala Ile Phe Trp Val Met	135	140	145	
gtt ccg ttg gtg ttt gtg gca agc ctg atc ggt acc ctg cgt ctg acc				595
Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly Thr Leu Arg Leu Thr	150	155	160	165
aac gtc agt gag cct aaa aag act cct ttg gat gtt att tcc ttc ctg				643
Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp Val Ile Ser Phe Leu	170	175	180	
att tcc gca gtg gct ttc ggt ggc ctt gtg tac gcc ttg agc tcg att				691
Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr Ala Leu Ser Ser Ile	185	190	195	
ggc atc att ttg gaa ggt gac aga agc gct ttg gtc gtg ttg gct gtc				739
Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu Val Val Leu Ala Val	200	205	210	
ggc atc att gcg ttg gtg gtg ttt gtg tgg cgc cag att gcc atg ggt				787
Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg Gln Ile Ala Met Gly	215	220	225	
aag cag gat aag gcg ctg ttg gat ctg cgt ccg ttg gcg att cgt gag				835
Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro Leu Ala Ile Arg Glu	230	235	240	245
tac acc att ccg ctg gtt gtg ctt ttg acg ctg ttc ggt gcg ctg ctc				883
Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu Phe Gly Ala Leu Leu	250	255	260	
ggg gtc atg aat aca ctg ccg ctc tac ctg cag gga tcc ttg atg gtc				931
Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln Gly Ser Leu Met Val	265	270	275	
acc gcc ttg gtc gcg ggt cta gtg ctg ttg cca ggt ggt ctt ttg gaa				979
Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro Gly Gly Leu Leu Glu	280	285	290	
ggg gtg ctg tcg cca ttt gtg ggt cga att tat gat cgt cat ggt cca				1027
Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr Asp Arg His Gly Pro	295	300	305	
cgc gga ctc gtg atc ggc ggt atg tca ctc gtt gtg atc tcc ctg ttt				1075
Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val Val Ile Ser Leu Phe	310	315	320	325

gca ctg tcc acc gtc gat gag ttc gcc aac gtg tgg ttc atc atc ggc 1123
 Ala Leu Ser Thr Val Asp Glu Phe Ala Asn Val Trp Phe Ile Ile Gly
 330 335 340

gta cac atc gtg ttc tcc atc ggc ctt gcg ctg ctg ttc acc cca ctg 1171
 Val His Ile Val Phe Ser Ile Gly Leu Ala Leu Leu Phe Thr Pro Leu
 345 350 355

atg aca gtc gcg ctc gca tcc gtc ccc gac aac atg tac ggc cac ggc 1219
 Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn Met Tyr Gly His Gly
 360 365 370

tcc gcg atc ctc aac acc ctc caa cag ctc gcc ggc gcc gca ggc acc 1267
 Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala Gly Ala Ala Gly Thr
 375 380 385

gcg gtc atg att gcg gtt tat tcc acc gtc agc aac aac gcg ctt atc 1315
 Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser Asn Asn Ala Leu Ile
 390 395 400 405

gac ggc gca acc caa caa acc gcc ctc gcc gac ggc gcc aac tct gca 1363
 Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp Gly Ala Asn Ser Ala
 410 415 420

ttc ttc gcc tca gcg tgc gtg gca gtg ttt gca ctg atc gtg ggc ttc 1411
 Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala Leu Ile Val Gly Phe
 425 430 435

ttt gta aag agg cca gcc cgc taagctaggt cgc atgatca gca 1455
 Phe Val Lys Arg Pro Ala Arg
 440

<210> 240

<211> 444

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Met Met Leu Asn Glu Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met
 1 5 10 15

Ala Asp Phe Asp Ile Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly
 20 25 30

Phe Met Leu Thr Met Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu
 35 40 45

Glu Arg Phe Thr Thr Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe
 50 55 60

Leu Ile Gly Thr Val Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met
 65 70 75 80

Leu Ala Ala Arg Val Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro
 85 90 95

Leu Leu Met Thr Val Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly
 100 105 110

Ala Val Met Gly Leu Ile Ala Val Val Met Ala Val Gly Pro Ala Leu
 115 120 125
 Gly Pro Ser Val Ala Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala
 130 135 140
 Ile Phe Trp Val Met Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly
 145 150 155 160
 Thr Leu Arg Leu Thr Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp
 165 170 175
 Val Ile Ser Phe Leu Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr
 180 185 190
 Ala Leu Ser Ser Ile Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu
 195 200 205
 Val Val Leu Ala Val Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg
 210 215 220
 Gln Ile Ala Met Gly Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro
 225 230 235 240
 Leu Ala Ile Arg Glu Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu
 245 250 255
 Phe Gly Ala Leu Leu Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln
 260 265 270
 Gly Ser Leu Met Val Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro
 275 280 285
 Gly Gly Leu Leu Glu Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr
 290 295 300
 Asp Arg His Gly Pro Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val
 305 310 315 320
 Val Ile Ser Leu Phe Ala Leu Ser Thr Val Asp Glu Phe Ala Asn Val
 325 330 335
 Trp Phe Ile Ile Gly Val His Ile Val Phe Ser Ile Gly Leu Ala Leu
 340 345 350
 Leu Phe Thr Pro Leu Met Thr Val Ala Leu Ala Ser Val Pro Asp Asn
 355 360 365
 Met Tyr Gly His Gly Ser Ala Ile Leu Asn Thr Leu Gln Gln Leu Ala
 370 375 380
 Gly Ala Ala Gly Thr Ala Val Met Ile Ala Val Tyr Ser Thr Val Ser
 385 390 395 400
 Asn Asn Ala Leu Ile Asp Gly Ala Thr Gln Gln Thr Ala Leu Ala Asp
 405 410 415
 Gly Ala Asn Ser Ala Phe Phe Ala Ser Ala Cys Val Ala Val Phe Ala
 420 425 430
 Leu Ile Val Gly Phe Phe Val Lys Arg Pro Ala Arg

435

440

<210> 241
 <211> 1093
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1093)
 <223> FRXA00565

<400> 241
 tggagccttg tcttcctcca gcaatcccac aacggagcag gttgggatcc cgagaaatgt 60
 tgatcatcatc ttggctgtat tagttttttac agcctttgtc atg atg ttg aat gag 115
 Met Met Leu Asn Glu
 1 5
 act act ctg gca gtc gcg ttg ccg tcg atc atg gcg gac ttt gac att 163
 Thr Thr Leu Ala Val Ala Leu Pro Ser Ile Met Ala Asp Phe Asp Ile
 10 15 20
 gag gcg aat act gcg cag tgg ttg ctc act ggt ttt atg ttg acc atg 211
 Glu Ala Asn Thr Ala Gln Trp Leu Leu Thr Gly Phe Met Leu Thr Met
 25 30 35
 gct gtg gtt ctt cca gct act ggt tgg atg ttg gaa cgt ttt acc act 259
 Ala Val Val Leu Pro Ala Thr Gly Trp Met Leu Glu Arg Phe Thr Thr
 40 45 50
 cgt agt gtg ttt att ttc gcc acg gtg gtc ttc ctg atc ggt act gtg 307
 Arg Ser Val Phe Ile Phe Ala Thr Val Val Phe Leu Ile Gly Thr Val
 55 60 65
 acg gct gcg ttg tct cct act ttt gcg att atg ctt gca gcc cgc gtc 355
 Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met Leu Ala Ala Arg Val
 70 75 80 85
 gct cag gcg att ggt acc gct gtg atc atg ccg ctg ctg atg act gtc 403
 Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro Leu Leu Met Thr Val
 90 95 100
 gcg atg acc gtt gtt cct cca gag cgc cgt ggc gcc gtc atg ggt ttg 451
 Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly Ala Val Met Gly Leu
 105 110 115
 att gcg gtc gtg atg gcc gtt ggt cct gct ctt gga cct agt gtg gct 499
 Ile Ala Val Val Met Ala Val Gly Pro Ala Leu Gly Pro Ser Val Ala
 120 125 130
 ggt ttc gta ctc agc ttg tct tcg tgg cac gcg att ttc tgg gtc atg 547
 Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala Ile Phe Trp Val Met
 135 140 145
 gtt ccg ttg gtg ttt gtg gca agc ctg atc ggt acc ctg cgt ctg acc 595
 Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly Thr Leu Arg Leu Thr
 150 155 160 165
 aac gtc agt gag cct aaa aag act cct ttg gat gtt att tcc ttc ctg 643

Asn	Val	Ser	Glu	Pro	Lys	Lys	Thr	Pro	Leu	Asp	Val	Ile	Ser	Phe	Leu		
				170					175					180			
att	tcc	gca	gtg	gct	ttc	ggc	ggc	ctt	gtg	tac	gcc	ttg	agc	tcg	att	691	
Ile	Ser	Ala	Val	Ala	Phe	Gly	Gly	Leu	Val	Tyr	Ala	Leu	Ser	Ser	Ile		
			185					190					195				
ggc	atc	att	ttg	gaa	ggc	gac	aga	agc	gct	ttg	gtc	gtg	ttg	gct	gtc	739	
Gly	Ile	Ile	Leu	Glu	Gly	Asp	Arg	Ser	Ala	Leu	Val	Val	Leu	Ala	Val		
		200					205					210					
ggc	atc	att	gcg	ttg	gtg	gtg	ttt	gtg	tgg	cgc	cag	att	gcc	atg	ggc	787	
Gly	Ile	Ile	Ala	Leu	Val	Val	Phe	Val	Trp	Arg	Gln	Ile	Ala	Met	Gly		
	215					220					225						
aag	cag	gat	aag	gcg	ctg	ttg	gat	ctg	cgt	ccg	ttg	gcg	att	cgt	gag	835	
Lys	Gln	Asp	Lys	Ala	Leu	Leu	Asp	Leu	Arg	Pro	Leu	Ala	Ile	Arg	Glu		
230					235				240						245		
tac	acc	att	ccg	ctg	ggt	gtg	ctt	ttg	acg	ctg	ttc	ggc	gcg	ctg	ctc	883	
Tyr	Thr	Ile	Pro	Leu	Val	Val	Leu	Leu	Thr	Leu	Phe	Gly	Ala	Leu	Leu		
				250					255					260			
ggc	gtc	atg	aat	aca	ctg	ccg	ctc	tac	ctg	cag	gga	tcc	ttg	atg	gtc	931	
Gly	Val	Met	Asn	Thr	Leu	Pro	Leu	Tyr	Leu	Gln	Gly	Ser	Leu	Met	Val		
			265					270					275				
acc	gcc	ttg	gtc	gcg	ggc	cta	gtg	ctg	ttg	cca	ggc	ggc	ctt	ttg	gaa	979	
Thr	Ala	Leu	Val	Ala	Gly	Leu	Val	Leu	Leu	Pro	Gly	Gly	Leu	Leu	Glu		
		280					285					290					
ggc	gtg	ctg	tcg	cca	ttt	gtg	ggc	cga	att	tat	gat	cgt	cat	ggc	cca	1027	
Gly	Val	Leu	Ser	Pro	Phe	Val	Gly	Arg	Ile	Tyr	Asp	Arg	His	Gly	Pro		
	295					300					305						
cgc	gga	ctc	gtg	atc	ggc	ggc	atg	tca	ctc	gtt	gtg	atc	tcc	ctg	ttt	1075	
Arg	Gly	Leu	Val	Ile	Gly	Gly	Met	Ser	Leu	Val	Val	Ile	Ser	Leu	Phe		
310					315					320					325		
gca	ctg	tcc	acc	gtc	gat											1093	
Ala	Leu	Ser	Thr	Val	Asp												
				330													

<210> 242

<211> 331

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Met	Met	Leu	Asn	Glu	Thr	Thr	Leu	Ala	Val	Ala	Leu	Pro	Ser	Ile	Met
1				5					10					15	

Ala	Asp	Phe	Asp	Ile	Glu	Ala	Asn	Thr	Ala	Gln	Trp	Leu	Leu	Thr	Gly
			20					25					30		

Phe	Met	Leu	Thr	Met	Ala	Val	Val	Leu	Pro	Ala	Thr	Gly	Trp	Met	Leu
		35					40					45			

Glu	Arg	Phe	Thr	Thr	Arg	Ser	Val	Phe	Ile	Phe	Ala	Thr	Val	Val	Phe
	50					55					60				

Leu Ile Gly Thr Val Thr Ala Ala Leu Ser Pro Thr Phe Ala Ile Met
 65 70 75 80
 Leu Ala Ala Arg Val Ala Gln Ala Ile Gly Thr Ala Val Ile Met Pro
 85 90 95
 Leu Leu Met Thr Val Ala Met Thr Val Val Pro Pro Glu Arg Arg Gly
 100 105 110
 Ala Val Met Gly Leu Ile Ala Val Val Met Ala Val Gly Pro Ala Leu
 115 120 125
 Gly Pro Ser Val Ala Gly Phe Val Leu Ser Leu Ser Ser Trp His Ala
 130 135 140
 Ile Phe Trp Val Met Val Pro Leu Val Phe Val Ala Ser Leu Ile Gly
 145 150 155 160
 Thr Leu Arg Leu Thr Asn Val Ser Glu Pro Lys Lys Thr Pro Leu Asp
 165 170 175
 Val Ile Ser Phe Leu Ile Ser Ala Val Ala Phe Gly Gly Leu Val Tyr
 180 185 190
 Ala Leu Ser Ser Ile Gly Ile Ile Leu Glu Gly Asp Arg Ser Ala Leu
 195 200 205
 Val Val Leu Ala Val Gly Ile Ile Ala Leu Val Val Phe Val Trp Arg
 210 215 220
 Gln Ile Ala Met Gly Lys Gln Asp Lys Ala Leu Leu Asp Leu Arg Pro
 225 230 235 240
 Leu Ala Ile Arg Glu Tyr Thr Ile Pro Leu Val Val Leu Leu Thr Leu
 245 250 255
 Phe Gly Ala Leu Leu Gly Val Met Asn Thr Leu Pro Leu Tyr Leu Gln
 260 265 270
 Gly Ser Leu Met Val Thr Ala Leu Val Ala Gly Leu Val Leu Leu Pro
 275 280 285
 Gly Gly Leu Leu Glu Gly Val Leu Ser Pro Phe Val Gly Arg Ile Tyr
 290 295 300
 Asp Arg His Gly Pro Arg Gly Leu Val Ile Gly Gly Met Ser Leu Val
 305 310 315 320
 Val Ile Ser Leu Phe Ala Leu Ser Thr Val Asp
 325 330

<210> 243

<211> 380

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(357)

<223> FRXA02878

<400> 243

tgc	ctg	tcc	acc	gtc	gat	gag	ttc	gcc	acg	tgt	tgg	tca	tca	ttc	gcg	48
Cys	Leu	Ser	Thr	Val	Asp	Glu	Phe	Ala	Thr	Cys	Trp	Ser	Ser	Phe	Ala	
1				5				10						15		
gac	aca	tcg	tgg	ttc	tca	tcg	gcc	ctt	gcg	ctg	ctg	ttc	acc	cca	ctg	96
Asp	Thr	Ser	Trp	Phe	Ser	Ser	Ala	Leu	Ala	Leu	Leu	Phe	Thr	Pro	Leu	
		20					25						30			
atg	aca	gtc	gcg	ctc	gca	tcc	gtc	ccc	gac	aac	atg	tac	ggc	cac	ggc	144
Met	Thr	Val	Ala	Leu	Ala	Ser	Val	Pro	Asp	Asn	Met	Tyr	Gly	His	Gly	
		35					40					45				
tcc	gcg	atc	ctc	aac	acc	ctc	caa	cag	ctc	gcc	ggc	gcc	gca	ggc	acc	192
Ser	Ala	Ile	Leu	Asn	Thr	Leu	Gln	Gln	Leu	Ala	Gly	Ala	Ala	Gly	Thr	
		50				55					60					
gcg	gtc	atg	att	gcg	gtt	tat	tcc	acc	gtc	agc	aac	aac	gcg	ctt	atc	240
Ala	Val	Met	Ile	Ala	Val	Tyr	Ser	Thr	Val	Ser	Asn	Asn	Ala	Leu	Ile	
65					70					75					80	
gac	ggc	gca	acc	caa	caa	acc	gcc	ctc	gcc	gac	ggc	gcc	aac	tct	gca	288
Asp	Gly	Ala	Thr	Gln	Gln	Thr	Ala	Leu	Ala	Asp	Gly	Ala	Asn	Ser	Ala	
				85				90						95		
ttc	ttc	gcc	tca	gcg	tgc	gtg	gca	gtg	ttt	gca	ctg	atc	gtg	ggc	ttc	336
Phe	Phe	Ala	Ser	Ala	Cys	Val	Ala	Val	Phe	Ala	Leu	Ile	Val	Gly	Phe	
		100					105						110			
ttt	gta	aag	agg	cca	gcc	cgc	taagctaggt	cgcatgatca	gca							380
Phe	Val	Lys	Arg	Pro	Ala	Arg										
		115														

<210> 244

<211> 119

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 244

Cys	Leu	Ser	Thr	Val	Asp	Glu	Phe	Ala	Thr	Cys	Trp	Ser	Ser	Phe	Ala
1				5					10					15	
Asp	Thr	Ser	Trp	Phe	Ser	Ser	Ala	Leu	Ala	Leu	Leu	Phe	Thr	Pro	Leu
		20						25					30		
Met	Thr	Val	Ala	Leu	Ala	Ser	Val	Pro	Asp	Asn	Met	Tyr	Gly	His	Gly
		35					40					45			
Ser	Ala	Ile	Leu	Asn	Thr	Leu	Gln	Gln	Leu	Ala	Gly	Ala	Ala	Gly	Thr
		50				55					60				
Ala	Val	Met	Ile	Ala	Val	Tyr	Ser	Thr	Val	Ser	Asn	Asn	Ala	Leu	Ile
65					70					75					80
Asp	Gly	Ala	Thr	Gln	Gln	Thr	Ala	Leu	Ala	Asp	Gly	Ala	Asn	Ser	Ala
				85				90						95	
Phe	Phe	Ala	Ser	Ala	Cys	Val	Ala	Val	Phe	Ala	Leu	Ile	Val	Gly	Phe

100	105	110	
Phe Val Lys Arg Pro Ala Arg			
115			
<210> 245			
<211> 1533			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1510)			
<223> RXA00648			
<400> 245			
gtttgccagc tattgcatct tgcacaaaat gtgtaccata cacataatgt catcgagtcc 60			
tcccgaatca gccacaccac agatcaaata cggcctgctg	gtg gtc act ctc gcc	115	
	Val Val Thr Leu Ala		
	1 5		
tca gct ggt atc act gtt tcc cta gcg cag acc ctg gtt att ccg atc	163		
Ser Ala Gly Ile Thr Val Ser Leu Ala Gln Thr Leu Val Ile Pro Ile			
	10 15 20		
att ggt cgg ttg ccc gag atc ttc aac acc acg gct gct aat gcc tct	211		
Ile Gly Arg Leu Pro Glu Ile Phe Asn Thr Thr Ala Ala Asn Ala Ser			
	25 30 35		
tgg atc att act gtg acg ctg ttg gtg ggc gca gtg gcg act cct gtg	259		
Trp Ile Ile Thr Val Thr Leu Leu Val Gly Ala Val Ala Thr Pro Val			
	40 45 50		
atg ggc agg ctt gca gat atg tac ggc aag aaa aag atg atg ctc atc	307		
Met Gly Arg Leu Ala Asp Met Tyr Gly Lys Lys Lys Met Met Leu Ile			
	55 60 65		
tca ctt gtc ccg ttc att ctt gga tca gtg atc tgc gct gtg tcg gtg	355		
Ser Leu Val Pro Phe Ile Leu Gly Ser Val Ile Cys Ala Val Ser Val			
	70 75 80 85		
gat ttg att ccg atg atc atc ggc cgt ggt ttt cag ggg ctt ggc tct	403		
Asp Leu Ile Pro Met Ile Ile Gly Arg Gly Phe Gln Gly Leu Gly Ser			
	90 95 100		
ggc ctg att cct ctt ggc att tct ctc atg cat gat ttg ttg ccc cgg	451		
Gly Leu Ile Pro Leu Gly Ile Ser Leu Met His Asp Leu Leu Pro Arg			
	105 110 115		
gag aaa gca ggg tct gcc att gct ttg atg agt tct tcc atg ggc att	499		
Glu Lys Ala Gly Ser Ala Ile Ala Leu Met Ser Ser Ser Met Gly Ile			
	120 125 130		
ggc ggt gca ctc ggt cta ccg ctg gct gct gct att gcc cag ttt gcg	547		
Gly Gly Ala Leu Gly Leu Pro Leu Ala Ala Ala Ile Ala Gln Phe Ala			
	135 140 145		
tcc tgg cgg gtg ctg ttc tgg ttc acc gct ctg gta gcg ctt aca gtt	595		
Ser Trp Arg Val Leu Phe Trp Phe Thr Ala Leu Val Ala Leu Thr Val			

150	155	160	165	
ggc gcg gtc att tgg aag gcg att cct gct aga ccc agg atc gtg agg				643
Gly Ala Val Ile Trp Lys Ala Ile Pro Ala Arg Pro Arg Ile Val Arg	170	175	180	
agt ggc ggc ttt gat tat ttc ggt gct ctc ggc ctt gca atg gga ctt				691
Ser Gly Gly Phe Asp Tyr Phe Gly Ala Leu Gly Leu Ala Met Gly Leu	185	190	195	
atc gca ttg ttg ctc gcg gtg tcc aag gga tca gaa tgg ggc tgg aga				739
Ile Ala Leu Leu Leu Ala Val Ser Lys Gly Ser Glu Trp Gly Trp Arg	200	205	210	
agt gcc ctg acc att ggg tta ttc gtg gca gcg ctg gtg att ttg gtg				787
Ser Ala Leu Thr Ile Gly Leu Phe Val Ala Ala Leu Val Ile Leu Val	215	220	225	
ggt tgg ggc tgg ttc gaa acc cgc cag aaa tcc cct ttg att gat ctg				835
Gly Trp Gly Trp Phe Glu Thr Arg Gln Lys Ser Pro Leu Ile Asp Leu	230	235	240	245
cgc acc act att cgg gcg acc gtg ttg atg aca aat att gcg tcc atc				883
Arg Thr Thr Ile Arg Ala Thr Val Leu Met Thr Asn Ile Ala Ser Ile	250	255	260	
ctc atc ggt ttc acc atg tat gga atg aat ctg atc ctg cct cag gtc				931
Leu Ile Gly Phe Thr Met Tyr Gly Met Asn Leu Ile Leu Pro Gln Val	265	270	275	
atg cag ctg cct gta att ctg ggc tac ggt cta ggc cag agc atg ctt				979
Met Gln Leu Pro Val Ile Leu Gly Tyr Gly Leu Gly Gln Ser Met Leu	280	285	290	
cag atg ggc atc tgg ctg atc ccg atg ggt cta ggc atg atg ttg att				1027
Gln Met Gly Ile Trp Leu Ile Pro Met Gly Leu Gly Met Met Leu Ile	295	300	305	
tcg aat gca ggt gca gcc att agc gct gct cat ggt cct cgt gtg acg				1075
Ser Asn Ala Gly Ala Ala Ile Ser Ala Ala His Gly Pro Arg Val Thr	310	315	320	325
ctg aca att gcg ggt gtt gtg atc gca gtc ggt tat gca ctt act gcc				1123
Leu Thr Ile Ala Gly Val Val Ile Ala Val Gly Tyr Ala Leu Thr Ala	330	335	340	
aca gtg ttg ttc act atc ggc aac cgc aca ccg gga gga gat gca gac				1171
Thr Val Leu Phe Thr Ile Gly Asn Arg Thr Pro Gly Gly Asp Ala Asp	345	350	355	
aac gca ctt att ttg acc acc ctg gtg ctg ttc tca gtg tgt agt ctc				1219
Asn Ala Leu Ile Leu Thr Thr Leu Val Leu Phe Ser Val Cys Ser Leu	360	365	370	
gtg gtc ggt atc ggc att ggc ctg gca ttt ggt tcc atg cct gcc ttg				1267
Val Val Gly Ile Gly Ile Gly Leu Ala Phe Gly Ser Met Pro Ala Leu	375	380	385	
atc atg ggt gcc gta cca gcc acg gag aaa gcc gca gcg aat ggt ttc				1315
Ile Met Gly Ala Val Pro Ala Thr Glu Lys Ala Ala Ala Asn Gly Phe	390	395	400	405

```

aac tct ctt atg cgt tca ctg ggc acc acc ggc tca tca gct gtc atc 1363
Asn Ser Leu Met Arg Ser Leu Gly Thr Thr Gly Ser Ser Ala Val Ile
      410                      415                      420

ggt gca gtg ttg gcc gga atg atg agt ggc gga gta ccc acc tta ggg 1411
Gly Ala Val Leu Ala Gly Met Met Ser Gly Gly Val Pro Thr Leu Gly
      425                      430                      435

gga ttc atg acc act ctg atc atc gga tgc tgc gcc gcg ctt gtg gct 1459
Gly Phe Met Thr Thr Leu Ile Ile Gly Cys Cys Ala Ala Leu Val Ala
      440                      445                      450

gcg gtc atc tcc tat ttc atc ccc acc aca acc act gtg gtg gaa gca 1507
Ala Val Ile Ser Tyr Phe Ile Pro Thr Thr Thr Thr Val Val Glu Ala
      455                      460                      465

aaa taatccccggc agcgactcga cca 1533
Lys
470

```

```

<210> 246
<211> 470
<212> PRT
<213> Corynebacterium glutamicum

```

```

<400> 246
Val Val Thr Leu Ala Ser Ala Gly Ile Thr Val Ser Leu Ala Gln Thr
  1              5              10              15

Leu Val Ile Pro Ile Ile Gly Arg Leu Pro Glu Ile Phe Asn Thr Thr
      20              25              30

Ala Ala Asn Ala Ser Trp Ile Ile Thr Val Thr Leu Leu Val Gly Ala
      35              40              45

Val Ala Thr Pro Val Met Gly Arg Leu Ala Asp Met Tyr Gly Lys Lys
      50              55              60

Lys Met Met Leu Ile Ser Leu Val Pro Phe Ile Leu Gly Ser Val Ile
      65              70              75              80

Cys Ala Val Ser Val Asp Leu Ile Pro Met Ile Ile Gly Arg Gly Phe
      85              90              95

Gln Gly Leu Gly Ser Gly Leu Ile Pro Leu Gly Ile Ser Leu Met His
      100              105              110

Asp Leu Leu Pro Arg Glu Lys Ala Gly Ser Ala Ile Ala Leu Met Ser
      115              120              125

Ser Ser Met Gly Ile Gly Gly Ala Leu Gly Leu Pro Leu Ala Ala Ala
      130              135              140

Ile Ala Gln Phe Ala Ser Trp Arg Val Leu Phe Trp Phe Thr Ala Leu
      145              150              155              160

Val Ala Leu Thr Val Gly Ala Val Ile Trp Lys Ala Ile Pro Ala Arg
      165              170              175

```

Pro Arg Ile Val Arg Ser Gly Gly Phe Asp Tyr Phe Gly Ala Leu Gly
 180 185 190
 Leu Ala Met Gly Leu Ile Ala Leu Leu Leu Ala Val Ser Lys Gly Ser
 195 200 205
 Glu Trp Gly Trp Arg Ser Ala Leu Thr Ile Gly Leu Phe Val Ala Ala
 210 215 220
 Leu Val Ile Leu Val Gly Trp Gly Trp Phe Glu Thr Arg Gln Lys Ser
 225 230 235 240
 Pro Leu Ile Asp Leu Arg Thr Thr Ile Arg Ala Thr Val Leu Met Thr
 245 250 255
 Asn Ile Ala Ser Ile Leu Ile Gly Phe Thr Met Tyr Gly Met Asn Leu
 260 265 270
 Ile Leu Pro Gln Val Met Gln Leu Pro Val Ile Leu Gly Tyr Gly Leu
 275 280 285
 Gly Gln Ser Met Leu Gln Met Gly Ile Trp Leu Ile Pro Met Gly Leu
 290 295 300
 Gly Met Met Leu Ile Ser Asn Ala Gly Ala Ala Ile Ser Ala Ala His
 305 310 315 320
 Gly Pro Arg Val Thr Leu Thr Ile Ala Gly Val Val Ile Ala Val Gly
 325 330 335
 Tyr Ala Leu Thr Ala Thr Val Leu Phe Thr Ile Gly Asn Arg Thr Pro
 340 345 350
 Gly Gly Asp Ala Asp Asn Ala Leu Ile Leu Thr Thr Leu Val Leu Phe
 355 360 365
 Ser Val Cys Ser Leu Val Val Gly Ile Gly Ile Gly Leu Ala Phe Gly
 370 375 380
 Ser Met Pro Ala Leu Ile Met Gly Ala Val Pro Ala Thr Glu Lys Ala
 385 390 395 400
 Ala Ala Asn Gly Phe Asn Ser Leu Met Arg Ser Leu Gly Thr Thr Gly
 405 410 415
 Ser Ser Ala Val Ile Gly Ala Val Leu Ala Gly Met Met Ser Gly Gly
 420 425 430
 Val Pro Thr Leu Gly Gly Phe Met Thr Thr Leu Ile Ile Gly Cys Cys
 435 440 445
 Ala Ala Leu Val Ala Ala Val Ile Ser Tyr Phe Ile Pro Thr Thr Thr
 450 455 460
 Thr Val Val Glu Ala Lys
 465 470

<210> 247

<211> 1770

<212> DNA

gga ctg tcc tcc atc ctt ggc cca ttg ctt ggt ggc tgg ttc act gac 691
Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Asp
185 190 195

ggt cca ggc tgg cgt tgg ggt ctg tgg ttg aac gtt cca atc ggc atc	739
Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn Val Pro Ile Gly Ile	
200 205 210	
atc gca ctg gtt gct atc gct gtg ctg ctg aaa ctt cca gct cgt gaa	787
Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys Leu Pro Ala Arg Glu	
215 220 225	
cgt ggc aag gtc tcc gtt gac tgg ttg gga agc atc ttc atg gct atc	835
Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser Ile Phe Met Ala Ile	
230 235 240 245	
gcc acc acc gca ttt gtc ctc gca gtg acc tgg ggt ggc aat gaa tat	883
Ala Thr Thr Ala Phe Val Leu Ala Val Thr Trp Gly Gly Asn Glu Tyr	
250 255 260	
gag tgg gca tca cca atg atc atc ggt ttg ttc atc acg aca ttg gtc	931
Glu Trp Ala Ser Pro Met Ile Ile Gly Leu Phe Ile Thr Thr Leu Val	
265 270 275	
gct gcg ata gtg ttc gtt ttc gtc gaa aag cgt gct gtt gac cca ctg	979
Ala Ala Ile Val Phe Val Phe Val Glu Lys Arg Ala Val Asp Pro Leu	
280 285 290	
gtc ccc atg ggc ctt ttc tcg aac cgc aac ttc gtg ctc acc gcc gtc	1027
Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe Val Leu Thr Ala Val	
295 300 305	
gcc ggt atc ggc gta ggc ctg ttt atg atg ggc acc atc gcg tac atg	1075
Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly Thr Ile Ala Tyr Met	
310 315 320 325	
cct acc tac ctg cag atg gtt cat ggt ctg aac cca acg caa gct ggt	1123
Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn Pro Thr Gln Ala Gly	
330 335 340	
ctg atg ctg atc cca atg atg atc ggc ctg att ggt aca tcc act gtg	1171
Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly Thr Ser Thr Val	
345 350 355	
gtg ggc aac atc gtg tcc aag act ggc aag tac aag tgg tac cca ttc	1219
Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys Trp Tyr Pro Phe	
360 365 370	
atc ggc atg ctc atc atg gtc ctt gcc cta gta ctg cta tcg acg ctg	1267
Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu Leu Ser Thr Leu	
375 380 385	
aca cct tcg gca agc ttg gct ctc att gga ctg tac ttc ttc gtc ttc	1315
Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr Phe Phe Val Phe	
390 395 400 405	
gga ttc ggc ctg ggc tgt gca atg cag att ttg gtt ctc atc gtg cag	1363
Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val Leu Ile Val Gln	
410 415 420	
aac tcc ttc cca atc acc atg gtt ggc acc gcg acc ggt tcc aac aac	1411
Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala Thr Gly Ser Asn Asn	
425 430 435	

ttc ttc cgc caa atc ggt gga gca gta ggt tcc gca ctg atc ggt ggc 1459
 Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala Leu Ile Gly Gly
 440 445 450
 ctg ttt atc tcc aac ctg tcc gac cga ttc acc gaa aac gtc ccc gca 1507
 Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu Asn Val Pro Ala
 455 460 465
 gca gtg gct tcc atg ggt gaa gaa ggc gca caa tac gcc tca gca atg 1555
 Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr Ala Ser Ala Met
 470 475 480 485
 tcc gat ttc tcc ggt gca tcc aac ctc act cca cac ctt gtt gaa tca 1603
 Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His Leu Val Glu Ser
 490 495 500
 ctt cca caa gca ctc cgt gaa gca att caa ctt tct tac aac gac gcc 1651
 Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu Ser Tyr Asn Asp Ala
 505 510 515
 ctg aca cca atc ttc ttg gcg ctc acc ccg atc gca gta gtc gcc gcg 1699
 Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala Val Val Ala Ala
 520 525 530
 atc ctc ctc ttt ttc atc cgt gaa gat cac ctc aag gaa acg cac gaa 1747
 Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu Lys Glu Thr His Glu
 535 540 545
 taatgacaca cgaaacttcc gtc 1770

<210> 248

<211> 549

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

Met Thr Ser Gln Val Lys Pro Asp Asp Glu Arg Pro Val Thr Thr Ile
 1 5 10 15
 Ser Lys Ser Gly Ala Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala
 20 25 30
 Ala Ala Thr Glu Glu Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly
 35 40 45
 Phe Ile Ile Ala Ala Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly
 50 55 60
 Gln Thr Ile Phe Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly
 65 70 75 80
 Gly Val Asn His Met Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln
 85 90 95
 Thr Ile Ser Leu Pro Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg
 100 105 110
 Lys Tyr Leu Phe Met Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile
 115 120 125

Ile Gly Ala Leu Ala Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala
 130 135 140
 Leu Gln Gly Ile Ala Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile
 145 150 155 160
 Thr Ala Asp Val Thr Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile
 165 170 175
 Met Gly Ser Val Phe Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly
 180 185 190
 Gly Trp Phe Thr Asp Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn
 195 200 205
 Val Pro Ile Gly Ile Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys
 210 215 220
 Leu Pro Ala Arg Glu Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser
 225 230 235 240
 Ile Phe Met Ala Ile Ala Thr Thr Ala Phe Val Leu Ala Val Thr Trp
 245 250 255
 Gly Gly Asn Glu Tyr Glu Trp Ala Ser Pro Met Ile Ile Gly Leu Phe
 260 265 270
 Ile Thr Thr Leu Val Ala Ala Ile Val Phe Val Phe Val Glu Lys Arg
 275 280 285
 Ala Val Asp Pro Leu Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe
 290 295 300
 Val Leu Thr Ala Val Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly
 305 310 315 320
 Thr Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn
 325 330 335
 Pro Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile
 340 345 350
 Gly Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr
 355 360 365
 Lys Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val
 370 375 380
 Leu Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu
 385 390 395 400
 Tyr Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu
 405 410 415
 Val Leu Ile Val Gln Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala
 420 425 430
 Thr Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser
 435 440 445
 Ala Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr

450	455	460
Glu Asn Val Pro Ala	Ala Val Ala Ser Met Gly	Glu Glu Gly Ala Gln
465	470	475 480
Tyr Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro	485 490	495
His Leu Val Glu Ser Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu	500 505	510
Ser Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile	515 520	525
Ala Val Val Ala Ala Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu	530 535	540
Lys Glu Thr His Glu		
545		

<210> 249
 <211> 841
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(841)
 <223> FRXA01314

<400> 249
 gtgaatggca cgacatgccca caaggcacgc aagctgattt ccaagcctgc tgtcgcaaag 60
 caattaaaaa tacttttctt cttagagggtg gattttcaga atg aca tca cag gtc 115
 Met Thr Ser Gln Val
 1 5
 aag ccg gac gac gaa cgt ccg gta aca aca att tca aaa agt ggt gca 163
 Lys Pro Asp Asp Glu Arg Pro Val Thr Thr Ile Ser Lys Ser Gly Ala
 10 15 20
 cct tcg gcc cac acc tca gca cca tat ggt gca gca gca act gaa gaa 211
 Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala Ala Ala Thr Glu Glu
 25 30 35
 gct gtc gag gaa aaa acc aaa ggt cgc gtt gga ttt atc atc gca gcc 259
 Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly Phe Ile Ile Ala Ala
 40 45 50
 ctc atg ttg gcg atg ctt ctt agc tcc ttg ggt cag acc att ttc ggt 307
 Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly Gln Thr Ile Phe Gly
 55 60 65
 tct gcc ctg cca acg att gtt ggt gag ctt ggc ggc gtt aac cac atg 355
 Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asn His Met
 70 75 80 85
 acc tgg gtg att acc gcc ttc ctc ttg ggc cag acc att tca ttg cct 403
 Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln Thr Ile Ser Leu Pro
 90 95 100

att ttc ggc aag ttg ggt gac cag ttt ggt cgc aaa tac ctc ttc atg 451
 Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg Lys Tyr Leu Phe Met
 105 110 115

ttt gcc atc gca ctg ttc gtg gtg ggt tcc atc atc ggt gct ttg gct 499
 Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile Ile Gly Ala Leu Ala
 120 125 130

cag aac atg acc acc ttg att gtg gct cgt gca ctg cag ggt atc gcc 547
 Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala Leu Gln Gly Ile Ala
 135 140 145

ggt ggt ggc ttg atg att ctt tct cag gca att acc gct gat gtc acc 595
 Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Thr Ala Asp Val Thr
 150 155 160 165

acc gcc cgt gag cgt gca aag tac atg ggc atc atg ggt tcc gtt ttc 643
 Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile Met Gly Ser Val Phe
 170 175 180

gga ctg tcc tcc atc ctt ggc cca ttg ctt ggt ggc tgg ttc act gac 691
 Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Asp
 185 190 195

ggt cca ggc tgg cgt tgg ggt ctg tgg ttg aac gtt cca atc ggc atc 739
 Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn Val Pro Ile Gly Ile
 200 205 210

atc gca ctg gtt gct atc gct gtg ctg ctg aaa ctt cca gct cgt gaa 787
 Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys Leu Pro Ala Arg Glu
 215 220 225

cgt ggc aag gtc tcc gtt gac tgg ttg gga agc atc ttc atg gct atc 835
 Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser Ile Phe Met Ala Ile
 230 235 240 245

gcc acc 841
 Ala Thr

<210> 250

<211> 247

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

Met Thr Ser Gln Val Lys Pro Asp Asp Glu Arg Pro Val Thr Thr Ile
 1 5 10 15

Ser Lys Ser Gly Ala Pro Ser Ala His Thr Ser Ala Pro Tyr Gly Ala
 20 25 30

Ala Ala Thr Glu Glu Ala Val Glu Glu Lys Thr Lys Gly Arg Val Gly
 35 40 45

Phe Ile Ile Ala Ala Leu Met Leu Ala Met Leu Leu Ser Ser Leu Gly
 50 55 60

Gln Thr Ile Phe Gly Ser Ala Leu Pro Thr Ile Val Gly Glu Leu Gly

65	70	75	80
Gly Val Asn His Met Thr Trp Val Ile Thr Ala Phe Leu Leu Gly Gln	85	90	95
Thr Ile Ser Leu Pro Ile Phe Gly Lys Leu Gly Asp Gln Phe Gly Arg	100	105	110
Lys Tyr Leu Phe Met Phe Ala Ile Ala Leu Phe Val Val Gly Ser Ile	115	120	125
Ile Gly Ala Leu Ala Gln Asn Met Thr Thr Leu Ile Val Ala Arg Ala	130	135	140
Leu Gln Gly Ile Ala Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile	145	150	155
Thr Ala Asp Val Thr Thr Ala Arg Glu Arg Ala Lys Tyr Met Gly Ile	165	170	175
Met Gly Ser Val Phe Gly Leu Ser Ser Ile Leu Gly Pro Leu Leu Gly	180	185	190
Gly Trp Phe Thr Asp Gly Pro Gly Trp Arg Trp Gly Leu Trp Leu Asn	195	200	205
Val Pro Ile Gly Ile Ile Ala Leu Val Ala Ile Ala Val Leu Leu Lys	210	215	220
Leu Pro Ala Arg Glu Arg Gly Lys Val Ser Val Asp Trp Leu Gly Ser	225	230	235
Ile Phe Met Ala Ile Ala Thr	245		

<210> 251
 <211> 803
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(780)
 <223> FRXA01320

<400> 251	
ggt gac cca ctg gtc ccc atg ggc ctt ttc tcg aac cgc aac ttc gtg	48
Val Asp Pro Leu Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe Val	
1 5 10 15	
ctc acc gcc gtc gcc ggt atc ggc gta ggc ctg ttt atg atg ggc acc	96
Leu Thr Ala Val Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly Thr	
20 25 30	
atc gcg tac atg cct acc tac ctg cag atg gtt cat ggt ctg aac cca	144
Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn Pro	
35 40 45	
acg caa gct ggt ctg atg ctg atc cca atg atg atc ggc ctg att ggt	192
Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly	

50	55	60	
aca tcc act gtg gtg ggc aac atc gtg tcc aag act ggc aag tac aag			240
Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys			
65	70	75	80
tgg tac cca ttc atc ggc atg ctc atc atg gtc ctt gcc cta gta ctg			288
Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu			
	85	90	95
cta tcg acg ctg aca cct tcg gca agc ttg gct ctc att gga ctg tac			336
Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr			
	100	105	110
ttc ttc gtc ttc gga ttc ggc ctg ggc tgt gca atg cag att ttg gtt			384
Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val			
	115	120	125
ctc atc gtg cag aac tcc ttc cca atc acc atg gtt ggc acc gcg acc			432
Leu Ile Val Gln Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala Thr			
	130	135	140
ggg tcc aac aac ttc ttc cgc caa atc ggt gga gca gta ggt tcc gca			480
Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala			
	145	150	160
ctg atc ggt ggc ctg ttt atc tcc aac ctg tcc gac cga ttc acc gaa			528
Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu			
	165	170	175
aac gtc ccc gca gca gtg gct tcc atg ggt gaa gaa ggc gca caa tac			576
Asn Val Pro Ala Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr			
	180	185	190
gcc tca gca atg tcc gat ttc tcc ggt gca tcc aac ctc act cca cac			624
Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His			
	195	200	205
ctt gtt gaa tca ctt cca caa gca ctc cgt gaa gca att caa ctt tct			672
Leu Val Glu Ser Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu Ser			
	210	215	220
tac aac gac gcc ctg aca cca atc ttc ttg gcg ctc acc ccg atc gca			720
Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala			
	225	230	240
gta gtc gcc gcg atc ctc ctc ttt ttc atc cgt gaa gat cac ctc aag			768
Val Val Ala Ala Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu Lys			
	245	250	255
gaa acg cac gaa taatgacaca cgaaacttcc gtc			803
Glu Thr His Glu			
	260		

<210> 252

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Val Asp Pro Leu Val Pro Met Gly Leu Phe Ser Asn Arg Asn Phe Val
 1 5 10 15
 Leu Thr Ala Val Ala Gly Ile Gly Val Gly Leu Phe Met Met Gly Thr
 20 25 30
 Ile Ala Tyr Met Pro Thr Tyr Leu Gln Met Val His Gly Leu Asn Pro
 35 40 45
 Thr Gln Ala Gly Leu Met Leu Ile Pro Met Met Ile Gly Leu Ile Gly
 50 55 60
 Thr Ser Thr Val Val Gly Asn Ile Val Ser Lys Thr Gly Lys Tyr Lys
 65 70 75 80
 Trp Tyr Pro Phe Ile Gly Met Leu Ile Met Val Leu Ala Leu Val Leu
 85 90 95
 Leu Ser Thr Leu Thr Pro Ser Ala Ser Leu Ala Leu Ile Gly Leu Tyr
 100 105 110
 Phe Phe Val Phe Gly Phe Gly Leu Gly Cys Ala Met Gln Ile Leu Val
 115 120 125
 Leu Ile Val Gln Asn Ser Phe Pro Ile Thr Met Val Gly Thr Ala Thr
 130 135 140
 Gly Ser Asn Asn Phe Phe Arg Gln Ile Gly Gly Ala Val Gly Ser Ala
 145 150 155 160
 Leu Ile Gly Gly Leu Phe Ile Ser Asn Leu Ser Asp Arg Phe Thr Glu
 165 170 175
 Asn Val Pro Ala Ala Val Ala Ser Met Gly Glu Glu Gly Ala Gln Tyr
 180 185 190
 Ala Ser Ala Met Ser Asp Phe Ser Gly Ala Ser Asn Leu Thr Pro His
 195 200 205
 Leu Val Glu Ser Leu Pro Gln Ala Leu Arg Glu Ala Ile Gln Leu Ser
 210 215 220
 Tyr Asn Asp Ala Leu Thr Pro Ile Phe Leu Ala Leu Thr Pro Ile Ala
 225 230 235 240
 Val Val Ala Ala Ile Leu Leu Phe Phe Ile Arg Glu Asp His Leu Lys
 245 250 255
 Glu Thr His Glu
 260

<210> 253

<211> 1755

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1732)

<223> RXN02926

<400> 253

```

ccctgacacc aatcttcttg gcgctcaccc cgatcgcaagt agtcgccgcg atcctcctct 60

ttttcatccg tgaagatcac ctcaaggaaa cgcacgaata atg aca cac gaa act 115
                                   Met Thr His Glu Thr
                                   1 5

tcc gtc ccc gga cct gcc gac gcg cag gtc gca gga gat acg aag ctg 163
Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala Gly Asp Thr Lys Leu
                10                15                20

cgc aaa ggc cgc gcg aag aag gaa aaa act cct tca tca atg acg cct 211
Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro Ser Ser Met Thr Pro
                25                30                35

gaa caa caa aag aaa gtc tgg tgg gtc ctc agc gcg ctg atg gtc gcc 259
Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser Ala Leu Met Val Ala
                40                45                50

atg atg atg gcc tcc ctt gac cag atg att ttc ggc aca gcc ctg cca 307
Met Met Met Ala Ser Leu Asp Gln Met Ile Phe Gly Thr Ala Leu Pro
                55                60                65

aca atc gtc ggt gaa ctc ggc ggc gtt gac cac atg atg tgg gtc atc 355
Thr Ile Val Gly Glu Leu Gly Gly Val Asp His Met Met Trp Val Ile
                70                75                80                85

acc gca tac cta ctt gcc gaa acc atc atg ctg ccg atc tac gga aag 403
Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu Pro Ile Tyr Gly Lys
                90                95                100

ctc ggc gac ctg gtt gga cgt aaa ggt ctc ttc atc gga gcc ctc ggc 451
Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe Ile Gly Ala Leu Gly
                105                110                115

atc ttc ctg atc ggc tcc gtc atc ggc ggg ctt gca gga aat atg acc 499
Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu Ala Gly Asn Met Thr
                120                125                130

tgg ttg atc gtc ggc cgt gcc gta cag ggc atc ggt ggc ggt gga ctg 547
Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile Gly Gly Gly Gly Leu
                135                140                145

atg atc ctc tcg cag gca atc atc gcg gac gtt gtt cca gca cgt gaa 595
Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val Val Pro Ala Arg Glu
                150                155                160                165

cgt ggc cgc tac atg ggt gtc atg ggt gga gtc ttc gga ctc tct gca 643
Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val Phe Gly Leu Ser Ala
                170                175                180

gtt ctt ggc cca cta ctc ggt ggc tgg ttc acc gaa gga cca ggc tgg 691
Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Glu Gly Pro Gly Trp
                185                190                195

cgc tgg gca ttc tgg atg aac atc cca ctg gga atc atc gcc atc ggt 739
Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly Ile Ile Ala Ile Gly
                200                205                210

gtc gcc att tac ttc ctg gac att cca aag aag agc gtc aag ttc cgc 787

```


Val	Ala	Ile	Tyr	Phe	Leu	Asp	Ile	Pro	Lys	Lys	Ser	Val	Lys	Phe	Arg	
215						220					225					
tgg	gat	tac	ctg	ggc	act	ttc	ttc	atg	atc	ggt	gcc	gca	acc	agc	ctg	835
Trp	Asp	Tyr	Leu	Gly	Thr	Phe	Phe	Met	Ile	Val	Ala	Ala	Thr	Ser	Leu	
230					235					240					245	
atc	ctg	ttc	acc	acc	tgg	ggt	gga	tcc	cag	tac	gag	tgg	tct	gat	cca	883
Ile	Leu	Phe	Thr	Thr	Trp	Gly	Gly	Ser	Gln	Tyr	Glu	Trp	Ser	Asp	Pro	
				250					255					260		
atc	atc	att	gga	ctg	atc	atc	acc	acc	atc	ggt	gcc	gct	gca	ctg	ctg	931
Ile	Ile	Ile	Gly	Leu	Ile	Ile	Thr	Thr	Ile	Val	Ala	Ala	Ala	Leu	Leu	
			265					270					275			
ggt	ggt	gtg	gaa	ctg	cgc	gca	aaa	gat	cca	ttg	ggt	cca	atg	tcc	ttc	979
Val	Val	Val	Glu	Leu	Arg	Ala	Lys	Asp	Pro	Leu	Val	Pro	Met	Ser	Phe	
		280					285					290				
ttc	caa	aac	cgc	aac	ttc	acg	ctc	acc	acc	att	gca	ggc	ctg	atc	ctg	1027
Phe	Gln	Asn	Arg	Asn	Phe	Thr	Leu	Thr	Thr	Ile	Ala	Gly	Leu	Ile	Leu	
	295					300					305					
ggt	atc	gca	atg	ttc	ggc	atc	atc	ggc	tac	ctt	ccg	acc	tac	ctc	cag	1075
Gly	Ile	Ala	Met	Phe	Gly	Ile	Ile	Gly	Tyr	Leu	Pro	Thr	Tyr	Leu	Gln	
310					315					320					325	
atg	gtc	cac	gga	atc	aac	gcc	acc	gaa	gcc	ggc	tac	atg	ctg	atc	cca	1123
Met	Val	His	Gly	Ile	Asn	Ala	Thr	Glu	Ala	Gly	Tyr	Met	Leu	Ile	Pro	
				330					335					340		
atg	atg	gtc	ggc	atg	atg	ggt	acc	tcc	atc	tgg	act	ggt	atc	cgc	atc	1171
Met	Met	Val	Gly	Met	Met	Gly	Thr	Ser	Ile	Trp	Thr	Gly	Ile	Arg	Ile	
			345					350					355			
tcc	aac	aca	gga	aag	tac	aaa	ctc	ttc	cca	cca	atc	ggc	atg	gtg	ggt	1219
Ser	Asn	Thr	Gly	Lys	Tyr	Lys	Leu	Phe	Pro	Pro	Ile	Gly	Met	Val	Val	
		360					365					370				
acc	ttc	gtg	gca	ctg	atc	ttc	ttt	gcc	cga	atg	gaa	gtg	tcc	acc	acc	1267
Thr	Phe	Val	Ala	Leu	Ile	Phe	Phe	Ala	Arg	Met	Glu	Val	Ser	Thr	Thr	
		375				380					385					
ctg	tgg	cag	atc	gga	atc	tac	ctc	ttc	gtc	ctc	ggc	gtc	ggc	ctg	ggt	1315
Leu	Trp	Gln	Ile	Gly	Ile	Tyr	Leu	Phe	Val	Leu	Gly	Val	Gly	Leu	Gly	
390					395					400					405	
cta	gcc	atg	cag	ggt	ctg	gtc	ctg	atc	ggt	cag	aac	acc	ctg	cca	acc	1363
Leu	Ala	Met	Gln	Val	Leu	Val	Leu	Ile	Val	Gln	Asn	Thr	Leu	Pro	Thr	
				410					415					420		
gcg	gtg	gtc	gga	tcc	gca	acc	gct	gtg	aac	aac	ttc	ttc	cgt	caa	atc	1411
Ala	Val	Val	Gly	Ser	Ala	Thr	Ala	Val	Asn	Asn	Phe	Phe	Arg	Gln	Ile	
			425					430					435			
ggt	tcc	tca	ctc	gga	tcc	gcg	ctg	gtc	ggt	ggc	atg	ttc	ggt	ggc	aac	1459
Gly	Ser	Ser	Leu	Gly	Ser	Ala	Leu	Val	Gly	Gly	Met	Phe	Val	Gly	Asn	
		440					445					450				
ttg	gga	acc	ctc	atg	gaa	gaa	aga	atg	cca	gca	gcc	atg	gca	caa	ctt	1507
Leu	Gly	Thr	Leu	Met	Glu	Glu	Arg	Met	Pro	Ala	Ala	Met	Ala	Gln	Leu	

455	460	465	
tca cca gaa gaa caa gcc gcc atg gca gcc caa ggc gga ctg gac tcc			1555
Ser Pro Glu Glu Gln Ala Ala Met Ala Ala Gln Gly Gly Leu Asp Ser			
470	475	480	485
aac gaa ttg acg ccg gca atc gtc aat caa ttg cca acc gcg ctc cac			1603
Asn Glu Leu Thr Pro Ala Ile Val Asn Gln Leu Pro Thr Ala Leu His			
	490	495	500
gat gcg ttc gcc ggt tcc tac aac gac gca ctc atc cca gtg ttc tac			1651
Asp Ala Phe Ala Gly Ser Tyr Asn Asp Ala Leu Ile Pro Val Phe Tyr			
	505	510	515
gtg atg atg cca ctg atc ggc atc gcg ctg ctt ctc ttg ctg ttt att			1699
Val Met Met Pro Leu Ile Gly Ile Ala Leu Leu Leu Leu Leu Phe Ile			
	520	525	530
aag caa gaa aaa cta cgc gaa acc acc aca gac taaacacaaa acaaatgaga			1752
Lys Gln Glu Lys Leu Arg Gln Thr Thr Thr Asp			
	535	540	
cct			1755

<210> 254

<211> 544

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Met Thr His Glu Thr Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala	
1 5 10 15	

Gly Asp Thr Lys Leu Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro	
20 25 30	

Ser Ser Met Thr Pro Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser	
35 40 45	

Ala Leu Met Val Ala Met Met Met Ala Ser Leu Asp Gln Met Ile Phe	
50 55 60	

Gly Thr Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asp His	
65 70 75 80	

Met Met Trp Val Ile Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu	
85 90 95	

Pro Ile Tyr Gly Lys Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe	
100 105 110	

Ile Gly Ala Leu Gly Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu	
115 120 125	

Ala Gly Asn Met Thr Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile	
130 135 140	

Gly Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val	
145 150 155 160	

Val Pro Ala Arg Glu Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val
 165 170 175
 Phe Gly Leu Ser Ala Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr
 180 185 190
 Glu Gly Pro Gly Trp Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly
 195 200 205
 Ile Ile Ala Ile Gly Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys
 210 215 220
 Ser Val Lys Phe Arg Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val
 225 230 235 240
 Ala Ala Thr Ser Leu Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr
 245 250 255
 Glu Trp Ser Asp Pro Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val
 260 265 270
 Ala Ala Ala Leu Leu Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu
 275 280 285
 Val Pro Met Ser Phe Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile
 290 295 300
 Ala Gly Leu Ile Leu Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu
 305 310 315 320
 Pro Thr Tyr Leu Gln Met Val His Gly Ile Asn Ala Thr Glu Ala Gly
 325 330 335
 Tyr Met Leu Ile Pro Met Met Val Gly Met Met Gly Thr Ser Ile Trp
 340 345 350
 Thr Gly Ile Arg Ile Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro
 355 360 365
 Ile Gly Met Val Val Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met
 370 375 380
 Glu Val Ser Thr Thr Leu Trp Gln Ile Gly Ile Tyr Leu Phe Val Leu
 385 390 395 400
 Gly Val Gly Leu Gly Leu Ala Met Gln Val Leu Val Leu Ile Val Gln
 405 410 415
 Asn Thr Leu Pro Thr Ala Val Val Gly Ser Ala Thr Ala Val Asn Asn
 420 425 430
 Phe Phe Arg Gln Ile Gly Ser Ser Leu Gly Ser Ala Leu Val Gly Gly
 435 440 445
 Met Phe Val Gly Asn Leu Gly Thr Leu Met Glu Glu Arg Met Pro Ala
 450 455 460
 Ala Met Ala Gln Leu Ser Pro Glu Glu Gln Ala Ala Met Ala Ala Gln
 465 470 475 480
 Gly Gly Leu Asp Ser Asn Glu Leu Thr Pro Ala Ile Val Asn Gln Leu

<400> 255															60
ccctgacacc aatcttcttgc gcgctcaccg cgatcgagc agtcgcgcgcg atcctcctct															
ttttcatccg tgaagatcac ctcaaggaaa cgcacgaata atg aca cac gaa act															115
Met Thr His Glu Thr															5
tcc gtc ccc gga cct gcc gac gcg cag gtc gca gga gat acg aag ctg															163
Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala Gly Asp Thr Lys Leu															20
cgc aaa ggc cgc gcg aag aag gaa aaa act cct tca tca atg acg cct															211
Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro Ser Ser Met Thr Pro															35
gaa caa caa aag aaa gtc tgg tgg gtc ctc agc gcg ctg atg gtc gcc															259
Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser Ala Leu Met Val Ala															50
atg atg atg gcc tcc ctt gac cag atg att ttc ggc aca gcc ctg cca															307
Met Met Met Ala Ser Leu Asp Gln Met Ile Phe Gly Thr Ala Leu Pro															65
aca atc gtc ggt gaa ctc ggc ggc gtt gac cac atg atg tgg gtc atc															355
Thr Ile Val Gly Glu Leu Gly Gly Val Asp His Met Met Trp Val Ile															85
acc gca tac cta ctt gcc gaa acc atc atg ctg ccg atc tac gga aag															403
Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu Pro Ile Tyr Gly Lys															100
ctc ggc gac ctg gtt gga cgt aaa ggt ctc ttc atc gga gcc ctc ggc															451
Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe Ile Gly Ala Leu Gly															115
atc ttc ctg atc ggc tcc gtc atc ggc ggg ctt gca gga aat atg acc															499
Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu Ala Gly Asn Met Thr															120
															125
															130

tgg ttg atc gtc ggc cgt gcc gta cag ggc atc ggt ggc ggt gga ctg	547
Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile Gly Gly Gly Leu	
135 140 145	
atg atc ctc tcg cag gca atc atc gcg gac gtt gtt cca gca cgt gaa	595
Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val Val Pro Ala Arg Glu	
150 155 160 165	
cgt ggc cgc tac atg ggt gtc atg ggt gga gtc ttc gga ctc tct gca	643
Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val Phe Gly Leu Ser Ala	
170 175 180	
gtt ctt ggc cca cta ctc ggt ggc tgg ttc acc gaa gga cca ggc tgg	691
Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr Glu Gly Pro Gly Trp	
185 190 195	
cgc tgg gca ttc tgg atg aac atc cca ctg gga atc atc gcc atc ggt	739
Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly Ile Ile Ala Ile Gly	
200 205 210	
gtc gcc att tac ttc ctg gac att cca aag aag agc gtc aag ttc cgc	787
Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys Ser Val Lys Phe Arg	
215 220 225	
tgg gat tac ctg ggc act ttc ttc atg atc gtt gcc gca acc agc ctg	835
Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val Ala Ala Thr Ser Leu	
230 235 240 245	
atc ctg ttc acc acc tgg ggt gga tcc cag tac gag tgg tct gat cca	883
Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr Glu Trp Ser Asp Pro	
250 255 260	
atc atc att gga ctg atc atc acc acc atc gtt gcc gct gca ctg ctg	931
Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val Ala Ala Ala Leu Leu	
265 270 275	
gtt gtt gtg gaa ctg cgc gca aaa gat cca ttg gtt cca atg tcc ttc	979
Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu Val Pro Met Ser Phe	
280 285 290	
ttc caa aac cgc aac ttc acg ctc acc acc att gca ggc ctg atc ctg	1027
Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile Ala Gly Leu Ile Leu	
295 300 305	
ggt atc gca atg ttc ggc atc atc ggc tac ctt ccg acc tac ctc cag	1075
Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu Pro Thr Tyr Leu Gln	
310 315 320 325	
atg gtc cac gga atc aac gcc acc gaa gcc ggc tac atg ctg atc cca	1123
Met Val His Gly Ile Asn Ala Thr Glu Ala Gly Tyr Met Leu Ile Pro	
330 335 340	
atg atg gtc ggc atg atg ggt acc tcc atc tgg act ggt atc cgc atc	1171
Met Met Val Gly Met Met Gly Thr Ser Ile Trp Thr Gly Ile Arg Ile	
345 350 355	
tcc aac aca gga aag tac aaa ctc ttc cca cca atc ggc atg gtg gtt	1219
Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro Ile Gly Met Val Val	
360 365 370	
acc ttc gtg gca ctg atc ttc ttt gcc cga atg gaa gtg tcc acc acc	1267

Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met Glu Val Ser Thr Thr
 375 380 385

ctg tgg cag atc gga atc tac ctc ttc
 Leu Trp Gln Ile Gly Ile Tyr Leu Phe
 390 395

1294

<210> 256
 <211> 398
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 256
 Met Thr His Glu Thr Ser Val Pro Gly Pro Ala Asp Ala Gln Val Ala
 1 5 10 15

Gly Asp Thr Lys Leu Arg Lys Gly Arg Ala Lys Lys Glu Lys Thr Pro
 20 25 30

Ser Ser Met Thr Pro Glu Gln Gln Lys Lys Val Trp Trp Val Leu Ser
 35 40 45

Ala Leu Met Val Ala Met Met Met Ala Ser Leu Asp Gln Met Ile Phe
 50 55 60

Gly Thr Ala Leu Pro Thr Ile Val Gly Glu Leu Gly Gly Val Asp His
 65 70 75 80

Met Met Trp Val Ile Thr Ala Tyr Leu Leu Ala Glu Thr Ile Met Leu
 85 90 95

Pro Ile Tyr Gly Lys Leu Gly Asp Leu Val Gly Arg Lys Gly Leu Phe
 100 105 110

Ile Gly Ala Leu Gly Ile Phe Leu Ile Gly Ser Val Ile Gly Gly Leu
 115 120 125

Ala Gly Asn Met Thr Trp Leu Ile Val Gly Arg Ala Val Gln Gly Ile
 130 135 140

Gly Gly Gly Gly Leu Met Ile Leu Ser Gln Ala Ile Ile Ala Asp Val
 145 150 155 160

Val Pro Ala Arg Glu Arg Gly Arg Tyr Met Gly Val Met Gly Gly Val
 165 170 175

Phe Gly Leu Ser Ala Val Leu Gly Pro Leu Leu Gly Gly Trp Phe Thr
 180 185 190

Glu Gly Pro Gly Trp Arg Trp Ala Phe Trp Met Asn Ile Pro Leu Gly
 195 200 205

Ile Ile Ala Ile Gly Val Ala Ile Tyr Phe Leu Asp Ile Pro Lys Lys
 210 215 220

Ser Val Lys Phe Arg Trp Asp Tyr Leu Gly Thr Phe Phe Met Ile Val
 225 230 235 240

Ala Ala Thr Ser Leu Ile Leu Phe Thr Thr Trp Gly Gly Ser Gln Tyr
 245 250 255

Glu Trp Ser Asp Pro Ile Ile Ile Gly Leu Ile Ile Thr Thr Ile Val
 260 265 270
 Ala Ala Ala Leu Leu Val Val Val Glu Leu Arg Ala Lys Asp Pro Leu
 275 280 285
 Val Pro Met Ser Phe Phe Gln Asn Arg Asn Phe Thr Leu Thr Thr Ile
 290 295 300
 Ala Gly Leu Ile Leu Gly Ile Ala Met Phe Gly Ile Ile Gly Tyr Leu
 305 310 315 320
 Pro Thr Tyr Leu Gln Met Val His Gly Ile Asn Ala Thr Glu Ala Gly
 325 330 335
 Tyr Met Leu Ile Pro Met Met Val Gly Met Met Gly Thr Ser Ile Trp
 340 345 350
 Thr Gly Ile Arg Ile Ser Asn Thr Gly Lys Tyr Lys Leu Phe Pro Pro
 355 360 365
 Ile Gly Met Val Val Thr Phe Val Ala Leu Ile Phe Phe Ala Arg Met
 370 375 380
 Glu Val Ser Thr Thr Leu Trp Gln Ile Gly Ile Tyr Leu Phe
 385 390 395

<210> 257
 <211> 1510
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (93)..(1487)
 <223> RXA01578

<400> 257
 tgacctcccc tcaaccactc actgaaaaga gaacactgat gtcacttcct gttcagccga 60
 gtaaaacctc ggccgccaca gtcataccat tg atg atc gcc ctg ctg gtc gcg 113
 Met Ile Ala Leu Leu Val Ala
 1 5
 gta ttc gcc ttc cag ctc aac gcc tcc atg ctg gcg ccg gca ctg gcc 161
 Val Phe Ala Phe Gln Leu Asn Ala Ser Met Leu Ala Pro Ala Leu Ala
 10 15 20
 acc atg gaa act gaa ctt aat gca aca gct gcc caa atc ggc atg acg 209
 Thr Met Glu Thr Glu Leu Asn Ala Thr Ala Ala Gln Ile Gly Met Thr
 25 30 35
 cag act gct ttc ttc acc gcg gcg gcg ctg ttt tcc ctg ttc ctg cca 257
 Gln Thr Ala Phe Phe Thr Ala Ala Ala Leu Phe Ser Leu Phe Leu Pro
 40 45 50 55
 cgt tgg ggc gat ctg att ggt cgc cgc aaa gtg ctg gtc ggc atg atg 305
 Arg Trp Gly Asp Leu Ile Gly Arg Arg Lys Val Leu Val Gly Met Met
 60 65 70

att gtc acc ggt att gga tgt gtt gtc gct gcc ttt gct ccg aat gtg	353
Ile Val Thr Gly Ile Gly Cys Val Val Ala Ala Phe Ala Pro Asn Val	
75 80 85	
acc atc ctc ttc ctg ggc cgc ctg att caa ggt gtt gct ggc cca acc	401
Thr Ile Leu Phe Leu Gly Arg Leu Ile Gln Gly Val Ala Gly Pro Thr	
90 95 100	
gtg cca ctg tgt ctg atc att ctg cgc cag cag gta acc aat gaa aag	449
Val Pro Leu Cys Leu Ile Ile Leu Arg Gln Gln Val Thr Asn Glu Lys	
105 110 115	
caa tat gcg cta ctt ctc gga att gtt acc tct gtc aac ggt ggt atc	497
Gln Tyr Ala Leu Leu Leu Gly Ile Val Thr Ser Val Asn Gly Gly Ile	
120 125 130 135	
ggc ggc gtg gac gcg ctt gct ggt ggc tgg ttg gct gaa aca ctt ggt	545
Gly Gly Val Asp Ala Leu Ala Gly Gly Trp Leu Ala Glu Thr Leu Gly	
140 145 150	
ttc cgt tcc atc ttc tgg gtc atg gct gct ttc tgc gct gtc gct gcc	593
Phe Arg Ser Ile Phe Trp Val Met Ala Ala Phe Cys Ala Val Ala Ala	
155 160 165	
ctc gca ctg cct ttc agc gtg aag gaa tcc acc gct gaa gaa acc ccg	641
Leu Ala Leu Pro Phe Ser Val Lys Glu Ser Thr Ala Glu Glu Thr Pro	
170 175 180	
aag atg gac tgg ctt ggt gtg ctg cca ctg gcg gtg tcc att gga tct	689
Lys Met Asp Trp Leu Gly Val Leu Pro Leu Ala Val Ser Ile Gly Ser	
185 190 195	
ttg ctc atg gct ttc aac gag gcc ggc aaa ctc ggt gcc gcg aac tgg	737
Leu Leu Met Ala Phe Asn Glu Ala Gly Lys Leu Gly Ala Ala Asn Trp	
200 205 210 215	
att ctg gtg gtt gtg ctg ttc atc atc ggt atc gcc gga gtc atc ttc	785
Ile Leu Val Val Val Leu Phe Ile Ile Gly Ile Ala Gly Val Ile Phe	
220 225 230	
ttc tac aac att gaa aag cgc gtt aag cac ccg ctg gtc agt gtt gaa	833
Phe Tyr Asn Ile Glu Lys Arg Val Lys His Pro Leu Val Ser Val Glu	
235 240 245	
tac ctc ggt caa cga cgc acc tgg gca ttg ctg ctg agc acc ctt ctc	881
Tyr Leu Gly Gln Arg Arg Thr Trp Ala Leu Leu Leu Ser Thr Leu Leu	
250 255 260	
aca atg acc ggt gta ttc gcc gta atg aat ggt ctg ctg ccc aac ctt	929
Thr Met Thr Gly Val Phe Ala Val Met Asn Gly Leu Leu Pro Asn Leu	
265 270 275	
gcg cag gat gct gcc aac ggt gcc ggc atg tca gcg agc gtg gtg tcc	977
Ala Gln Asp Ala Ala Asn Gly Ala Gly Met Ser Ala Ser Val Val Ser	
280 285 290 295	
tgg tgg aca ctt acc cca tat gcg ctg gct ggc ttg gta ttc ggt cca	1025
Trp Trp Thr Leu Thr Pro Tyr Ala Leu Ala Gly Leu Val Phe Gly Pro	
300 305 310	

atc gcc gga att ctc gcc gga aaa ttt gga tac aag atc gtc ctg caa 1073
 ile ala gly ile leu ala gly lys phe gly tyr lys ile val leu gln
 315 320 325

 att ggt atc gct gcc acc atc atc ggc gtt gcc gga gcc acc ttc tta 1121
 ile gly ile ala ala thr ile ile gly val ala gly ala thr phe leu
 330 335 340

 gtc gga agc acc tcg cat ctc gcg tac ctc ggc atc tcc atc ttc gtg 1169
 val gly ser thr ser his leu ala tyr leu gly ile ser ile phe val
 345 350 355

 ggt att acc tat gca ggt att gcc aac atc atg ctc aac ggc ctg ggc 1217
 gly ile thr tyr ala gly ile ala asn ile met leu asn gly leu gly
 360 365 370 375

 atc gtg ctc tcc cct gct aac aac caa ggc tat ctg cct ggc atg aac 1265
 ile val leu ser pro ala asn asn gln gly tyr leu pro gly met asn
 380 385 390

 gca ggt gcc ttc aac cta ggt gca ggt att tcc ttc gcc atc ctc ttc 1313
 ala gly ala phe asn leu gly ala gly ile ser phe ala ile leu phe
 395 400 405

 gca gtt tcc acg gca ttc agt gac aac ggc gga gga tac gcc gca ggc 1361
 ala val ser thr ala phe ser asp asn gly gly gly tyr ala ala gly
 410 415 420

 atg tgg gct ggc gtg atc atc ttg gtc cta gcc ttc ctc tgc tcc ctg 1409
 met trp ala gly val ile ile leu val leu ala phe leu cys ser leu
 425 430 435

 ctg atc cca cgc cca gaa tca atc acc gat aca gtg gca gcc aaa gtc 1457
 leu ile pro arg pro glu ser ile thr asp thr val ala ala lys val
 440 445 450 455

 cag gct gaa gaa gcc gct caa gcc gcc agc taaatccaca aactgaacta 1507
 gln ala glu glu ala ala gln ala ala ser
 460 465

 agg 1510

<210> 258

<211> 465

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

Met ile ala leu leu val ala val phe ala phe gln leu asn ala ser
 1 5 10 15

Met leu ala pro ala leu ala thr met glu thr glu leu asn ala thr
 20 25 30

ala ala gln ile gly met thr gln thr ala phe phe thr ala ala ala
 35 40 45

leu phe ser leu phe leu pro arg trp gly asp leu ile gly arg arg
 50 55 60

Lys Val Leu Val Gly Met Met Ile Val Thr Gly Ile Gly Cys Val Val
 65 70 75 80
 Ala Ala Phe Ala Pro Asn Val Thr Ile Leu Phe Leu Gly Arg Leu Ile
 85 90 95
 Gln Gly Val Ala Gly Pro Thr Val Pro Leu Cys Leu Ile Ile Leu Arg
 100 105 110
 Gln Gln Val Thr Asn Glu Lys Gln Tyr Ala Leu Leu Leu Gly Ile Val
 115 120 125
 Thr Ser Val Asn Gly Gly Ile Gly Gly Val Asp Ala Leu Ala Gly Gly
 130 135 140
 Trp Leu Ala Glu Thr Leu Gly Phe Arg Ser Ile Phe Trp Val Met Ala
 145 150 155 160
 Ala Phe Cys Ala Val Ala Ala Leu Ala Leu Pro Phe Ser Val Lys Glu
 165 170 175
 Ser Thr Ala Glu Glu Thr Pro Lys Met Asp Trp Leu Gly Val Leu Pro
 180 185 190
 Leu Ala Val Ser Ile Gly Ser Leu Leu Met Ala Phe Asn Glu Ala Gly
 195 200 205
 Lys Leu Gly Ala Ala Asn Trp Ile Leu Val Val Val Leu Phe Ile Ile
 210 215 220
 Gly Ile Ala Gly Val Ile Phe Phe Tyr Asn Ile Glu Lys Arg Val Lys
 225 230 235 240
 His Pro Leu Val Ser Val Glu Tyr Leu Gly Gln Arg Arg Thr Trp Ala
 245 250 255
 Leu Leu Leu Ser Thr Leu Leu Thr Met Thr Gly Val Phe Ala Val Met
 260 265 270
 Asn Gly Leu Leu Pro Asn Leu Ala Gln Asp Ala Ala Asn Gly Ala Gly
 275 280 285
 Met Ser Ala Ser Val Val Ser Trp Trp Thr Leu Thr Pro Tyr Ala Leu
 290 295 300
 Ala Gly Leu Val Phe Gly Pro Ile Ala Gly Ile Leu Ala Gly Lys Phe
 305 310 315 320
 Gly Tyr Lys Ile Val Leu Gln Ile Gly Ile Ala Ala Thr Ile Ile Gly
 325 330 335
 Val Ala Gly Ala Thr Phe Leu Val Gly Ser Thr Ser His Leu Ala Tyr
 340 345 350
 Leu Gly Ile Ser Ile Phe Val Gly Ile Thr Tyr Ala Gly Ile Ala Asn
 355 360 365
 Ile Met Leu Asn Gly Leu Gly Ile Val Leu Ser Pro Ala Asn Asn Gln
 370 375 380
 Gly Tyr Leu Pro Gly Met Asn Ala Gly Ala Phe Asn Leu Gly Ala Gly

385		390		395		400
Ile Ser Phe Ala	Ile Leu Phe Ala Val	Ser Thr Ala Phe Ser Asp Asn				
	405	410			415	
Gly Gly Gly Tyr	Ala Ala Gly Met Trp	Ala Gly Val Ile Ile Leu Val				
	420	425			430	
Leu Ala Phe Leu Cys	Ser Leu Leu Ile Pro Arg Pro	Glu Ser Ile Thr				
	435	440			445	
Asp Thr Val Ala Ala Lys	Val Gln Ala Glu Glu Ala Ala Gln Ala Ala					
	450	455			460	

Ser
465

<210> 259
 <211> 1470
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1447)
 <223> RXA02087

<400> 259
 aatcggattc atgctgtgtg gtgtgatcag tttgctggct gcggtcgcac ggatcttcgg 60
 ccgggagacg ctgccaacgg cgaaagtcga gcaggtataa atg acg cca att gtg 115
 Met Thr Pro Ile Val
 1 5
 gag tcc agg gcg tgg aaa gct ctg ggc gct tta agt gtt ggg ctg ttt 163
 Glu Ser Arg Ala Trp Lys Ala Leu Gly Ala Leu Ser Val Gly Leu Phe
 10 15 20
 ctc aca ctg ctt gac caa tcg ttg gtg gct gtc gcg ctg cca aag att 211
 Leu Thr Leu Leu Asp Gln Ser Leu Val Ala Val Ala Leu Pro Lys Ile
 25 30 35
 caa gag gat ttg ggt gcg agc ctg aac caa gcg gtg tgg gtg tca gcg 259
 Gln Glu Asp Leu Gly Ala Ser Leu Asn Gln Ala Val Trp Val Ser Ala
 40 45 50
 gtt tat ttg ctc act ttt gcg gtg cca ctg ttg att act ggg cgc ttg 307
 Val Tyr Leu Leu Thr Phe Ala Val Pro Leu Leu Ile Thr Gly Arg Leu
 55 60 65
 ggt gat cgt tat gga cag cga aat att tat ctt gcc gcc atg gct gtg 355
 Gly Asp Arg Tyr Gly Gln Arg Asn Ile Tyr Leu Ala Gly Met Ala Val
 70 75 80 85
 ttt acc ctc gcg gcg ttg gcc tgt gta ttt gca cca agc atc gaa tgg 403
 Phe Thr Leu Ala Ala Leu Ala Cys Val Phe Ala Pro Ser Ile Glu Trp
 90 95 100
 ttg att gct gct cgc gcg gtg cag ggc ctg ggc gga tct ctt ctt aat 451
 Leu Ile Ala Ala Arg Ala Val Gln Gly Leu Gly Gly Ser Leu Leu Asn

105						110						115						
ccg	cag	ccc	ctg	agc	atc	att	cac	aag	att	ttc	gcg	cat	gat	cgt	agg	499		
Pro	Gln	Pro	Leu	Ser	Ile	Ile	His	Lys	Ile	Phe	Ala	His	Asp	Arg	Arg			
		120					125					130						
gga	gcc	gcc	acc	ggg	gtg	tgg	agt	gct	gtt	gcc	tca	tca	gct	gga	ctt	547		
Gly	Ala	Ala	Thr	Gly	Val	Trp	Ser	Ala	Val	Ala	Ser	Ser	Ala	Gly	Leu			
	135					140					145							
ttc	ggg	cca	gtt	atc	ggg	ggg	gtt	ctg	gtg	ggg	tgg	atc	agc	tgg	cgt	595		
Phe	Gly	Pro	Val	Ile	Gly	Gly	Val	Leu	Val	Gly	Trp	Ile	Ser	Trp	Arg			
150					155					160					165			
gct	gtg	ttc	ttg	gtt	tat	gtg	ccg	ctc	gga	ttg	atc	tcc	cta	ttt	atg	643		
Ala	Val	Phe	Leu	Val	Tyr	Val	Pro	Leu	Gly	Leu	Ile	Ser	Leu	Phe	Met			
				170					175					180				
gtg	gcg	cgt	tat	gtg	cct	aaa	ctt	ccc	acg	gga	acc	tcg	aag	atc	gat	691		
Val	Ala	Arg	Tyr	Val	Pro	Lys	Leu	Pro	Thr	Gly	Thr	Ser	Lys	Ile	Asp			
			185					190					195					
tgg	ctc	tcg	ggg	gcg	gtc	tca	ctt	gtt	gct	gta	ctt	ggg	gtg	gtt	ctt	739		
Trp	Leu	Ser	Gly	Ala	Val	Ser	Leu	Val	Ala	Val	Leu	Gly	Val	Val	Leu			
		200					205					210						
gcc	ttg	cag	cag	ggg	cca	gaa	ctt	ggg	tgg	gga	aca	ctg	att	tgg	gtg	787		
Ala	Leu	Gln	Gln	Gly	Pro	Glu	Leu	Gly	Trp	Gly	Thr	Leu	Ile	Trp	Val			
	215					220					225							
tcc	ctt	gcc	gtt	ggg	att	gct	gca	gct	gtg	ctc	ttt	ata	tgg	atg	caa	835		
Ser	Leu	Ala	Val	Gly	Ile	Ala	Ala	Ala	Val	Leu	Phe	Ile	Trp	Met	Gln			
230					235					240					245			
aca	aga	tcc	aag	gcg	cca	ctg	atg	ccg	ttg	agg	att	ttc	aag	acg	cgc	883		
Thr	Arg	Ser	Lys	Ala	Pro	Leu	Met	Pro	Leu	Arg	Ile	Phe	Lys	Thr	Arg			
			250					255						260				
aac	ttc	gcg	atc	ggg	gca	ttt	tcg	atc	ttc	agc	ctg	ggc	ttt	acg	gtg	931		
Asn	Phe	Ala	Ile	Gly	Ala	Phe	Ser	Ile	Phe	Ser	Leu	Gly	Phe	Thr	Val			
			265					270					275					
tat	tcc	gtt	aat	ttg	ccc	atc	atg	ttg	tat	ctg	caa	acg	gct	cag	gga	979		
Tyr	Ser	Val	Asn	Leu	Pro	Ile	Met	Leu	Tyr	Leu	Gln	Thr	Ala	Gln	Gly			
		280					285					290						
atg	tcg	tcg	cag	ttg	gcc	ggg	ttg	atg	ttg	gtt	ccg	atg	ggc	atc	atc	1027		
Met	Ser	Ser	Gln	Leu	Ala	Gly	Leu	Met	Leu	Val	Pro	Met	Gly	Ile	Ile			
	295					300					305							
tct	gtg	gtg	atg	tca	cca	gta	att	gga	cga	ttg	gtg	gat	cgc	ctg	gca	1075		
Ser	Val	Val	Met	Ser	Pro	Val	Ile	Gly	Arg	Leu	Val	Asp	Arg	Leu	Ala			
310					315					320					325			
cca	gga	atg	atc	tcc	aag	atc	gga	ttc	ggc	gcg	ctg	att	ttc	tcg	atg	1123		
Pro	Gly	Met	Ile	Ser	Lys	Ile	Gly	Phe	Gly	Ala	Leu	Ile	Phe	Ser	Met			
				330					335					340				
gcg	ttg	atg	gct	gtc	ttt	atg	atc	gcc	aac	cta	tcg	ccg	tgg	tgg	cta	1171		
Ala	Leu	Met	Ala	Val	Phe	Met	Ile	Ala	Asn	Leu	Ser	Pro	Trp	Trp	Leu			
			345					350					355					

ctc atc ccg att att ttg ttc ggt agc tcc aac gcg atg agt ttt gca 1219
 Leu Ile Pro Ile Ile Leu Phe Gly Ser Ser Asn Ala Met Ser Phe Ala
 360 365 370
 ccg aac tct gtg att gct ctg cgt gat gtt ccg cag gat tta gtg ggc 1267
 Pro Asn Ser Val Ile Ala Leu Arg Asp Val Pro Gln Asp Leu Val Gly
 375 380 385
 tct gct tct ggt ttt tac aac acc tca cgc cag gtg ggc gct gtt ttg 1315
 Ser Ala Ser Gly Phe Tyr Asn Thr Ser Arg Gln Val Gly Ala Val Leu
 390 395 400 405
 ggc gcc gct acc ttg ggc gct gtg atg caa ata gga gtg ggc acg gtg 1363
 Gly Ala Ala Thr Leu Gly Ala Val Met Gln Ile Gly Val Gly Thr Val
 410 415 420
 tcc ttc ggt gtt gcc atg ggt gcg gca atc ctg gtg aca ctc gtg ccc 1411
 Ser Phe Gly Val Ala Met Gly Ala Ala Ile Leu Val Thr Leu Val Pro
 425 430 435
 tta atc ttt ggg ttc cta gcg gta acc caa ttt aga tagttgctcc 1457
 Leu Ile Phe Gly Phe Leu Ala Val Thr Gln Phe Arg
 440 445
 gattttctca cga 1470

<210> 260

<211> 449

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 260

Met Thr Pro Ile Val Glu Ser Arg Ala Trp Lys Ala Leu Gly Ala Leu
 1 5 10 15
 Ser Val Gly Leu Phe Leu Thr Leu Leu Asp Gln Ser Leu Val Ala Val
 20 25 30
 Ala Leu Pro Lys Ile Gln Glu Asp Leu Gly Ala Ser Leu Asn Gln Ala
 35 40 45
 Val Trp Val Ser Ala Val Tyr Leu Leu Thr Phe Ala Val Pro Leu Leu
 50 55 60
 Ile Thr Gly Arg Leu Gly Asp Arg Tyr Gly Gln Arg Asn Ile Tyr Leu
 65 70 75 80
 Ala Gly Met Ala Val Phe Thr Leu Ala Ala Leu Ala Cys Val Phe Ala
 85 90 95
 Pro Ser Ile Glu Trp Leu Ile Ala Ala Arg Ala Val Gln Gly Leu Gly
 100 105 110
 Gly Ser Leu Leu Asn Pro Gln Pro Leu Ser Ile Ile His Lys Ile Phe
 115 120 125
 Ala His Asp Arg Arg Gly Ala Ala Thr Gly Val Trp Ser Ala Val Ala
 130 135 140

Ser Ser Ala Gly Leu Phe Gly Pro Val Ile Gly Gly Val Leu Val Gly
 145 150 155 160
 Trp Ile Ser Trp Arg Ala Val Phe Leu Val Tyr Val Pro Leu Gly Leu
 165 170 175
 Ile Ser Leu Phe Met Val Ala Arg Tyr Val Pro Lys Leu Pro Thr Gly
 180 185 190
 Thr Ser Lys Ile Asp Trp Leu Ser Gly Ala Val Ser Leu Val Ala Val
 195 200 205
 Leu Gly Val Val Leu Ala Leu Gln Gln Gly Pro Glu Leu Gly Trp Gly
 210 215 220
 Thr Leu Ile Trp Val Ser Leu Ala Val Gly Ile Ala Ala Ala Val Leu
 225 230 235 240
 Phe Ile Trp Met Gln Thr Arg Ser Lys Ala Pro Leu Met Pro Leu Arg
 245 250 255
 Ile Phe Lys Thr Arg Asn Phe Ala Ile Gly Ala Phe Ser Ile Phe Ser
 260 265 270
 Leu Gly Phe Thr Val Tyr Ser Val Asn Leu Pro Ile Met Leu Tyr Leu
 275 280 285
 Gln Thr Ala Gln Gly Met Ser Ser Gln Leu Ala Gly Leu Met Leu Val
 290 295 300
 Pro Met Gly Ile Ile Ser Val Val Met Ser Pro Val Ile Gly Arg Leu
 305 310 315 320
 Val Asp Arg Leu Ala Pro Gly Met Ile Ser Lys Ile Gly Phe Gly Ala
 325 330 335
 Leu Ile Phe Ser Met Ala Leu Met Ala Val Phe Met Ile Ala Asn Leu
 340 345 350
 Ser Pro Trp Trp Leu Leu Ile Pro Ile Ile Leu Phe Gly Ser Ser Asn
 355 360 365
 Ala Met Ser Phe Ala Pro Asn Ser Val Ile Ala Leu Arg Asp Val Pro
 370 375 380
 Gln Asp Leu Val Gly Ser Ala Ser Gly Phe Tyr Asn Thr Ser Arg Gln
 385 390 395 400
 Val Gly Ala Val Leu Gly Ala Ala Thr Leu Gly Ala Val Met Gln Ile
 405 410 415
 Gly Val Gly Thr Val Ser Phe Gly Val Ala Met Gly Ala Ala Ile Leu
 420 425 430
 Val Thr Leu Val Pro Leu Ile Phe Gly Phe Leu Ala Val Thr Gln Phe
 435 440 445

Arg

<400> 261															
agagcacccca agcgacatttg ttcgataata tgttctatta ttgggtattaa tactgggtcag															60
ctagatataa aagggggcgca gggctagcct tgggtgtgaa atg tta act caa aaa															115
Met Leu Thr Gln Lys															1 5
ata gaa tta gag gct aaa cca aaa atc cca gag gag atc tgg gtg ctg															163
Ile Glu Leu Glu Ala Lys Pro Lys Ile Pro Glu Glu Ile Trp Val Leu															10 15 20
gtt gtg gct gcg ttt att att gcg ctg ggc tat ggc ctg att gcg ccg															211
Val Val Ala Ala Phe Ile Ile Ala Leu Gly Tyr Gly Leu Ile Ala Pro															25 30 35
att ttg cca cag ttt gtg gtc ggt ttt gat gta agt ttt gca gct gcc															259
Ile Leu Pro Gln Phe Val Val Gly Phe Asp Val Ser Phe Ala Ala Ala															40 45 50
agt gcg gtg gtg tcc atc ttt gcg ggc gcc cgg ttg ttg ttt gcg ccg															307
Ser Ala Val Val Ser Ile Phe Ala Gly Ala Arg Leu Leu Phe Ala Pro															55 60 65
atg tcg ggg agt ttg atc gat aag atc ggt tcc cgt cgt gtg tat ctc															355
Met Ser Gly Ser Leu Ile Asp Lys Ile Gly Ser Arg Arg Val Tyr Leu															70 75 80 85
act ggt tta ctc acc gtg gct atc acc acg ggg ctt gtt gcg ttg gcg															403
Thr Gly Leu Leu Thr Val Ala Ile Thr Thr Gly Leu Val Ala Leu Ala															90 95 100
cag gaa tac tgg cag att ctg ctg ctt cgt ggc atc gca ggt att ggt															451
Gln Glu Tyr Trp Gln Ile Leu Leu Leu Arg Gly Ile Ala Gly Ile Gly															105 110 115
tcc acc atg ttt acg gtc tct gcc atg ggc ctg atc gtg aag atg gcg															499
Ser Thr Met Phe Thr Val Ser Ala Met Gly Leu Ile Val Lys Met Ala															120 125 130
ccg gtg gag atc cgc ggg cgg tgt tcg tcg gta tat gcc agt tcg ttc															547
Pro Val Glu Ile Arg Gly Arg Cys Ser Ser Val Tyr Ala Ser Ser Phe															135 140 145
ctg ttt ggc aat att att ggc ccg gtt gtg ggt gct gcg atg tcc ggt															595
Leu Phe Gly Asn Ile Ile Gly Pro Val Val Gly Ala Ala Met Ser Gly															150 155 160 165
ttg ggc atg cgg tgg ccg ttc gcg att tat ggt gct tcc gtt ggc tta															643
Leu Gly Met Arg Trp Pro Phe Ala Ile Tyr Gly Ala Ser Val Gly Leu															170 175 180

gct gca ctt gtt gtg tgg tgg cgg atg ccg aaa acc aac gat tca ctt	691
Ala Ala Leu Val Val Trp Trp Arg Met Pro Lys Thr Asn Asp Ser Leu	
185 190 195	
cgg aag gct gat agc aat agt gtg ccg gcg ttg cgc ttt gct gag gca	739
Arg Lys Ala Asp Ser Asn Ser Val Pro Ala Leu Arg Phe Ala Glu Ala	
200 205 210	
att aag gat tct gcc tac cgc tcg gcg ttg ttt agt gct ttt gcc aat	787
Ile Lys Asp Ser Ala Tyr Arg Ser Ala Leu Phe Ser Ala Phe Ala Asn	
215 220 225	
ggg tgg tcg aac ttt ggt gtg cgt gtg gcg gtt ctt cca ctg ttt gcc	835
Gly Trp Ser Asn Phe Gly Val Arg Val Ala Val Leu Pro Leu Phe Ala	
230 235 240 245	
gca gct gca ttt agc aat ggc gga gct att gcg ggt ttt gcc atg gct	883
Ala Ala Ala Phe Ser Asn Gly Gly Ala Ile Ala Gly Phe Ala Met Ala	
250 255 260	
gcg ttc gcc gct gga aat gct ttg tgt ctg caa ttc gcg ggc gat ctc	931
Ala Phe Ala Ala Gly Asn Ala Leu Cys Leu Gln Phe Ala Gly Asp Leu	
265 270 275	
tca gat cgc att ggc cgt aaa ccg atg att att tcc ggg ctg atc gtc	979
Ser Asp Arg Ile Gly Arg Lys Pro Met Ile Ile Ser Gly Leu Ile Val	
280 285 290	
aat gca gtg ttc acg gca atg atc gga ttc ggc aca gaa gtg tgg atc	1027
Asn Ala Val Phe Thr Ala Met Ile Gly Phe Gly Thr Glu Val Trp Ile	
295 300 305	
ctg atc acg gta tct gcg ttg gca ggt gct ggt gcg ggc ttg ctt aat	1075
Leu Ile Thr Val Ser Ala Leu Ala Gly Ala Gly Ala Gly Leu Leu Asn	
310 315 320 325	
cca agt cag cag gcg gtg ctc gct gat gtt ata gat tcc cgc ccc ggc	1123
Pro Ser Gln Gln Ala Val Leu Ala Asp Val Ile Asp Ser Arg Pro Gly	
330 335 340	
gga aaa gtc tta gcg aat ttc caa atg gcg cag gat ttc ggt gcg att	1171
Gly Lys Val Leu Ala Asn Phe Gln Met Ala Gln Asp Phe Gly Ala Ile	
345 350 355	
gtt ggc ccg att ctc gta ggc atg atc gca gaa cag gca ggc ttc caa	1219
Val Gly Pro Ile Leu Val Gly Met Ile Ala Glu Gln Ala Gly Phe Gln	
360 365 370	
atc gga ttc atg ctg tgt ggt gtg atc agt ttg ctg gct gcg gtc gca	1267
Ile Gly Phe Met Leu Cys Gly Val Ile Ser Leu Leu Ala Ala Val Ala	
375 380 385	
tgg atc ttc ggc ccg gag acg ctg cca acg gcg aaa gtc gag cag gta	1315
Trp Ile Phe Gly Arg Glu Thr Leu Pro Thr Ala Lys Val Glu Gln Val	
390 395 400 405	
taaatgacgc caattgtgga gtc	1338

<210> 262

<211> 405

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 262

```

Met Leu Thr Gln Lys Ile Glu Leu Glu Ala Lys Pro Lys Ile Pro Glu
 1             5             10             15

Glu Ile Trp Val Leu Val Val Ala Ala Phe Ile Ile Ala Leu Gly Tyr
      20             25             30

Gly Leu Ile Ala Pro Ile Leu Pro Gln Phe Val Val Gly Phe Asp Val
      35             40             45

Ser Phe Ala Ala Ala Ser Ala Val Val Ser Ile Phe Ala Gly Ala Arg
      50             55             60

Leu Leu Phe Ala Pro Met Ser Gly Ser Leu Ile Asp Lys Ile Gly Ser
      65             70             75             80

Arg Arg Val Tyr Leu Thr Gly Leu Leu Thr Val Ala Ile Thr Thr Gly
      85             90             95

Leu Val Ala Leu Ala Gln Glu Tyr Trp Gln Ile Leu Leu Leu Arg Gly
      100            105            110

Ile Ala Gly Ile Gly Ser Thr Met Phe Thr Val Ser Ala Met Gly Leu
      115            120            125

Ile Val Lys Met Ala Pro Val Glu Ile Arg Gly Arg Cys Ser Ser Val
      130            135            140

Tyr Ala Ser Ser Phe Leu Phe Gly Asn Ile Ile Gly Pro Val Val Gly
      145            150            155            160

Ala Ala Met Ser Gly Leu Gly Met Arg Trp Pro Phe Ala Ile Tyr Gly
      165            170            175

Ala Ser Val Gly Leu Ala Ala Leu Val Val Trp Trp Arg Met Pro Lys
      180            185            190

Thr Asn Asp Ser Leu Arg Lys Ala Asp Ser Asn Ser Val Pro Ala Leu
      195            200            205

Arg Phe Ala Glu Ala Ile Lys Asp Ser Ala Tyr Arg Ser Ala Leu Phe
      210            215            220

Ser Ala Phe Ala Asn Gly Trp Ser Asn Phe Gly Val Arg Val Ala Val
      225            230            235            240

Leu Pro Leu Phe Ala Ala Ala Ala Phe Ser Asn Gly Gly Ala Ile Ala
      245            250            255

Gly Phe Ala Met Ala Ala Phe Ala Ala Gly Asn Ala Leu Cys Leu Gln
      260            265            270

Phe Ala Gly Asp Leu Ser Asp Arg Ile Gly Arg Lys Pro Met Ile Ile
      275            280            285

Ser Gly Leu Ile Val Asn Ala Val Phe Thr Ala Met Ile Gly Phe Gly
      290            295            300

```

Thr Glu Val Trp Ile Leu Ile Thr Val Ser Ala Leu Ala Gly Ala Gly
 305 310 315 320
 Ala Gly Leu Leu Asn Pro Ser Gln Gln Ala Val Leu Ala Asp Val Ile
 325 330 335
 Asp Ser Arg Pro Gly Gly Lys Val Leu Ala Asn Phe Gln Met Ala Gln
 340 345 350
 Asp Phe Gly Ala Ile Val Gly Pro Ile Leu Val Gly Met Ile Ala Glu
 355 360 365
 Gln Ala Gly Phe Gln Ile Gly Phe Met Leu Cys Gly Val Ile Ser Leu
 370 375 380
 Leu Ala Ala Val Ala Trp Ile Phe Gly Arg Glu Thr Leu Pro Thr Ala
 385 390 395 400
 Lys Val Glu Gln Val
 405

<210> 263
 <211> 1239
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1216)
 <223> RXA00764

<400> 263
 tactgcgtcg gatccgctga tgcttgcaga atcggacagt gatgggccgt ctgcgcctgc 60
 acctgggacg actggattat taggggtgga attttcgctc atg aca ctc aag act 115
 Met Thr Leu Lys Thr
 1 5
 agc gtt ttg gca cta ctc tta gat aac gtg cat gtt ctt ctg att gcg 163
 Ser Val Leu Ala Leu Leu Leu Asp Asn Val His Val Leu Leu Ile Ala
 10 15 20
 aat cct gag tcg acc acg cag acg cag aaa ctt ttc cgt cgt gtg gtg 211
 Asn Pro Glu Ser Thr Thr Gln Thr Gln Lys Leu Phe Arg Arg Val Val
 25 30 35
 cct gcg ttg atg gcg ctt gat ggt gtg tcg ctt gaa gcg agg ttt acg 259
 Pro Ala Leu Met Ala Leu Asp Gly Val Ser Leu Glu Ala Arg Phe Thr
 40 45 50
 cac tat gga ggc cat gcg gag gaa atg gtt gcg ggt ttg acg gtg gat 307
 His Tyr Gly Gly His Ala Glu Glu Met Val Ala Gly Leu Thr Val Asp
 55 60 65
 gat ttt gat gtg att atc ccc gcg ggt ggg gac ggc acc gtc aac gaa 355
 Asp Phe Asp Val Ile Ile Pro Ala Gly Gly Asp Gly Thr Val Asn Glu
 70 75 80 85
 gtg ata aat ggg tta ctt ggg tcg gcg gaa ggt gat ttt aga aac ctt 403
 Val Ile Asn Gly Leu Leu Gly Ser Ala Glu Gly Asp Phe Arg Asn Leu

90						95						100						
gag	gat	ttg	ccg	gcg	att	gcg	gtg	ttg	cca	acg	ggg	tct	gcc	aat	gtg	451		
Glu	Asp	Leu	Pro	Ala	Ile	Ala	Val	Leu	Pro	Thr	Gly	Ser	Ala	Asn	Val			
			105				110						115					
ttt	gcc	cgt	gcg	ctt	ggt	tac	ccc	act	gac	ccg	tat	gct	gcc	gct	gat	499		
Phe	Ala	Arg	Ala	Leu	Gly	Tyr	Pro	Thr	Asp	Pro	Tyr	Ala	Ala	Ala	Asp			
			120				125						130					
gcc	ctg	gtg	gag	ttg	att	cgg	aag	aac	cac	acc	aga	act	atc	acc	ttg	547		
Ala	Leu	Val	Glu	Leu	Ile	Arg	Lys	Asn	His	Thr	Arg	Thr	Ile	Thr	Leu			
			135				140						145					
ggt	acg	tgg	aag	ggt	gat	gat	cag	ggg	act	cgt	tgg	ttc	gcg	gtt	aat	595		
Gly	Thr	Trp	Lys	Gly	Asp	Asp	Gln	Gly	Thr	Arg	Trp	Phe	Ala	Val	Asn			
				155						160			165					
gct	ggg	ttt	ggt	att	gat	gcg	gat	gtt	att	gcc	agg	gtc	gaa	cgg	gcg	643		
Ala	Gly	Phe	Gly	Ile	Asp	Ala	Asp	Val	Ile	Ala	Arg	Val	Glu	Arg	Ala			
			170						175			180						
aga	tct	ttc	ggc	ttt	gcg	gct	tca	ccg	ttg	ttg	tat	ctg	cag	gtg	agt	691		
Arg	Ser	Phe	Gly	Phe	Ala	Ala	Ser	Pro	Leu	Leu	Tyr	Leu	Gln	Val	Ser			
			185						190			195						
ctt	cgg	gcg	tgg	gtg	aaa	act	cag	att	aag	cca	ccg	aaa	att	acc	gtg	739		
Leu	Arg	Ala	Trp	Val	Lys	Thr	Gln	Ile	Lys	Pro	Pro	Lys	Ile	Thr	Val			
			200						205			210						
gag	gcg	gtg	gac	agc	aaa	ggg	cac	aaa	ttg	caa	aaa	gag	gaa	gtg	cca	787		
Glu	Ala	Val	Asp	Ser	Lys	Gly	His	Lys	Leu	Gln	Lys	Glu	Glu	Val	Pro			
			215			220						225						
atg	ctg	ctt	gcc	tcg	aat	acc	aat	ccg	tgg	act	ttt	ttg	ggt	ccg	ctt	835		
Met	Leu	Leu	Ala	Ser	Asn	Thr	Asn	Pro	Trp	Thr	Phe	Leu	Gly	Pro	Leu			
			230			235			240			245						
cct	gtg	gtg	aca	aat	ccg	cag	aat	tct	ttt	gac	aca	ggt	ctg	ggg	ctt	883		
Pro	Val	Val	Thr	Asn	Pro	Gln	Asn	Ser	Phe	Asp	Thr	Gly	Leu	Gly	Leu			
			250						255			260						
ttt	ggc	ttg	act	agt	gtg	cga	gga	ttc	ggg	gga	gtg	gca	gcg	atg	atg	931		
Phe	Gly	Leu	Thr	Ser	Val	Arg	Gly	Phe	Gly	Gly	Val	Ala	Ala	Met	Met			
			265						270			275						
cac	ctg	att	ggc	gtg	ggg	cat	ggt	cgg	aag	ttg	gag	aag	ttg	atc	gct	979		
His	Leu	Ile	Gly	Val	Gly	His	Gly	Arg	Lys	Leu	Glu	Lys	Leu	Ile	Ala			
			280			285						290						
aag	cgc	acc	att	gct	ttt	gat	gat	gcg	gag	aaa	gta	acg	ctc	acg	tgc	1027		
Lys	Arg	Thr	Ile	Ala	Phe	Asp	Asp	Ala	Glu	Lys	Val	Thr	Leu	Thr	Cys			
			295			300						305						
gac	agc	gat	cag	cgt	ttc	caa	gtt	gat	ggt	gag	tat	gaa	ggc	aaa	cca	1075		
Asp	Ser	Asp	Gln	Arg	Phe	Gln	Val	Asp	Gly	Glu	Tyr	Glu	Gly	Lys	Pro			
			310			315			320			325						
aca	aag	gtg	gtg	ttg	gaa	tca	atc	act	gat	gcg	gtg	cga	gtg	tat				

ccg aag acg cat ccg aca ccg ccg atc atg aat tgg gct gtc cat ttg 1171
 Pro Lys Thr His Pro Thr Pro Pro Ile Met Asn Trp Ala Val His Leu
 345 350 355

ttt aag cac gtc cgt gat ttc ctc cgg gtg cgc acg ttt ggc atc 1216
 Phe Lys His Val Arg Asp Phe Leu Arg Val Arg Thr Phe Gly Ile
 360 365 370

taggattcat cggagttttc ttc 1239

<210> 264

<211> 372

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 264

Met Thr Leu Lys Thr Ser Val Leu Ala Leu Leu Leu Asp Asn Val His
 1 5 10 15

Val Leu Leu Ile Ala Asn Pro Glu Ser Thr Thr Gln Thr Gln Lys Leu
 20 25 30

Phe Arg Arg Val Val Pro Ala Leu Met Ala Leu Asp Gly Val Ser Leu
 35 40 45

Glu Ala Arg Phe Thr His Tyr Gly Gly His Ala Glu Glu Met Val Ala
 50 55 60

Gly Leu Thr Val Asp Asp Phe Asp Val Ile Ile Pro Ala Gly Gly Asp
 65 70 75 80

Gly Thr Val Asn Glu Val Ile Asn Gly Leu Leu Gly Ser Ala Glu Gly
 85 90 95

Asp Phe Arg Asn Leu Glu Asp Leu Pro Ala Ile Ala Val Leu Pro Thr
 100 105 110

Gly Ser Ala Asn Val Phe Ala Arg Ala Leu Gly Tyr Pro Thr Asp Pro
 115 120 125

Tyr Ala Ala Ala Asp Ala Leu Val Glu Leu Ile Arg Lys Asn His Thr
 130 135 140

Arg Thr Ile Thr Leu Gly Thr Trp Lys Gly Asp Asp Gln Gly Thr Arg
 145 150 155 160

Trp Phe Ala Val Asn Ala Gly Phe Gly Ile Asp Ala Asp Val Ile Ala
 165 170 175

Arg Val Glu Arg Ala Arg Ser Phe Gly Phe Ala Ala Ser Pro Leu Leu
 180 185 190

Tyr Leu Gln Val Ser Leu Arg Ala Trp Val Lys Thr Gln Ile Lys Pro
 195 200 205

Pro Lys Ile Thr Val Glu Ala Val Asp Ser Lys Gly His Lys Leu Gln
 210 215 220

Lys Glu Glu Val Pro Met Leu Leu Ala Ser Asn Thr Asn Pro Trp Thr

225	230	235	240
Phe Leu Gly Pro	Leu Pro Val Val Thr	Asn Pro Gln Asn Ser	Phe Asp
	245	250	255
Thr Gly Leu Gly	Leu Phe Gly Leu Thr	Ser Val Arg Gly	Phe Gly Gly
	260	265	270
Val Ala Ala Met	Met His Leu Ile Gly	Val Gly His Gly	Arg Lys Leu
	275	280	285
Glu Lys Leu Ile	Ala Lys Arg Thr	Ile Ala Phe Asp	Asp Ala Glu Lys
	290	295	300
Val Thr Leu Thr	Cys Asp Ser Asp	Gln Arg Phe Gln	Val Asp Gly Glu
305	310	315	320
Tyr Glu Gly Lys	Pro Thr Lys Val	Val Leu Glu Ser	Ile Thr Asp Ala
	325	330	335
Val Arg Val Tyr	Ala Pro Lys Thr	His Pro Thr Pro	Pro Ile Met Asn
	340	345	350
Trp Ala Val His	Leu Phe Lys His	Val Arg Asp Phe	Leu Arg Val Arg
	355	360	365
Thr Phe Gly Ile			
370			

<210> 265
 <211> 271
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(271)
 <223> RXN03125

<400> 265
 tgacaccggc gcgacgtatg gcattactgg cgtcacccca atttacgatg acatctctgc 60
 tcgcctcggc gacgtcctgg ttccttacgt tctgatcggt ttg gtt cta gcg ttc 115
 Leu Val Leu Ala Phe
 1 5
 ctc gtg ctg ttg ctc gtg ttc cgg tcc att tgg gtc cca ttg atc gcg 163
 Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp Val Pro Leu Ile Ala
 10 15 20
 gct ctg ggc ttt ggc ttg tca gtt ctg gct acc ttt ggt gct acc gtg 211
 Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr Phe Gly Ala Thr Val
 25 30 35
 gcg atc ttc caa gaa ggt gct ttc ggc atc atc gac gat cct cag cca 259
 Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile Asp Asp Pro Gln Pro
 40 45 50
 ctg ctg tgc ttc 271
 Leu Leu Cys Phe

55

<210> 266

<211> 57

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Leu Val Leu Ala Phe Leu Val Leu Leu Leu Val Phe Arg Ser Ile Trp
 1 5 10 15

Val Pro Leu Ile Ala Ala Leu Gly Phe Gly Leu Ser Val Leu Ala Thr
 20 25 30

Phe Gly Ala Thr Val Ala Ile Phe Gln Glu Gly Ala Phe Gly Ile Ile
 35 40 45

Asp Asp Pro Gln Pro Leu Leu Cys Phe
 50 55

<210> 267

<211> 1443

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1420)

<223> RXN01553

<400> 267

atgatgatgt cctcagcaag tccaagcgcc aagccatgct ggaaacaatt ctcgagctga 60

taccaagcca gacttaaatt tctaccttaa agtcttgagc atg act gtt cag gaa 115
 Met Thr Val Gln Glu
 1 5

ttc gac cgc gcg acc aaa ccc aca cca aaa ccc cca att gtt tct tgg 163
 Phe Asp Arg Ala Thr Lys Pro Thr Pro Lys Pro Pro Ile Val Ser Trp
 10 15 20

gcg ttt tgg gat tgg ggt tcc gcc tct ttc aac gcg gtc ctc gtg acc 211
 Ala Phe Trp Asp Trp Gly Ser Ala Ser Phe Asn Ala Val Leu Val Thr
 25 30 35

ttt att ttc tcg gtc tat ctc act gat tca gtc ggc gcc acc ctc ccc 259
 Phe Ile Phe Ser Val Tyr Leu Thr Asp Ser Val Gly Ala Thr Leu Pro
 40 45 50

gag ggt tcc aac gcc aca tca ctg tat tcg atg gcg gtc gcc atc gct 307
 Glu Gly Ser Asn Ala Thr Ser Leu Tyr Ser Met Ala Val Ala Ile Ala
 55 60 65

ggc gtc att gtt gcg gtt gtt gcc cca gtc atg ggc agg cga tca gat 355
 Gly Val Ile Val Ala Val Val Ala Pro Val Met Gly Arg Arg Ser Asp
 70 75 80 85

atc aag ggc act cgc cgc agg tca ctg cgc atg tgg aca ctt gtc acc 403
 Ile Lys Gly Thr Arg Arg Arg Ser Leu Arg Met Trp Thr Leu Val Thr

90								95				100				
gtg	ttc	ttg	atg	ttt	tgt	ctc	ttt	aca	gta	aag	aac	act	gat	ccc	aca	451
Val	Phe	Leu	Met	Phe	Cys	Leu	Phe	Thr	Val	Lys	Asn	Thr	Asp	Pro	Thr	
			105					110					115			
ttt	ttc	tgg	ttt	ggg	gta	gcc	atc	atg	gcg	atc	gcc	aac	atc	acc	ttt	499
Phe	Phe	Trp	Phe	Gly	Val	Ala	Ile	Met	Ala	Ile	Ala	Asn	Ile	Thr	Phe	
		120					125					130				
gag	ttc	gct	gaa	gtt	cag	tac	tat	gcg	cag	ctc	tcc	caa	atc	tcg	acc	547
Glu	Phe	Ala	Glu	Val	Gln	Tyr	Tyr	Ala	Gln	Leu	Ser	Gln	Ile	Ser	Thr	
	135					140					145					
cgc	gaa	aac	gtg	ggc	cga	ggt	tct	ggg	ttc	ggc	tgg	tcc	atg	ggg	tac	595
Arg	Glu	Asn	Val	Gly	Arg	Val	Ser	Gly	Phe	Gly	Trp	Ser	Met	Gly	Tyr	
150					155					160					165	
ttc	ggg	ggc	atc	gtt	cta	ctg	ctt	gtt	tgt	tac	cta	ggg	ttt	gtt	gcc	643
Phe	Gly	Gly	Ile	Val	Leu	Leu	Leu	Val	Cys	Tyr	Leu	Gly	Phe	Val	Ala	
				170					175					180		
ggg	gat	ggc	gat	acc	cgc	gga	ttc	cta	aac	ctg	ccc	atc	gaa	gac	ggc	691
Gly	Asp	Gly	Asp	Thr	Arg	Gly	Phe	Leu	Asn	Leu	Pro	Ile	Glu	Asp	Gly	
			185					190					195			
atg	aat	atc	cgc	ctc	gtc	gca	gtg	ctt	gca	gcc	gtt	tgg	ttc	ttg	gtc	739
Met	Asn	Ile	Arg	Leu	Val	Ala	Val	Leu	Ala	Ala	Val	Trp	Phe	Leu	Val	
		200					205					210				
tct	gcg	att	ccg	gca	ctt	ctt	cga	gtc	cca	gaa	att	gag	gca	cag	gta	787
Ser	Ala	Ile	Pro	Ala	Leu	Leu	Arg	Val	Pro	Glu	Ile	Glu	Ala	Gln	Val	
	215					220					225					
gct	gcc	gaa	gac	cac	ccc	aaa	ggc	ctc	ata	gct	gcc	tac	aag	gat	ctc	835
Ala	Ala	Glu	Asp	His	Pro	Lys	Gly	Leu	Ile	Ala	Ala	Tyr	Lys	Asp	Leu	
230					235					240					245	
ttt	ggg	cag	atc	gct	gag	ctg	tgg	aaa	caa	gac	cgc	aac	tcc	gtg	tat	883
Phe	Gly	Gln	Ile	Ala	Glu	Leu	Trp	Lys	Gln	Asp	Arg	Asn	Ser	Val	Tyr	
				250					255					260		
ttc	ctc	atc	gca	gca	act	gtt	ttc	cgt	gac	gga	ctc	gcc	gga	gta	ttt	931
Phe	Leu	Ile	Ala	Ala	Thr	Val	Phe	Arg	Asp	Gly	Leu	Ala	Gly	Val	Phe	
			265					270					275			
acc	ttc	ggg	gcc	atc	ctt	gcg	gtc	tct	gtg	tac	gga	cta	tct	gcc	ggg	979
Thr	Phe	Gly	Ala	Ile	Leu	Ala	Val	Ser	Val	Tyr	Gly	Leu	Ser	Ala	Gly	
		280					285					290				
gat	gtc	ctc	ctc	ttc	ggg	gtc	gca	gcc	aac	gtg	gtc	tct	gcg	ttg	gga	1027
Asp	Val	Leu	Leu	Phe	Gly	Val	Ala	Ala	Asn	Val	Val	Ser	Ala	Leu	Gly	
	295					300					305					
gca	ctc	ctc	gga	gga	ttc	cta	gac	gat	cgc	gtc	ggg	cca	aaa	ccc	atc	1075
Ala	Leu	Leu	Gly	Gly	Phe	Leu	Asp	Asp	Arg	Val	Gly	Pro	Lys	Pro	Ile	
310					315					320					325	
atc	ttg	att	tct	ctt	gcc	atc	atg	atc	gcc	gat	gct	gca	att	ctc	ttc	1123
Ile	Leu	Ile	Ser	Leu	Ala	Ile	Met	Ile	Ala	Asp	Ala	Ala	Ile	Leu	Phe	
				330					335					340		

```

ttc gtt gaa ggc ccc act aat ttc tgg atc ttc gga tta atc ctc tgt 1171
Phe Val Glu Gly Pro Thr Asn Phe Trp Ile Phe Gly Leu Ile Leu Cys
345 350 355

gcg ttt gtg gga cct gca cag tca gcg tcg aga agc tat tta aca cgt 1219
Ala Phe Val Gly Pro Ala Gln Ser Ala Ser Arg Ser Tyr Leu Thr Arg
360 365 370

ctt tcc cca gat ggc cag gaa ggc cag ctc ttc ggc ctt tat gcc act 1267
Leu Ser Pro Asp Gly Gln Glu Gly Gln Leu Phe Gly Leu Tyr Ala Thr
375 380 385

acc ggc cgt gcc gtg agt tgg atg gtg ccg tcg ctg ttt ggt gta ttt 1315
Thr Gly Arg Ala Val Ser Trp Met Val Pro Ser Leu Phe Gly Val Phe
390 395 400 405

gtg ggg ctc acc ggc gat gac cgc act ggt att ttg gcc atc gcg ctg 1363
Val Gly Leu Thr Gly Asp Asp Arg Thr Gly Ile Leu Ala Ile Ala Leu
410 415 420

att ctg cta ttc ggt att gtg ctg ctg agc atg gtg aag cca ccg cac 1411
Ile Leu Leu Phe Gly Ile Val Leu Leu Ser Met Val Lys Pro Pro His
425 430 435

aag gtg aag tagacaaagc gcccacaagg att 1443
Lys Val Lys
440

```

<210> 268

<211> 440

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 268

```

Met Thr Val Gln Glu Phe Asp Arg Ala Thr Lys Pro Thr Pro Lys Pro
1 5 10 15

Pro Ile Val Ser Trp Ala Phe Trp Asp Trp Gly Ser Ala Ser Phe Asn
20 25 30

Ala Val Leu Val Thr Phe Ile Phe Ser Val Tyr Leu Thr Asp Ser Val
35 40 45

Gly Ala Thr Leu Pro Glu Gly Ser Asn Ala Thr Ser Leu Tyr Ser Met
50 55 60

Ala Val Ala Ile Ala Gly Val Ile Val Ala Val Val Ala Pro Val Met
65 70 75 80

Gly Arg Arg Ser Asp Ile Lys Gly Thr Arg Arg Arg Ser Leu Arg Met
85 90 95

Trp Thr Leu Val Thr Val Phe Leu Met Phe Cys Leu Phe Thr Val Lys
100 105 110

Asn Thr Asp Pro Thr Phe Phe Trp Phe Gly Val Ala Ile Met Ala Ile
115 120 125

Ala Asn Ile Thr Phe Glu Phe Ala Glu Val Gln Tyr Tyr Ala Gln Leu

```


130					135					140					
Ser	Gln	Ile	Ser	Thr	Arg	Glu	Asn	Val	Gly	Arg	Val	Ser	Gly	Phe	Gly
145					150					155					160
Trp	Ser	Met	Gly	Tyr	Phe	Gly	Gly	Ile	Val	Leu	Leu	Leu	Val	Cys	Tyr
			165					170						175	
Leu	Gly	Phe	Val	Ala	Gly	Asp	Gly	Asp	Thr	Arg	Gly	Phe	Leu	Asn	Leu
			180					185					190		
Pro	Ile	Glu	Asp	Gly	Met	Asn	Ile	Arg	Leu	Val	Ala	Val	Leu	Ala	Ala
		195					200					205			
Val	Trp	Phe	Leu	Val	Ser	Ala	Ile	Pro	Ala	Leu	Leu	Arg	Val	Pro	Glu
	210					215					220				
Ile	Glu	Ala	Gln	Val	Ala	Ala	Glu	Asp	His	Pro	Lys	Gly	Leu	Ile	Ala
225						230				235					240
Ala	Tyr	Lys	Asp	Leu	Phe	Gly	Gln	Ile	Ala	Glu	Leu	Trp	Lys	Gln	Asp
			245						250					255	
Arg	Asn	Ser	Val	Tyr	Phe	Leu	Ile	Ala	Ala	Thr	Val	Phe	Arg	Asp	Gly
			260					265					270		
Leu	Ala	Gly	Val	Phe	Thr	Phe	Gly	Ala	Ile	Leu	Ala	Val	Ser	Val	Tyr
		275					280					285			
Gly	Leu	Ser	Ala	Gly	Asp	Val	Leu	Leu	Phe	Gly	Val	Ala	Ala	Asn	Val
	290					295					300				
Val	Ser	Ala	Leu	Gly	Ala	Leu	Leu	Gly	Gly	Phe	Leu	Asp	Asp	Arg	Val
305						310					315				320
Gly	Pro	Lys	Pro	Ile	Ile	Leu	Ile	Ser	Leu	Ala	Ile	Met	Ile	Ala	Asp
			325						330					335	
Ala	Ala	Ile	Leu	Phe	Phe	Val	Glu	Gly	Pro	Thr	Asn	Phe	Trp	Ile	Phe
			340					345					350		
Gly	Leu	Ile	Leu	Cys	Ala	Phe	Val	Gly	Pro	Ala	Gln	Ser	Ala	Ser	Arg
		355					360					365			
Ser	Tyr	Leu	Thr	Arg	Leu	Ser	Pro	Asp	Gly	Gln	Glu	Gly	Gln	Leu	Phe
	370					375					380				
Gly	Leu	Tyr	Ala	Thr	Thr	Gly	Arg	Ala	Val	Ser	Trp	Met	Val	Pro	Ser
385						390					395				400
Leu	Phe	Gly	Val	Phe	Val	Gly	Leu	Thr	Gly	Asp	Asp	Arg	Thr	Gly	Ile
			405					410						415	
Leu	Ala	Ile	Ala	Leu	Ile	Leu	Leu	Phe	Gly	Ile	Val	Leu	Leu	Ser	Met
			420					425					430		
Val	Lys	Pro	Pro	His	Lys	Val	Lys								
		435					440								

<400> 269																
aatcgcatgg ggcaccgtgg tcagacaccg gatcgcgctc cgcaccccaa aagatggctc																60
cctaaggagc tcaccttttac tcaatgctct gatgacaccg atg tgg tgg gca ggc																115
Met Trp Trp Ala Gly																5
1																
atg agt acc gcg atg ctg gca tat ttc tta caa aca gta gca ctt ggt																163
Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln Thr Val Ala Leu Gly																20
10 15																
ttc ggc acc ctc ttg gta gtg caa cca gtg ctt gtc ctg tcg ctg atg																211
Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu Val Leu Ser Leu Met																35
25 30																
ttc acg ctg ccg ctc tca gca cga ttc aat ggc tac cga cta cgc cga																259
Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly Tyr Arg Leu Arg Arg																50
40 45																
act gaa atc ttc tgg gct acc ctc ctc acc gta gcc gtg ggc atc atg																307
Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val Ala Val Gly Ile Met																65
55 60																
atc gtt ttg gga cgc ccc ctt ccc gga aac ccc cac ccc cca ctc gat																355
Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro His Pro Pro Leu Asp																85
70 75 80																
cga tgg att cca gta ctt tta gtc ggc gtt gca gta atg ggt gga atg																403
Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala Val Met Gly Gly Met																100
90 95																
tgg ctg ctt gcg gaa tac gta tta aag aag gac aaa gcc ctc atc ctt																451
Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp Lys Ala Leu Ile Leu																115
105 110																
ggc ctt gtg acg ggt gca ttg ttt ggc tac gta gca gtg atg tcc aaa																499
Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val Ala Val Met Ser Lys																130
120 125																
gcc gcg gtg gat ctt ttt gtc cat caa ggc ata acg gga ctc atc ttg																547
Ala Ala Val Asp Leu Phe Val His Gln Gly Ile Thr Gly Leu Ile Leu																145
135 140																
aac tgg gaa ggc tac ggc cta atc ctc acc gca tta ctt gga aca atc																595
Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala Leu Leu Gly Thr Ile																165
150 155 160																
gtg cag cag tat tcc ttt aac gct ggc gaa cta caa aaa tcg cta ccc																643
Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu Gln Lys Ser Leu Pro																180
170 175																
gcc atg acc att gcc gaa cca att gtt gcc ttc agt ttg ggc tac ttg																691

Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe Ser Leu Gly Tyr Leu
 185 190 195

gtt ctg ggc gaa aaa ttc caa gtc gtg gac tgg gaa tgg atc gcc atg 739
 Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp Glu Trp Ile Ala Met
 200 205 210

ggc atc gca cta ctg gtg atg att gtt tcc acc att gca ctg tct cgt 787
 Gly Ile Ala Leu Leu Val Met Ile Val Ser Thr Ile Ala Leu Ser Arg
 215 220 225

aca agc aca atg ccg gcc gga tcg aaa agg taaaactcca aagttccccc 837
 Thr Ser Thr Met Pro Ala Gly Ser Lys Arg
 230 235

cga 840

<210> 270
 <211> 239
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 270
 Met Trp Trp Ala Gly Met Ser Thr Ala Met Leu Ala Tyr Phe Leu Gln
 1 5 10 15

Thr Val Ala Leu Gly Phe Gly Thr Leu Leu Val Val Gln Pro Val Leu
 20 25 30

Val Leu Ser Leu Met Phe Thr Leu Pro Leu Ser Ala Arg Phe Asn Gly
 35 40 45

Tyr Arg Leu Arg Arg Thr Glu Ile Phe Trp Ala Thr Leu Leu Thr Val
 50 55 60

Ala Val Gly Ile Met Ile Val Leu Gly Arg Pro Leu Pro Gly Asn Pro
 65 70 75 80

His Pro Pro Leu Asp Arg Trp Ile Pro Val Leu Leu Val Gly Val Ala
 85 90 95

Val Met Gly Gly Met Trp Leu Leu Ala Glu Tyr Val Leu Lys Lys Asp
 100 105 110

Lys Ala Leu Ile Leu Gly Leu Val Thr Gly Ala Leu Phe Gly Tyr Val
 115 120 125

Ala Val Met Ser Lys Ala Ala Val Asp Leu Phe Val His Gln Gly Ile
 130 135 140

Thr Gly Leu Ile Leu Asn Trp Glu Gly Tyr Gly Leu Ile Leu Thr Ala
 145 150 155 160

Leu Leu Gly Thr Ile Val Gln Gln Tyr Ser Phe Asn Ala Gly Glu Leu
 165 170 175

Gln Lys Ser Leu Pro Ala Met Thr Ile Ala Glu Pro Ile Val Ala Phe
 180 185 190

Ser Leu Gly Tyr Leu Val Leu Gly Glu Lys Phe Gln Val Val Asp Trp

195	200	205	
Glu Trp Ile Ala Met Gly	Ile Ala Leu Leu Val	Met Ile Val Ser Thr	
210	215	220	
Ile Ala Leu Ser Arg Thr	Ser Thr Met Pro Ala Gly	Ser Lys Arg	
225	230	235	
 <210> 271			
<211> 2472			
<212> DNA			
<213> Corynebacterium glutamicum			
 <220>			
<221> CDS			
<222> (101)..(2449)			
<223> RXN00453			
 <400> 271			
tagtggggcg tgaaaaaata gctcatttaa gaggagaagc aaccccgtgg cgaaattgct			60
attcaggttg gggcgatggt cctataatcg caagtggatt			115
		gtg att tcg gca tgg	
		Val Ile Ser Ala Trp	
		1 5	
cta ctt att ttg gcc att gtt ggt ggt ctg gcc ctg acg atg cag aag			163
Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala Leu Thr Met Gln Lys			
	10	15	20
ggg ttc agt aac tct ttc act att gaa gac acc cct tcg att gat gcc			211
Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr Pro Ser Ile Asp Ala			
	25	30	35
act gtt tct ctg gtt gaa aat ttc cct gat cag acg aac ccg gtg acg			259
Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln Thr Asn Pro Val Thr			
	40	45	50
gcc gcc gga gtt aac gtg gtt ttc caa tcc ccg gaa gga acc acg ctt			307
Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro Glu Gly Thr Thr Leu			
	55	60	65
gat gat cct cag atg atg act gcg atg gat gca gtc gtt gat tac att			355
Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala Val Val Asp Tyr Ile			
	70	75	80
gag gac aat ttg cct gat ttt ggt ggg gga gag cgc ttc ggc aat cct			403
Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu Arg Phe Gly Asn Pro			
	90	95	100
gtt gag gtg tct cct gcg ttg gaa gag atg gtc atc gag cag atg acc			451
Val Glu Val Ser Pro Ala Leu Glu Glu Met Val Ile Glu Gln Met Thr			
	105	110	115
agc atg ggg ctt cct gag gaa acc gct gca aag gat gct gcc aat ctg			499
Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys Asp Ala Ala Asn Leu			
	120	125	130
gcg gtg ttg agc gaa gac aaa acc att ggc tac acc tct ttc aac att			547
Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr Thr Ser Phe Asn Ile			
	135	140	145

gat gtt gag gcc gca gaa tat gtg gag caa aaa cac cgc gat gtg atc	595
Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys His Arg Asp Val Ile	
150 155 160 165	
aac gaa gcg atg caa atc ggt gaa gat tta ggt gtc cgg gtg gaa gcc	643
Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly Val Arg Val Glu Ala	
170 175 180	
ggt gga cct gct ttc ggt gat cca att cag att gaa acc acc agt gag	691
Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile Glu Thr Thr Ser Glu	
185 190 195	
atc atc ggt att ggc atc gcg ttc atc gtg ttg att ttc acc ttt ggt	739
Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu Ile Phe Thr Phe Gly	
200 205 210	
tct ttg att gct gca ggc ttg cct ttg att acc gcg gtg atc ggc gtg	787
Ser Leu Ile Ala Ala Gly Leu Pro Leu Ile Thr Ala Val Ile Gly Val	
215 220 225	
ggc att ggt gcg ctg gca att gtg ctg gcc acg gcg ttt act gat ctc	835
Gly Ile Gly Ala Leu Ala Ile Val Leu Ala Thr Ala Phe Thr Asp Leu	
230 235 240 245	
aac aat gtg act cca gtg ctc gca gtg atg att ggc ctg gcc gtg ggc	883
Asn Asn Val Thr Pro Val Leu Ala Val Met Ile Gly Leu Ala Val Gly	
250 255 260	
att gac tac gcg ctg ttt att ttg tct agg tac cgt gcg gag tat aag	931
Ile Asp Tyr Ala Leu Phe Ile Leu Ser Arg Tyr Arg Ala Glu Tyr Lys	
265 270 275	
cgc atg cca cgt gcc gat gct gcc gga atg gcg gtg ggc aca gct ggt	979
Arg Met Pro Arg Ala Asp Ala Ala Gly Met Ala Val Gly Thr Ala Gly	
280 285 290	
agt gcg gtg gtg ttt gct ggc gcg acg gtg att atc gcg ctg gta gcc	1027
Ser Ala Val Val Phe Ala Gly Ala Thr Val Ile Ile Ala Leu Val Ala	
295 300 305	
ctc atc att gcg gat atc gga ttc ctc acg gcc atg ggt att tct gcg	1075
Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala Met Gly Ile Ser Ala	
310 315 320 325	
gcg ttt acg gtg ttc gtg gct gtg ctc att gcg ttg acg ttt atc ccg	1123
Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala Leu Thr Phe Ile Pro	
330 335 340	
gcg ctg ttg ggt gtg ttt ggt ggt cat gcg ttc aag ggc aag atc cct	1171
Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe Lys Gly Lys Ile Pro	
345 350 355	
gga att ggt gga aac cca acg cca aag cag acg tgg gag caa gcg ctt	1219
Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr Trp Glu Gln Ala Leu	
360 365 370	
aat cgt cgt tcc aag ggt cgc tca tgg gtc aag ctt gta cag aaa gca	1267
Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys Leu Val Gln Lys Ala	
375 380 385	

ccg ggt ctt gtg gtg gca gtg gtg gtc ttg ggt ctt ggt gcc ttg acc	1315
Pro Gly Leu Val Val Ala Val Val Val Leu Gly Leu Gly Ala Leu Thr	
390 395 400 405	
att cct gca atg aac ctg cag ttg tca ctg cct tct gac tcc acc tcc	1363
Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro Ser Asp Ser Thr Ser	
410 415 420	
aat att gat acc act cag cgt cag tcg gct gat ttg atg gca gag ggc	1411
Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp Leu Met Ala Glu Gly	
425 430 435	
ttt ggc gcg ggc gtt aat gcg ccg ttc ttg gtc atc gtc gat acg cat	1459
Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val Ile Val Asp Thr His	
440 445 450	
gag gtc aat gct gat tcc acc gca ttg cag cca ctg att gag gca cag	1507
Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro Leu Ile Glu Ala Gln	
455 460 465	
gag cct gaa gag ggc gag ttc gat cgg gag cag gcg gct cgt ttt gct	1555
Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln Ala Ala Arg Phe Ala	
470 475 480 485	
acc tat atg tat gtc acc cag acc tac aat tcc aac atc gat gtg aag	1603
Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser Asn Ile Asp Val Lys	
490 495 500	
aat gcg cag atc atc agc gtc aat gat gat ttc act gcg gcg cag att	1651
Asn Ala Gln Ile Ile Ser Val Asn Asp Phe Thr Ala Ala Gln Ile	
505 510 515	
ctc gtg act cca tac acc gga cct gcg gat aaa gag acc cct gag ttg	1699
Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys Glu Thr Pro Glu Leu	
520 525 530	
atg cac gtg ctg cgt gcg cag gaa gct cag att gag gat gtt acg gga	1747
Met His Val Leu Arg Ala Gln Glu Ala Gln Ile Glu Asp Val Thr Gly	
535 540 545	
act gaa ctg ggt acc act ggg ttt acg gcg gtt cag ttg gac att act	1795
Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val Gln Leu Asp Ile Thr	
550 555 560 565	
gag cag ctg gaa gac gca atg ccg gtt tac ctc gct gtg gtt gtt ggt	1843
Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu Ala Val Val Val Gly	
570 575 580	
ttg gct att ttc ctc ctc att ctg gtg ttc cgt tcc ctg ctt gtt ccg	1891
Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg Ser Leu Leu Val Pro	
585 590 595	
ctg gtt gct ggc ctt ggc ttc ttg ttg tct gtg ggt gcg gcc ttc ggt	1939
Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val Gly Ala Ala Phe Gly	
600 605 610	
gcg acg gtg ttg gtc tgg cag gag ggc ttc ggt ggc ttt gtg aac acc	1987
Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly Gly Phe Val Asn Thr	
615 620 625	
cct ggt ccg ctg att tcc ttc atg ccg atc ttc ctc atc ggc gtg acc	2035

Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe Leu Ile Gly Val Thr
630 635 640 645

ttc ggt ttg gcc atg gac tat cag gtg ttc ctt gtg act cgc atg cgc 2083
Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu Val Thr Arg Met Arg
650 655 660

gag cac tac acc cac cac aat ggc aag gga cag cct ggt tcc aag tac 2131
Glu His Tyr Thr His His Asn Gly Lys Gly Gln Pro Gly Ser Lys Tyr
665 670 675

acc ccg gtt gag cag tca gtg att gaa ggc ttc acg cag ggc tcc cgc 2179
Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe Thr Gln Gly Ser Arg
680 685 690

gtg gtt aca gca gcg gca ctg atc atg att gcc gtg ttc gtg gcg ttt 2227
Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala Val Phe Val Ala Phe
695 700 705

att gat cag ccg ttg cca ttt att aag atc ttc ggt ttc gcg ttg ggt 2275
Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe Gly Phe Ala Leu Gly
710 715 720 725

gcg ggc gtg ttt ttc gat gct ttc ttc att cgc atg ggt ctg gtc ccc 2323
Ala Gly Val Phe Phe Asp Ala Phe Phe Ile Arg Met Gly Leu Val Pro
730 735 740

gcg tcg atg ttc ctg atg ggc aag gcc acg tgg tgg atg cct aag tgg 2371
Ala Ser Met Phe Leu Met Gly Lys Ala Thr Trp Trp Met Pro Lys Trp
745 750 755

ctg gat cga att ctg cca agt ttg gac att gaa ggc acc gca ctg gag 2419
Leu Asp Arg Ile Leu Pro Ser Leu Asp Ile Glu Gly Thr Ala Leu Glu
760 765 770

aag gaa tgg gag gag aag cag gct gca cgt tagacttggc acctatgtca 2469
Lys Glu Trp Glu Glu Lys Gln Ala Ala Arg
775 780

gat 2472

<210> 272

<211> 783

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 272

Val Ile Ser Ala Trp Leu Leu Ile Leu Ala Ile Val Gly Gly Leu Ala
1 5 10 15

Leu Thr Met Gln Lys Gly Phe Ser Asn Ser Phe Thr Ile Glu Asp Thr
20 25 30

Pro Ser Ile Asp Ala Thr Val Ser Leu Val Glu Asn Phe Pro Asp Gln
35 40 45

Thr Asn Pro Val Thr Ala Ala Gly Val Asn Val Val Phe Gln Ser Pro
50 55 60

Glu Gly Thr Thr Leu Asp Asp Pro Gln Met Met Thr Ala Met Asp Ala

65	70	75	80
Val Val Asp Tyr	Ile Glu Asp Asn Leu Pro Asp Phe Gly Gly Gly Glu		
	85	90	95
Arg Phe Gly Asn Pro Val Glu Val Ser Pro Ala Leu Glu Glu Met Val			
	100	105	110
Ile Glu Gln Met Thr Ser Met Gly Leu Pro Glu Glu Thr Ala Ala Lys			
	115	120	125
Asp Ala Ala Asn Leu Ala Val Leu Ser Glu Asp Lys Thr Ile Gly Tyr			
	130	135	140
Thr Ser Phe Asn Ile Asp Val Glu Ala Ala Glu Tyr Val Glu Gln Lys			
	145	150	155
His Arg Asp Val Ile Asn Glu Ala Met Gln Ile Gly Glu Asp Leu Gly			
	165	170	175
Val Arg Val Glu Ala Gly Gly Pro Ala Phe Gly Asp Pro Ile Gln Ile			
	180	185	190
Glu Thr Thr Ser Glu Ile Ile Gly Ile Gly Ile Ala Phe Ile Val Leu			
	195	200	205
Ile Phe Thr Phe Gly Ser Leu Ile Ala Ala Gly Leu Pro Leu Ile Thr			
	210	215	220
Ala Val Ile Gly Val Gly Ile Gly Ala Leu Ala Ile Val Leu Ala Thr			
	225	230	235
Ala Phe Thr Asp Leu Asn Asn Val Thr Pro Val Leu Ala Val Met Ile			
	245	250	255
Gly Leu Ala Val Gly Ile Asp Tyr Ala Leu Phe Ile Leu Ser Arg Tyr			
	260	265	270
Arg Ala Glu Tyr Lys Arg Met Pro Arg Ala Asp Ala Ala Gly Met Ala			
	275	280	285
Val Gly Thr Ala Gly Ser Ala Val Val Phe Ala Gly Ala Thr Val Ile			
	290	295	300
Ile Ala Leu Val Ala Leu Ile Ile Ala Asp Ile Gly Phe Leu Thr Ala			
	305	310	315
Met Gly Ile Ser Ala Ala Phe Thr Val Phe Val Ala Val Leu Ile Ala			
	325	330	335
Leu Thr Phe Ile Pro Ala Leu Leu Gly Val Phe Gly Gly His Ala Phe			
	340	345	350
Lys Gly Lys Ile Pro Gly Ile Gly Gly Asn Pro Thr Pro Lys Gln Thr			
	355	360	365
Trp Glu Gln Ala Leu Asn Arg Arg Ser Lys Gly Arg Ser Trp Val Lys			
	370	375	380
Leu Val Gln Lys Ala Pro Gly Leu Val Val Ala Val Val Val Leu Gly			
	385	390	395
			400

Leu Gly Ala Leu Thr Ile Pro Ala Met Asn Leu Gln Leu Ser Leu Pro
 405 410 415
 Ser Asp Ser Thr Ser Asn Ile Asp Thr Thr Gln Arg Gln Ser Ala Asp
 420 425 430
 Leu Met Ala Glu Gly Phe Gly Ala Gly Val Asn Ala Pro Phe Leu Val
 435 440 445
 Ile Val Asp Thr His Glu Val Asn Ala Asp Ser Thr Ala Leu Gln Pro
 450 455 460
 Leu Ile Glu Ala Gln Glu Pro Glu Glu Gly Glu Phe Asp Arg Glu Gln
 465 470 475 480
 Ala Ala Arg Phe Ala Thr Tyr Met Tyr Val Thr Gln Thr Tyr Asn Ser
 485 490 495
 Asn Ile Asp Val Lys Asn Ala Gln Ile Ile Ser Val Asn Asp Asp Phe
 500 505 510
 Thr Ala Ala Gln Ile Leu Val Thr Pro Tyr Thr Gly Pro Ala Asp Lys
 515 520 525
 Glu Thr Pro Glu Leu Met His Val Leu Arg Ala Gln Glu Ala Gln Ile
 530 535 540
 Glu Asp Val Thr Gly Thr Glu Leu Gly Thr Thr Gly Phe Thr Ala Val
 545 550 555 560
 Gln Leu Asp Ile Thr Glu Gln Leu Glu Asp Ala Met Pro Val Tyr Leu
 565 570 575
 Ala Val Val Val Gly Leu Ala Ile Phe Leu Leu Ile Leu Val Phe Arg
 580 585 590
 Ser Leu Leu Val Pro Leu Val Ala Gly Leu Gly Phe Leu Leu Ser Val
 595 600 605
 Gly Ala Ala Phe Gly Ala Thr Val Leu Val Trp Gln Glu Gly Phe Gly
 610 615 620
 Gly Phe Val Asn Thr Pro Gly Pro Leu Ile Ser Phe Met Pro Ile Phe
 625 630 635 640
 Leu Ile Gly Val Thr Phe Gly Leu Ala Met Asp Tyr Gln Val Phe Leu
 645 650 655
 Val Thr Arg Met Arg Glu His Tyr Thr His His Asn Gly Lys Gly Gln
 660 665 670
 Pro Gly Ser Lys Tyr Thr Pro Val Glu Gln Ser Val Ile Glu Gly Phe
 675 680 685
 Thr Gln Gly Ser Arg Val Val Thr Ala Ala Ala Leu Ile Met Ile Ala
 690 695 700
 Val Phe Val Ala Phe Ile Asp Gln Pro Leu Pro Phe Ile Lys Ile Phe
 705 710 715 720

<400> 273															60	
cccaattaat ttatgcactt cggtgaggtt actcacaag agtagcgtgc aaagcccagc																
aataaggtga tgtttcaacg attaggttac ggtaggggcc															115	
Met Thr Pro Gln Lys															5	
1																
ctt	cac	cgt	ttt	gca	gcc	ctt	tta	gaa	atg	ggt	acc	tgg	acc	ctg	ctg	163
Leu	His	Arg	Phe	Ala	Ala	Leu	Leu	Glu	Met	Gly	Thr	Trp	Thr	Leu	Leu	20
10 15																
atc	atc	ggc	atg	atc	tta	aaa	tac	agt	gga	gtg	aca	gac	gcc	gta	acc	211
Ile	Ile	Gly	Met	Ile	Leu	Lys	Tyr	Ser	Gly	Val	Thr	Asp	Ala	Val	Thr	25 30 35
cct att gcc ggc ggt atc cac ggc ttt ggc ttc ctc tgt ttt gca gcc															259	
Pro	Ile	Ala	Gly	Gly	Ile	His	Gly	Phe	Gly	Phe	Leu	Cys	Phe	Ala	Ala	40 45 50
atc acc atc acc gtg tgg atc aat aat aag tgg aca ttc ccg cag ggt															307	
Ile	Thr	Ile	Thr	Val	Trp	Ile	Asn	Asn	Lys	Trp	Thr	Phe	Pro	Gln	Gly	55 60 65
atc gca ggt ttg atc gtc tct gtt atc ccg tgg gct gca ttg cca ttt															355	
Ile	Ala	Gly	Leu	Ile	Val	Ser	Val	Ile	Pro	Trp	Ala	Ala	Leu	Pro	Phe	70 75 80 85
gca ttg tgg gca gac aag aag ggc ctc gtt gcc ggc gga tgg cgc ttt															403	
Ala	Leu	Trp	Ala	Asp	Lys	Lys	Gly	Leu	Val	Ala	Gly	Gly	Trp	Arg	Phe	90 95 100
tca gat ccg tcc gaa aag cca cac act ttc ttt gac aag atc ttg gct															451	
Ser	Asp	Pro	Ser	Glu	Lys	Pro	His	Thr	Phe	Phe	Asp	Lys	Ile	Leu	Ala	105 110 115
caa ttg gtc agg cac cca atc cga tcc att tta att ctg ctg gtg att															499	
Gln	Leu	Val	Arg	His	Pro	Ile	Arg	Ser	Ile	Leu	Ile	Leu	Leu	Val	Ile	120 125 130

atc gcc gtc gtc ttc tct atc ttg ctg gcg atg gga cca cct tat gat 547
 Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met Gly Pro Pro Tyr Asp
 135 140 145

cca gat gcc atc gca aac act gtg gat taaacaacag cctccttcac 594
 Pro Asp Ala Ile Ala Asn Thr Val Asp
 150 155

atg 597

<210> 274

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

Met Thr Pro Gln Lys Leu His Arg Phe Ala Ala Leu Leu Glu Met Gly
 1 5 10 15

Thr Trp Thr Leu Leu Ile Ile Gly Met Ile Leu Lys Tyr Ser Gly Val
 20 25 30

Thr Asp Ala Val Thr Pro Ile Ala Gly Gly Ile His Gly Phe Gly Phe
 35 40 45

Leu Cys Phe Ala Ala Ile Thr Ile Thr Val Trp Ile Asn Asn Lys Trp
 50 55 60

Thr Phe Pro Gln Gly Ile Ala Gly Leu Ile Val Ser Val Ile Pro Trp
 65 70 75 80

Ala Ala Leu Pro Phe Ala Leu Trp Ala Asp Lys Lys Gly Leu Val Ala
 85 90 95

Gly Gly Trp Arg Phe Ser Asp Pro Ser Glu Lys Pro His Thr Phe Phe
 100 105 110

Asp Lys Ile Leu Ala Gln Leu Val Arg His Pro Ile Arg Ser Ile Leu
 115 120 125

Ile Leu Leu Val Ile Ile Ala Val Val Phe Ser Ile Leu Leu Ala Met
 130 135 140

Gly Pro Pro Tyr Asp Pro Asp Ala Ile Ala Asn Thr Val Asp
 145 150 155

<210> 275

<211> 534

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (65)..(511)

<223> RXN03022

<400> 275

acgcctgtgt catccttttc attagagtgg agaaaagccc atacagaaag ttggcgcccg 60

```

agca gtg atc atc acc gct ggc atc ttg gta gcg acc gcg acc gcc ctc 109
Val Ile Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu
1 5 10 15

cta atg atc acc gcg gtc agc gag tca acg tac atc gtc atc tcc ctc 157
Leu Met Ile Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu
20 25 30

gcc ggc ttc tcc ctt tat ggc ctt ggc ctc gga ctc ttc gcc acc cca 205
Ala Gly Phe Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro
35 40 45

gtc acc gat act gcg ctt gga aca ctt ccc aaa gac cgt acc ggc gct 253
Val Thr Asp Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala
50 55 60

ggg gca ggt gta ttc aag atg tcc tct tcc ctc ggc gca gca ctc ggc 301
Gly Ala Gly Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly
65 70 75

atc gca atc tcc act tca gtg ttc ctc gca ctt cgc gac ggc acc tcc 349
Ile Ala Ile Ser Thr Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser
80 85 90 95

atc aac tcc gac gtc gca ctc gcc gga aca gtt tca ctt ggc atc aac 397
Ile Asn Ser Asp Val Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn
100 105 110

gtt gta ttc gca gca aca gcc acc atc acc gca gca gtc ctt att cca 445
Val Val Phe Ala Ala Thr Ala Thr Ile Thr Ala Ala Val Leu Ile Pro
115 120 125

aaa gcc gct ggc aaa gtc tca caa acc agc atc acc ctt cct gag cca 493
Lys Ala Ala Gly Lys Val Ser Gln Thr Ser Ile Thr Leu Pro Glu Pro
130 135 140

gct atc gct gta aaa atc taaaacttca ccaggacaga taa 534
Ala Ile Ala Val Lys Ile
145

```

<210> 276

<211> 149

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 276

```

Val Ile Ile Thr Ala Gly Ile Leu Val Ala Thr Ala Thr Ala Leu Leu
1 5 10 15

Met Ile Thr Ala Val Ser Glu Ser Thr Tyr Ile Val Ile Ser Leu Ala
20 25 30

Gly Phe Ser Leu Tyr Gly Leu Gly Leu Gly Leu Phe Ala Thr Pro Val
35 40 45

Thr Asp Thr Ala Leu Gly Thr Leu Pro Lys Asp Arg Thr Gly Ala Gly
50 55 60

Ala Gly Val Phe Lys Met Ser Ser Ser Leu Gly Ala Ala Leu Gly Ile

```

65		70		75		80
Ala Ile Ser Thr	Ser Val Phe Leu Ala Leu Arg Asp Gly Thr Ser Ile					
	85		90		95	
Asn Ser Asp Val	Ala Leu Ala Gly Thr Val Ser Leu Gly Ile Asn Val					
	100		105		110	
Val Phe Ala Ala Thr	Ala Thr Ile Thr Ala Ala Val Leu Ile Pro Lys					
	115		120		125	
Ala Ala Gly Lys Val Ser	Gln Thr Ser Ile Thr Leu Pro Glu Pro Ala					
	130		135		140	
Ile Ala Val Lys Ile						
145						

<210> 277
 <211> 586
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(586)
 <223> RXN03151

<400> 277
 ccgaacttgg agcttttgctg ttggaggcag ccaaatagtc ccaatgtaaa cgactggggt 60
 agtatttggt taaccatcca cctcaaggag taaaacgcac gtg ctt tcc cac atc 115
 Val Leu Ser His Ile
 1 5
 att gat gtc ctc gcc gac ccg atc gat ggc acc cca ctt gta ggc gcc 163
 Ile Asp Val Leu Ala Asp Pro Ile Asp Gly Thr Pro Leu Val Gly Ala
 10 15 20
 gaa gat ttc tca cgg ttg gtg tct gaa tct ggg cat tcc tac gat gtt 211
 Glu Asp Phe Ser Arg Leu Val Ser Glu Ser Gly His Ser Tyr Asp Val
 25 30 35
 gct cgt caa ggg tat gtc acc ctg gct ggt ggc gca ggt ctg cgc tat 259
 Ala Arg Gln Gly Tyr Val Thr Leu Ala Gly Gly Ala Gly Leu Arg Tyr
 40 45 50
 tca ggc gat gat gca cag atg atc gcg gat cgg gaa acc ttc ctt tct 307
 Ser Gly Asp Asp Ala Gln Met Ile Ala Asp Arg Glu Thr Phe Leu Ser
 55 60 65
 ggc ggt cac ttc gcg ccc ttc gtg gaa gct gtc acc gag cat gtt caa 355
 Gly Gly His Phe Ala Pro Phe Val Glu Ala Val Thr Glu His Val Gln
 70 75 80 85
 gat gtc gtt gac cag gca ggc ctt agc gat gac gca cag cca gtg gtc 403
 Asp Val Val Asp Gln Ala Gly Leu Ser Asp Asp Ala Gln Pro Val Val
 90 95 100
 tgc gaa atc ggc gcg gga acc ggc tac tac ttg tcc cat acc ctt gat 451
 Cys Glu Ile Gly Ala Gly Thr Gly Tyr Tyr Leu Ser His Thr Leu Asp

105	110	115	
tct gtt gca gga tct cgc gga att ggc att gac gtt tcc gtg cac gcc			499
Ser Val Ala Gly Ser Arg Gly Ile Gly Ile Asp Val Ser Val His Ala			
120	125	130	
gca aag cgt ttg gca aag tgt cac cct cgc gtc ggc gca gtc atc gcg			547
Ala Lys Arg Leu Ala Lys Cys His Pro Arg Val Gly Ala Val Ile Ala			
135	140	145	
aac gca tgg gca cgc ctg ccg att gca gat aac tcc tcg			586
Asn Ala Trp Ala Arg Leu Pro Ile Ala Asp Asn Ser Ser			
150	155	160	

<210> 278
 <211> 162
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 278
 Val Leu Ser His Ile Ile Asp Val Leu Ala Asp Pro Ile Asp Gly Thr
 1 5 10 15
 Pro Leu Val Gly Ala Glu Asp Phe Ser Arg Leu Val Ser Glu Ser Gly
 20 25 30
 His Ser Tyr Asp Val Ala Arg Gln Gly Tyr Val Thr Leu Ala Gly Gly
 35 40 45
 Ala Gly Leu Arg Tyr Ser Gly Asp Asp Ala Gln Met Ile Ala Asp Arg
 50 55 60
 Glu Thr Phe Leu Ser Gly Gly His Phe Ala Pro Phe Val Glu Ala Val
 65 70 75 80
 Thr Glu His Val Gln Asp Val Val Asp Gln Ala Gly Leu Ser Asp Asp
 85 90 95
 Ala Gln Pro Val Val Cys Glu Ile Gly Ala Gly Thr Gly Tyr Tyr Leu
 100 105 110
 Ser His Thr Leu Asp Ser Val Ala Gly Ser Arg Gly Ile Gly Ile Asp
 115 120 125
 Val Ser Val His Ala Ala Lys Arg Leu Ala Lys Cys His Pro Arg Val
 130 135 140
 Gly Ala Val Ile Ala Asn Ala Trp Ala Arg Leu Pro Ile Ala Asp Asn
 145 150 155 160
 Ser Ser

<210> 279
 <211> 543
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>

<221> CDS
 <222> (1)..(543)
 <223> RXN02832

<400> 279

cgc ggg cca gtg atg gat tat aca aat caa tca tta gta gca ttt ttc	48
Arg Gly Pro Val Met Asp Tyr Thr Asn Gln Ser Leu Val Ala Phe Phe	
1 5 10 15	
ttt aaa gca tta acg tca tat tta aag aaa cac aat tgt tta tat gtc	96
Phe Lys Ala Leu Thr Ser Tyr Leu Lys Lys His Asn Cys Leu Tyr Val	
20 25 30	
ctt gta gat cca tat tta att gaa aat tta cgc aat gca gac ggt gaa	144
Leu Val Asp Pro Tyr Leu Ile Glu Asn Leu Arg Asn Ala Asp Gly Glu	
35 40 45	
att gtt aaa tct tat gat aac cga gca ttt gtt aga aca atg gat aaa	192
Ile Val Lys Ser Tyr Asp Asn Arg Ala Phe Val Arg Thr Met Asp Lys	
50 55 60	
tta ggt tat aaa cac caa ggt ttc cct gta ggt tat gat tca atg agc	240
Leu Gly Tyr Lys His Gln Gly Phe Pro Val Gly Tyr Asp Ser Met Ser	
65 70 75 80	
caa atc cgt tgg ctg tca gtg tta gat tta aaa gat aag act gaa gac	288
Gln Ile Arg Trp Leu Ser Val Leu Asp Leu Lys Asp Lys Thr Glu Asp	
85 90 95	
caa ctt tta aaa gaa atg gat tat caa acg aga cgt aat att aaa aaa	336
Gln Leu Leu Lys Glu Met Asp Tyr Gln Thr Arg Arg Asn Ile Lys Lys	
100 105 110	
aca tat gat att ggt gtc aaa act aaa acg tta acg att gat gaa acg	384
Thr Tyr Asp Ile Gly Val Lys Thr Lys Thr Leu Thr Ile Asp Glu Thr	
115 120 125	
caa act ttt ttc gac tta ttc cat atg gct gag gaa aag cac ggt ttc	432
Gln Thr Phe Phe Asp Leu Phe His Met Ala Glu Glu Lys His Gly Phe	
130 135 140	
aaa ttc cgt gag tta cca tac ttt gaa gaa atg caa aag tta tac gat	480
Lys Phe Arg Glu Leu Pro Tyr Phe Glu Glu Met Gln Lys Leu Tyr Asp	
145 150 155 160	
gac cac gcc atg tta aag ttg gcg tat att gat tta aac gag tat tta	528
Asp His Ala Met Leu Lys Leu Ala Tyr Ile Asp Leu Asn Glu Tyr Leu	
165 170 175	
aaa acg ttg caa tta	543
Lys Thr Leu Gln Leu	
180	

<210> 280
 <211> 181
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 280

Arg Gly Pro Val Met Asp Tyr Thr Asn Gln Ser Leu Val Ala Phe Phe

```
<210> 281
<211> 1539
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1516)
<223> RXN00165
```

<400> 281
aaacctcccc gggcccggcg cgcgaccgtc caagatgccg gcgttggatg ccaaattatg 60

gactctcaaa gtggcgttgt cgcagcggcc gtggagcttt gtg gcg tct gct ggc 115
Val Ala Ser Ala Gly
1 5

atg gcg gcg tct ttt atc tgc aat ggg tta acg cct gtg att gtg ggt 163
Met Ala Ala Ser Phe Ile Cys Asn Gly Leu Thr Pro Val Ile Val Gly
10 15 20

aag gcg gtg gat gag gct att ggc acg agc gat ctg cag cga ttg tgg 211
Lys Ala Val Asp Glu Ala Ile Gly Thr Ser Asp Leu Gln Arg Leu Trp
25 30 35

ttc tgg att gcc atg ttg gcg gtt ctt ttc tta acg gcg atg acg gtg	259
Phe Trp Ile Ala Met Leu Ala Val Leu Phe Leu Thr Ala Met Thr Val	
40 45 50	
aac tgg att gct cgg tac atg ttg gtg cgg agc cag cag ttg gtc agc	307
Asn Trp Ile Ala Arg Tyr Met Leu Val Arg Ser Gln Gln Leu Val Ser	
55 60 65	
cat gat ttg cgc atg ttg gtg act gat cgg att caa gat ccg cgt ggt	355
His Asp Leu Arg Met Leu Val Thr Asp Arg Ile Gln Asp Pro Arg Gly	
70 75 80 85	
ttt gct gga aaa gag cgc act gcg ggt gga ttg ttg tcg att gcg tca	403
Phe Ala Gly Lys Glu Arg Thr Ala Gly Gly Leu Leu Ser Ile Ala Ser	
90 95 100	
tcg gat acg cag cgg gtg ggc gat atc gtc atg atg acg gtg ttc ccg	451
Ser Asp Thr Gln Arg Val Gly Asp Ile Val Met Met Thr Val Phe Pro	
105 110 115	
gtg gcg gaa ttg gcg tcg att att tat ggc gcc gtg gtg atg tac agc	499
Val Ala Glu Leu Ala Ser Ile Ile Tyr Gly Ala Val Val Met Tyr Ser	
120 125 130	
att aat ccg tgg ttg agt gtg gct gtg ctg att ggt gga ccg ctg ctg	547
Ile Asn Pro Trp Leu Ser Val Ala Val Leu Ile Gly Gly Pro Leu Leu	
135 140 145	
gtt gtg gtg gct att cag gtc tca aag ccg ttg cag aag cgt tcg ggt	595
Val Val Val Ala Ile Gln Val Ser Lys Pro Leu Gln Lys Arg Ser Gly	
150 155 160 165	
gct cgt cag cag gcg gtg gca cag gct gcg gct act gca act gat gtg	643
Ala Arg Gln Gln Ala Val Ala Gln Ala Ala Thr Ala Thr Asp Val	
170 175 180	
gtg cag ggc ttg aga att ttg aag ggt ttg ggc gcg att gtc acg gtg	691
Val Gln Gly Leu Arg Ile Leu Lys Gly Leu Gly Ala Ile Val Thr Val	
185 190 195	
cgc cgt cgg tac gag gcg att tct ggt gag gct tat ccg aag acg gtt	739
Arg Arg Arg Tyr Glu Ala Ile Ser Gly Glu Ala Tyr Arg Lys Thr Val	
200 205 210	
cat gcg gat gct gcg gaa gct cgc ttg aat ggt gtc acc gat gcg gcg	787
His Ala Asp Ala Ala Glu Ala Arg Leu Asn Gly Val Thr Asp Ala Ala	
215 220 225	
ggc gcc atc ttt gtg tcc gcg ttg ggt att gga gca gga ttt ttg gcg	835
Gly Ala Ile Phe Val Ser Ala Leu Gly Ile Gly Ala Gly Phe Leu Ala	
230 235 240 245	
ctg caa ggt cag atg agt att ggt gat ttg atc acg gtt gtg gga ctc	883
Leu Gln Gly Gln Met Ser Ile Gly Asp Leu Ile Thr Val Val Gly Leu	
250 255 260	
aca cag ttt ttg atc atg ccg atg acc atg ctt ggt cga aat gtg gca	931
Thr Gln Phe Leu Ile Met Pro Met Thr Met Leu Gly Arg Asn Val Ala	
265 270 275	
tcg cgc tgg gca tcg gcg gag gcg tcg gca aag cgt att agg gga gtg	979

```

Ser Arg Trp Ala Ser Ala Glu Ala Ser Ala Lys Arg Ile Arg Gly Val
280                               285                               290

ctc ggt gct gat ttt gag aga gtg tct gcg cat gat gcg gac aag gct 1027
Leu Gly Ala Asp Phe Glu Arg Val Ser Ala His Asp Ala Asp Lys Ala
295                               300                               305

gag gag att atc caa caa ctt gcc aaa ggt ttg acg gtt att cga ggc 1075
Glu Glu Ile Ile Gln Gln Leu Ala Lys Gly Leu Thr Val Ile Arg Gly
310                               315                               320                               325

act gat gag cag ctc gtt gag gta tta gag cag ttg cca cgt act cgg 1123
Thr Asp Glu Gln Leu Val Glu Val Leu Glu Gln Leu Pro Arg Thr Arg
330                               335                               340

gtg att gtg gct cct cat gcg gcg gat ctt ttt gat caa agt gtc agg 1171
Val Ile Val Ala Pro His Ala Ala Asp Leu Phe Asp Gln Ser Val Arg
345                               350                               355

gac aat gtg cat ccc gtg gca gag gtc gcg gag aaa gcc att gaa gtt 1219
Asp Asn Val His Pro Val Ala Glu Val Ala Glu Lys Ala Ile Glu Val
360                               365                               370

gcc tcc tgt gac gat att cca ggt ggt agt tcc aag att gtg ggc gag 1267
Ala Ser Cys Asp Asp Ile Pro Gly Gly Ser Ser Lys Ile Val Gly Glu
375                               380                               385

ggt gga cgg ttg ctc tcg ggt ggt cag cgt cag cgc gtt gca ctg gct 1315
Gly Gly Arg Leu Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Leu Ala
390                               395                               400                               405

cgg gcg att gct ttt gat cca gag gtg ttg gtg ctt caa gat ccc aca 1363
Arg Ala Ile Ala Phe Asp Pro Glu Val Leu Val Leu Gln Asp Pro Thr
410                               415                               420

acg gca gtg gat tct gtg acg gag caa aac att gct cag caa gtg gca 1411
Thr Ala Val Asp Ser Val Thr Glu Gln Asn Ile Ala Gln Gln Val Ala
425                               430                               435

gca cac cgt gca gga aaa gtg acc att gtg ttt agt gag gca ccc gcg 1459
Ala His Arg Ala Gly Lys Val Thr Ile Val Phe Ser Glu Ala Pro Ala
440                               445                               450

tgg agt gcg gtg gct gat caa cac gtt gag gca gct gct ttg cgg gag 1507
Trp Ser Ala Val Ala Asp Gln His Val Glu Ala Ala Ala Leu Arg Glu
455                               460                               465

gtt atg aaa tgagtgggga gacgtcgaaa agc 1539
Val Met Lys
470

```

<210> 282

<211> 472

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 282

```

Val Ala Ser Ala Gly Met Ala Ala Ser Phe Ile Cys Asn Gly Leu Thr
1           5           10           15

```

Pro Val Ile Val Gly Lys Ala Val Asp Glu Ala Ile Gly Thr Ser Asp
 20 25 30
 Leu Gln Arg Leu Trp Phe Trp Ile Ala Met Leu Ala Val Leu Phe Leu
 35 40 45
 Thr Ala Met Thr Val Asn Trp Ile Ala Arg Tyr Met Leu Val Arg Ser
 50 55 60
 Gln Gln Leu Val Ser His Asp Leu Arg Met Leu Val Thr Asp Arg Ile
 65 70 75 80
 Gln Asp Pro Arg Gly Phe Ala Gly Lys Glu Arg Thr Ala Gly Gly Leu
 85 90 95
 Leu Ser Ile Ala Ser Ser Asp Thr Gln Arg Val Gly Asp Ile Val Met
 100 105 110
 Met Thr Val Phe Pro Val Ala Glu Leu Ala Ser Ile Ile Tyr Gly Ala
 115 120 125
 Val Val Met Tyr Ser Ile Asn Pro Trp Leu Ser Val Ala Val Leu Ile
 130 135 140
 Gly Gly Pro Leu Leu Val Val Val Ala Ile Gln Val Ser Lys Pro Leu
 145 150 155 160
 Gln Lys Arg Ser Gly Ala Arg Gln Gln Ala Val Ala Gln Ala Ala Ala
 165 170 175
 Thr Ala Thr Asp Val Val Gln Gly Leu Arg Ile Leu Lys Gly Leu Gly
 180 185 190
 Ala Ile Val Thr Val Arg Arg Arg Tyr Glu Ala Ile Ser Gly Glu Ala
 195 200 205
 Tyr Arg Lys Thr Val His Ala Asp Ala Ala Glu Ala Arg Leu Asn Gly
 210 215 220
 Val Thr Asp Ala Ala Gly Ala Ile Phe Val Ser Ala Leu Gly Ile Gly
 225 230 235 240
 Ala Gly Phe Leu Ala Leu Gln Gly Gln Met Ser Ile Gly Asp Leu Ile
 245 250 255
 Thr Val Val Gly Leu Thr Gln Phe Leu Ile Met Pro Met Thr Met Leu
 260 265 270
 Gly Arg Asn Val Ala Ser Arg Trp Ala Ser Ala Glu Ala Ser Ala Lys
 275 280 285
 Arg Ile Arg Gly Val Leu Gly Ala Asp Phe Glu Arg Val Ser Ala His
 290 295 300
 Asp Ala Asp Lys Ala Glu Glu Ile Ile Gln Gln Leu Ala Lys Gly Leu
 305 310 315 320
 Thr Val Ile Arg Gly Thr Asp Glu Gln Leu Val Glu Val Leu Glu Gln
 325 330 335
 Leu Pro Arg Thr Arg Val Ile Val Ala Pro His Ala Ala Asp Leu Phe

340	345	350
Asp Gln Ser Val Arg Asp Asn Val His Pro Val Ala Glu Val Ala Glu		
355	360	365
Lys Ala Ile Glu Val Ala Ser Cys Asp Asp Ile Pro Gly Gly Ser Ser		
370	375	380
Lys Ile Val Gly Glu Gly Gly Arg Leu Leu Ser Gly Gly Gln Arg Gln		
385	390	395
Arg Val Ala Leu Ala Arg Ala Ile Ala Phe Asp Pro Glu Val Leu Val		
405	410	415
Leu Gln Asp Pro Thr Thr Ala Val Asp Ser Val Thr Glu Gln Asn Ile		
420	425	430
Ala Gln Gln Val Ala Ala His Arg Ala Gly Lys Val Thr Ile Val Phe		
435	440	445
Ser Glu Ala Pro Ala Trp Ser Ala Val Ala Asp Gln His Val Glu Ala		
450	455	460
Ala Ala Leu Arg Glu Val Met Lys		
465	470	

<210> 283

<211> 1470

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1447)

<223> RXN01190

<400> 283

cagggttttg atgagaacaa cacacaccgc ttcaagcatt ctgcgaagaa tgatcaggcg 60

gcagcggggc aaggttgcg	ttggcgcat	ctttttgggg	atg	tgg	cag	ctg	tgc	115
			Met	Trp	Gln	Leu	Ser	
			1				5	

gaa gca ttg gtg ccg att gcg att ggt ttg atc gtt gat cat gcg gtt	163
Glu Ala Leu Val Pro Ile Ala Ile Gly Leu Ile Val Asp His Ala Val	
10 15 20	

ctc aca aaa gat ctc cgc cga tta gtg gtc ggg ctt gtc gct ttt gtt	211
Leu Thr Lys Asp Leu Arg Arg Leu Val Val Gly Leu Val Ala Phe Val	
25 30 35	

gtg ctg ttt gtg gtg ttg agt ttt tct aat cgt ttc ggt tcg cgc gcg	259
Val Leu Phe Val Val Leu Ser Phe Ser Asn Arg Phe Gly Ser Arg Ala	
40 45 50	

ttg aat agg gcc gtg aac ttt gaa tcc cat gcg ctc cgc gta gag gta	307
Leu Asn Arg Ala Val Asn Phe Glu Ser His Ala Leu Arg Val Glu Val	
55 60 65	

gcc gat cat gcg ttg aag aat ctg gat ccg cgc aat ttg gtg cct ggc	355
---	-----

Ala	Asp	His	Ala	Leu	Lys	Asn	Leu	Asp	Pro	Arg	Asn	Leu	Val	Pro	Gly		
70					75					80					85		
gag	gtg	atg	tcg	cgg	tcc	acc	gca	gat	gcg	gat	tct	tcg	acg	cgt	att	403	
Glu	Val	Met	Ser	Arg	Ser	Thr	Ala	Asp	Ala	Asp	Ser	Ser	Thr	Arg	Ile		
				90					95					100			
ttc	ggg	cag	atc	gga	acc	ggg	gtt	tcg	gct	gcg	acg	gga	ttt	ctt	ggg	451	
Phe	Gly	Gln	Ile	Gly	Thr	Gly	Val	Ser	Ala	Ala	Thr	Gly	Phe	Leu	Gly		
			105					110					115				
gca	gcg	acc	tac	ctg	ttg	atc	agt	gac	tgg	ctg	gtc	ggg	ttg	ttg	gtg	499	
Ala	Ala	Thr	Tyr	Leu	Leu	Ile	Ser	Asp	Trp	Leu	Val	Gly	Leu	Leu	Val		
		120					125					130					
ctt	gtg	ctg	gta	ccg	atc	att	tcg	gga	gtg	gtt	gca	ctg	gct	agc	aag	547	
Leu	Val	Leu	Val	Pro	Ile	Ile	Ser	Gly	Val	Val	Ala	Leu	Ala	Ser	Lys		
	135					140					145						
ggc	att	tct	aaa	agg	agt	gtc	acc	cag	cag	gag	aag	ttg	gcg	gag	tct	595	
Gly	Ile	Ser	Lys	Arg	Ser	Val	Thr	Gln	Gln	Glu	Lys	Leu	Ala	Glu	Ser		
150					155					160					165		
ggg	gcg	cag	gca	agt	gac	atc	atg	atg	ggg	ctg	cgc	gtg	atc	aag	gcg	643	
Gly	Ala	Gln	Ala	Ser	Asp	Ile	Met	Met	Gly	Leu	Arg	Val	Ile	Lys	Ala		
				170					175					180			
atc	ggg	ggc	gag	cgt	tgg	gcc	gtg	aag	act	ttt	gaa	aag	gcg	tcg	cag	691	
Ile	Gly	Gly	Glu	Arg	Trp	Ala	Val	Lys	Thr	Phe	Glu	Lys	Ala	Ser	Gln		
			185					190					195				
gca	tca	gcg	aga	gcg	gcg	gtt	gat	act	gca	gtt	gct	tcg	ggc	aaa	gtc	739	
Ala	Ser	Ala	Arg	Ala	Ala	Val	Asp	Thr	Ala	Val	Ala	Ser	Gly	Lys	Val		
		200					205					210					
gct	ggg	att	ggg	gag	ttg	tcc	att	gcg	gtg	aat	ttg	gct	gcg	gtg	ttg	787	
Ala	Gly	Ile	Gly	Glu	Leu	Ser	Ile	Ala	Val	Asn	Leu	Ala	Ala	Val	Leu		
	215					220					225						
ttg	ctt	gct	ggg	tgg	cgg	gtc	acc	acg	ggg	gag	ttg	ggg	cct	ggc	cag	835	
Leu	Leu	Ala	Gly	Trp	Arg	Val	Thr	Thr	Gly	Glu	Leu	Gly	Pro	Gly	Gln		
230					235					240					245		
ttg	atc	gca	att	gtg	ggg	gtg	gcg	gtg	tat	ttg	tca	gag	ccg	att	cgc	883	
Leu	Ile	Ala	Ile	Val	Gly	Val	Ala	Val	Tyr	Leu	Ser	Glu	Pro	Ile	Arg		
				250					255					260			
ttg	ctg	agc	aac	tcg	att	aat	gcc	tca	gct	att	gcg	cac	ggg	gca	gcg	931	
Leu	Leu	Ser	Asn	Ser	Ile	Asn	Ala	Ser	Ala	Ile	Ala	His	Gly	Ala	Ala		
			265				270						275				
gag	cgg	gtg	gct	aat	ttc	tta	aac	ctc	gac	gaa	tct	cag	gca	cag	tac	979	
Glu	Arg	Val	Ala	Asn	Phe	Leu	Asn	Leu	Asp	Glu	Ser	Gln	Ala	Gln	Tyr		
		280					285					290					
gaa	agc	agc	gaa	aca	atc	aat	gac	ggc	gaa	ttc	ctc	gtc	atc	gtg	ccc	1027	
Glu	Ser	Ser	Glu	Thr	Ile	Asn	Asp	Gly	Glu	Phe	Leu	Val	Ile	Val	Pro		
	295					300					305						
cca	gcc	agc	acg	ctt	cca	cac	ggc	gac	aat	atc	ttg	gct	aca	cct	cat	1075	
Pro	Ala	Ser	Thr	Leu	Pro	His	Gly	Asp	Asn	Ile	Leu	Ala	Thr	Pro	His		

310	315	320	325	
gct gcc gac att ttc gaa ggt acc ttg cgg tca aat att tcc atg aat				1123
Ala Ala Asp Ile Phe Glu Gly Thr Leu Arg Ser Asn Ile Ser Met Asn	330	335	340	
cat gag gac aac gtg cca att gat ccg cag gta att cgc gct tct ggt				1171
His Glu Asp Asn Val Pro Ile Asp Pro Gln Val Ile Arg Ala Ser Gly	345	350	355	
ctg act gac atc att gag gtg gac gga ctt gat gcg ccg gtg cgc gat				1219
Leu Thr Asp Ile Ile Glu Val Asp Gly Leu Asp Ala Pro Val Arg Asp	360	365	370	
acg gga agc aat tta tcg ggt ggg cag cgt cag cga gtg gct ttg gcc				1267
Thr Gly Ser Asn Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Leu Ala	375	380	385	
agg gcg ttg cat gca gac gcg gaa gta ctg gtg ctg atg gat cca acc				1315
Arg Ala Leu His Ala Asp Ala Glu Val Leu Val Leu Met Asp Pro Thr	395	400	405	
agc gcg gtg gat tca gtg acg gag gtg tct atc gcg cag ggg att aag				1363
Ser Ala Val Asp Ser Val Thr Glu Val Ser Ile Ala Gln Gly Ile Lys	410	415	420	
cag ctg cga gca ggc aaa acc acc att gtg gtg agt tct tcg ccc gcg				1411
Gln Leu Arg Ala Gly Lys Thr Thr Ile Val Val Ser Ser Ser Pro Ala	425	430	435	
ttt tac aac ttg gcg gat ccg gtg att tca cat gtc taatttgatg				1457
Phe Tyr Asn Leu Ala Asp Arg Val Ile Ser His Val	440	445		
gcacatcatcga cac				1470

<210> 284

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

Met	Trp	Gln	Leu	Ser	Glu	Ala	Leu	Val	Pro	Ile	Ala	Ile	Gly	Leu	Ile
1				5					10					15	

Val	Asp	His	Ala	Val	Leu	Thr	Lys	Asp	Leu	Arg	Arg	Leu	Val	Val	Gly
			20					25					30		

Leu	Val	Ala	Phe	Val	Val	Leu	Phe	Val	Val	Leu	Ser	Phe	Ser	Asn	Arg
		35					40					45			

Phe	Gly	Ser	Arg	Ala	Leu	Asn	Arg	Ala	Val	Asn	Phe	Glu	Ser	His	Ala
	50					55				60					

Leu	Arg	Val	Glu	Val	Ala	Asp	His	Ala	Leu	Lys	Asn	Leu	Asp	Pro	Arg
65					70					75				80	

Asn	Leu	Val	Pro	Gly	Glu	Val	Met	Ser	Arg	Ser	Thr	Ala	Asp	Ala	Asp
				85					90					95	

Ser Ser Thr Arg Ile Phe Gly Gln Ile Gly Thr Gly Val Ser Ala Ala
 100 105 110
 Thr Gly Phe Leu Gly Ala Ala Thr Tyr Leu Leu Ile Ser Asp Trp Leu
 115 120 125
 Val Gly Leu Leu Val Leu Val Leu Val Pro Ile Ile Ser Gly Val Val
 130 135 140
 Ala Leu Ala Ser Lys Gly Ile Ser Lys Arg Ser Val Thr Gln Gln Glu
 145 150 155 160
 Lys Leu Ala Glu Ser Gly Ala Gln Ala Ser Asp Ile Met Met Gly Leu
 165 170 175
 Arg Val Ile Lys Ala Ile Gly Gly Glu Arg Trp Ala Val Lys Thr Phe
 180 185 190
 Glu Lys Ala Ser Gln Ala Ser Ala Arg Ala Ala Val Asp Thr Ala Val
 195 200 205
 Ala Ser Gly Lys Val Ala Gly Ile Gly Glu Leu Ser Ile Ala Val Asn
 210 215 220
 Leu Ala Ala Val Leu Leu Leu Ala Gly Trp Arg Val Thr Thr Gly Glu
 225 230 235 240
 Leu Gly Pro Gly Gln Leu Ile Ala Ile Val Gly Val Ala Val Tyr Leu
 245 250 255
 Ser Glu Pro Ile Arg Leu Leu Ser Asn Ser Ile Asn Ala Ser Ala Ile
 260 265 270
 Ala His Gly Ala Ala Glu Arg Val Ala Asn Phe Leu Asn Leu Asp Glu
 275 280 285
 Ser Gln Ala Gln Tyr Glu Ser Ser Glu Thr Ile Asn Asp Gly Glu Phe
 290 295 300
 Leu Val Ile Val Pro Pro Ala Ser Thr Leu Pro His Gly Asp Asn Ile
 305 310 315 320
 Leu Ala Thr Pro His Ala Ala Asp Ile Phe Glu Gly Thr Leu Arg Ser
 325 330 335
 Asn Ile Ser Met Asn His Glu Asp Asn Val Pro Ile Asp Pro Gln Val
 340 345 350
 Ile Arg Ala Ser Gly Leu Thr Asp Ile Ile Glu Val Asp Gly Leu Asp
 355 360 365
 Ala Pro Val Arg Asp Thr Gly Ser Asn Leu Ser Gly Gly Gln Arg Gln
 370 375 380
 Arg Val Ala Leu Ala Arg Ala Leu His Ala Asp Ala Glu Val Leu Val
 385 390 395 400
 Leu Met Asp Pro Thr Ser Ala Val Asp Ser Val Thr Glu Val Ser Ile
 405 410 415
 Ala Gln Gly Ile Lys Gln Leu Arg Ala Gly Lys Thr Thr Ile Val Val

	420		425		430
Ser Ser Ser Pro Ala Phe Tyr Asn Leu Ala Asp Arg Val Ile Ser His					
435		440		445	

Val

<210> 285
 <211> 1368
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1345)
 <223> RXN01102

<400> 285
 attctatggg tgttgggaga gatgacttaa tttggaatca cgggcttttaa cacgcgctga 60
 cattgagcaa cttcccagca tgtggaaaag cccaggtttc gtg gct gtc ctc gtg 115
 Val Ala Val Leu Val 5
 1
 gcg gtt gca gca gcg ttc ggc agt tgg tca ctc ctt ctt ccc gtc gta 163
 Ala Val Ala Ala Ala Phe Gly Ser Trp Ser Leu Leu Leu Pro Val Val 20
 10 15
 ccg cta gcg gtc ctc aac aac ggc gga tca agc gct gtc gcc ggt gcc 211
 Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser Ala Val Ala Gly Ala 35
 25 30
 acc act ggc atc ttc atg gca gct aca gtg atc act cag att ttc act 259
 Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile Thr Gln Ile Phe Thr 50
 40 45
 ccc gct gcg ctg cgg aaa att ggc tac acc cca gtg atg gct ttc gcc 307
 Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro Val Met Ala Phe Ala 65
 55 60
 gca ttc atg ctg ggt gtg cca gcc atc ggg tac atc ttc agc gtc gag 355
 Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr Ile Phe Ser Val Glu 85
 70 75 80
 cca att cca gtg ctg gta gtg tcc gca ctt cga gga att ggg ttc ggt 403
 Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg Gly Ile Gly Phe Gly 100
 90 95
 gcg ctc acc gtc gca gaa tct gcg ttg gtg gct gaa ctc gtt ccc gta 451
 Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala Glu Leu Val Pro Val 115
 105 110
 cgc ttc ttg ggc aaa gct tct gga atg ttg ggc gta ttt att ggc ctt 499
 Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly Val Phe Ile Gly Leu 130
 120 125
 tcc caa atg ctt ttc ctg cct gcc ggg ttg gcg tta ggt gac caa ttt 547
 Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala Leu Gly Asp Gln Phe 145
 135 140

ggc tac aac gtg gtc tat gtt tta ggt gcc gtt atc gca cta gtt gca	595
Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val Ile Ala Leu Val Ala	
150 155 160 165	
gcg gtg atg tgt ctg cgt att ccg cag gtt aag gca gcg gca aag cag	643
Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys Ala Ala Lys Gln	
170 175 180	
caa cca cag gtg agc gaa cag gag cgt tct gtt tcc acc tgg aag ttg	691
Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val Ser Thr Trp Lys Leu	
185 190 195	
gtg ctg gtt ccc tcc ttg gct gtt acc agt ttg tca atg act ttt ggc	739
Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu Ser Met Thr Phe Gly	
200 205 210	
gca gtg tct tca ttc ctt cca gct gca gtc att gag tta gat cca gga	787
Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile Glu Leu Asp Pro Gly	
215 220 225	
tta ggt gct gca tta gcg ggt att att tta tcc att acc ggt ggt tct	835
Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser Ile Thr Gly Gly Ser	
230 235 240 245	
tca atg gtg ttc cgc tac ctg tcc ggc gtt atc gct gac cgc cgc ggt	883
Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile Ala Asp Arg Arg Gly	
250 255 260	
gtg cct ggt acc acg atg att cct gct cag atc att ggg ttc tta ggt	931
Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile Ile Gly Phe Leu Gly	
265 270 275	
gtc gtt tta atc acc gtc aca atc ttc caa ggc tgg tcc gtg tgg ctt	979
Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly Trp Ser Val Trp Leu	
280 285 290	
ttg att ata ggt gca gtg atg ttt ggt ggt gct ttt ggc atg gtg caa	1027
Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala Phe Gly Met Val Gln	
295 300 305	
aac gaa gcg ttg ctt tca atg ttt ttc cgg ctt cct cgc act aga gtc	1075
Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu Pro Arg Thr Arg Val	
310 315 320 325	
tcc gaa gcc tcc gcc atc tgg aat atc gcc ttt gat tcg gga aca gga	1123
Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe Asp Ser Gly Thr Gly	
330 335 340	
atc gga agc ttc ctc ctt ggc ata gtt gcc gca tcg ctt gct tac agt	1171
Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala Ser Leu Ala Tyr Ser	
345 350 355	
ggg gct ttt ggt tcc gga gcc gtg gtg att ttg ttt gga atc gtt ttg	1219
Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu Phe Gly Ile Val Leu	
360 365 370	
acc acc gcc gat cga atc att ggg cgg cac cgc att act gaa tac aac	1267
Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg Ile Thr Glu Tyr Asn	
375 380 385	

aac acc cgc gcg cgt ttg cgc cag gtg cca gtc gct cgg cgt gca gtg 1315
 Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val Ala Arg Arg Ala Val
 390 395 400 405

caa ggg ctg cgc aac agg cgc aaa gat cgc taaaacgctt ttcgacgcca 1365
 Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
 410 415

ccc 1368

<210> 286

<211> 415

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

Val Ala Val Leu Val Ala Val Ala Ala Phe Gly Ser Trp Ser Leu
 1 5 10 15

Leu Leu Pro Val Val Pro Leu Ala Val Leu Asn Asn Gly Gly Ser Ser
 20 25 30

Ala Val Ala Gly Ala Thr Thr Gly Ile Phe Met Ala Ala Thr Val Ile
 35 40 45

Thr Gln Ile Phe Thr Pro Ala Ala Leu Arg Lys Ile Gly Tyr Thr Pro
 50 55 60

Val Met Ala Phe Ala Ala Phe Met Leu Gly Val Pro Ala Ile Gly Tyr
 65 70 75 80

Ile Phe Ser Val Glu Pro Ile Pro Val Leu Val Val Ser Ala Leu Arg
 85 90 95

Gly Ile Gly Phe Gly Ala Leu Thr Val Ala Glu Ser Ala Leu Val Ala
 100 105 110

Glu Leu Val Pro Val Arg Phe Leu Gly Lys Ala Ser Gly Met Leu Gly
 115 120 125

Val Phe Ile Gly Leu Ser Gln Met Leu Phe Leu Pro Ala Gly Leu Ala
 130 135 140

Leu Gly Asp Gln Phe Gly Tyr Asn Val Val Tyr Val Leu Gly Ala Val
 145 150 155 160

Ile Ala Leu Val Ala Ala Val Met Cys Leu Arg Ile Pro Gln Val Lys
 165 170 175

Ala Ala Ala Lys Gln Gln Pro Gln Val Ser Glu Gln Glu Arg Ser Val
 180 185 190

Ser Thr Trp Lys Leu Val Leu Val Pro Ser Leu Ala Val Thr Ser Leu
 195 200 205

Ser Met Thr Phe Gly Ala Val Ser Ser Phe Leu Pro Ala Ala Val Ile
 210 215 220

Glu Leu Asp Pro Gly Leu Gly Ala Ala Leu Ala Gly Ile Ile Leu Ser
 225 230 235 240

Ile Thr Gly Gly Ser Ser Met Val Phe Arg Tyr Leu Ser Gly Val Ile
 245 250 255
 Ala Asp Arg Arg Gly Val Pro Gly Thr Thr Met Ile Pro Ala Gln Ile
 260 265 270
 Ile Gly Phe Leu Gly Val Val Leu Ile Thr Val Thr Ile Phe Gln Gly
 275 280 285
 Trp Ser Val Trp Leu Leu Ile Ile Gly Ala Val Met Phe Gly Gly Ala
 290 295 300
 Phe Gly Met Val Gln Asn Glu Ala Leu Leu Ser Met Phe Phe Arg Leu
 305 310 315 320
 Pro Arg Thr Arg Val Ser Glu Ala Ser Ala Ile Trp Asn Ile Ala Phe
 325 330 335
 Asp Ser Gly Thr Gly Ile Gly Ser Phe Leu Leu Gly Ile Val Ala Ala
 340 345 350
 Ser Leu Ala Tyr Ser Gly Ala Phe Gly Ser Gly Ala Val Val Ile Leu
 355 360 365
 Phe Gly Ile Val Leu Thr Thr Ala Asp Arg Ile Ile Gly Arg His Arg
 370 375 380
 Ile Thr Glu Tyr Asn Asn Thr Arg Ala Arg Leu Arg Gln Val Pro Val
 385 390 395 400
 Ala Arg Arg Ala Val Gln Gly Leu Arg Asn Arg Arg Lys Asp Arg
 405 410 415

<210> 287

<211> 348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(325)

<223> RXN00788

<400> 287

cgcatccctc tagttttcca tcacctcaat gaacggcgct aactccggtt cattgcgcaa 60

ttgatccagc actgcttgca gtgaggcctc attagttggc atg gcc tcc tcc atc 115
 Met Ala Ser Ser Ile
 1 5

aac atc gga gtg ttc aac ctt gga aat gct gtt gct gcc tgg ctt gct 163
 Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val Ala Ala Trp Leu Ala
 10 15 20

ggt gca acc atc acc act tcc ctt gga ctc aca tca gcc gga tta gtt 211
 Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr Ser Ala Gly Leu Val
 25 30 35

ggc ggt ttg atg acg tcc ctc gga cta gtg ttg gcc atc gtg gct gtg 259

Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu Ala Ile Val Ala Val
 40 45 50

gtt ttg cgt cga aaa gcg caa ggc acc caa gcg acc atc agc gtt gtg 307
 Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala Thr Ile Ser Val Val
 55 60 65

gag cac cag ccc gcc caa taaataattt ctctcttcta att 348
 Glu His Gln Pro Ala Gln
 70 75

<210> 288

<211> 75

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

Met Ala Ser Ser Ile Asn Ile Gly Val Phe Asn Leu Gly Asn Ala Val
 1 5 10 15

Ala Ala Trp Leu Ala Gly Ala Thr Ile Thr Thr Ser Leu Gly Leu Thr
 20 25 30

Ser Ala Gly Leu Val Gly Gly Leu Met Thr Ser Leu Gly Leu Val Leu
 35 40 45

Ala Ile Val Ala Val Val Leu Arg Arg Lys Ala Gln Gly Thr Gln Ala
 50 55 60

Thr Ile Ser Val Val Glu His Gln Pro Ala Gln
 65 70 75

<210> 289

<211> 1764

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1741)

<223> RXN02119

<400> 289

ttcgggtccgc tctggcaaaa atggctggct gccacctcgg cgcagcagct taagggctgg 60

gcttaaattg cttgtcgacg cctagtgccca caatggagac atg acc gaa aca ctt 115
 Met Thr Glu Thr Leu
 1 5

gtg gtg aat ggc ctt gca ggc ggc tat ggg cac cgc aca tta ttt aac 163
 Val Val Asn Gly Leu Ala Gly Gly Tyr Gly His Arg Thr Leu Phe Asn
 10 15 20

gat gtg aat ctc acc gta gct gcc ggc gat gtc gtg ggc gtt gtc ggc 211
 Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val Val Gly Val Val Gly
 25 30 35

gtc aat ggc gct ggt aaa tcc aca ttt cta aaa att ctg gcg ggc gtg 259
 Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys Ile Leu Ala Gly Val

40	45	50	
gaa aag cca ctg gct gga act atc gcg ctt tcg cca gcc gat gct ttt Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser Pro Ala Asp Ala Phe 55 60 65			307
gtg ggc tac ttg cca cag gaa cac acc cgc acg tct gga gag acg atc Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr Ser Gly Glu Thr Ile 70 75 80 85			355
gca gtt tac att gct cgt cga acc ggc tgc caa gct gca aca act gcc Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln Ala Ala Thr Thr Ala 90 95 100			403
atg gat gac acc gcc gaa gcg ttt ggt gcg gat cca gac aac gct gcc Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp Pro Asp Asn Ala Ala 105 110 115			451
ttg gcc gat gca tac gcc gag gcg ctg gat cgg tgg atg gcc agt ggc Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg Trp Met Ala Ser Gly 120 125 130			499
gca gcc gat ttg gat gaa cgc atc ccc atc gtg ctc gct gat ttg ggc Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val Leu Ala Asp Leu Gly 135 140 145			547
ttt gag ctt ccc acc tcg acg ctg atg gaa gga ctt tca ggc ggg cag Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly Leu Ser Gly Gly Gln 150 155 160 165			595
gca gcc cgg gtc ggg ctg gcg gcg tta ctg ttg tca cgt ttt gac att Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu Ser Arg Phe Asp Ile 170 175 180			643
gtg ctt ctc gac gag ccc acc aac gat ttg gat ctc gac ggt ctt gag Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Leu Asp Gly Leu Glu 185 190 195			691
caa ctg gag aat ttt gtt cag ggg ctt cgc ggg gga gtc gta ctg gtc Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly Gly Val Val Leu Val 200 205 210			739
agc cat gat cgt gag ttt ctt tcc agg tgt gtg acc act gtg ctg gaa Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val Thr Thr Val Leu Glu 215 220 225			787
ctc gat ctg cac caa aat tcc cac cat gtt tat ggc ggt gga tat gat Leu Asp Leu His Gln Asn Ser His His Val Tyr Gly Gly Gly Tyr Asp 230 235 240 245			835
tcc tac ctt gag gaa cgc gca gtg cta cgc cag cac gcc cgt gac caa Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln His Ala Arg Asp Gln 250 255 260			883
tat gag gaa ttt gcg gaa aag aag aag gac ctt gtg gca cgt gct cga Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu Val Ala Arg Ala Arg 265 270 275			931
acg cag cgt gaa tgg tct agt cac ggt gtc cgc aat gct att aaa cgt Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg Asn Ala Ile Lys Arg 280 285 290			979

gca cct gac aac gac aaa ctt cgg aag aaa gcc gct gcg gaa tcc agt	1027
Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala Ala Ala Glu Ser Ser	
295 300 305	
gaa aag cag gct caa aaa gtc cgc cag atg gaa agc cgc atc gct cgg	1075
Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu Ser Arg Ile Ala Arg	
310 315 320 325	
tta gaa gaa gtt gaa gag cca cgt aaa gaa tgg aaa ctg cag ttc agc	1123
Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp Lys Leu Gln Phe Ser	
330 335 340	
gtc ggt aag gcg tcg cgg tca agt tct gtt gtt tcc acg ttg aat gat	1171
Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val Ser Thr Leu Asn Asp	
345 350 355	
gca agc ttc acc caa ggc gat ttc acc ttg gga cca gta tcc atc caa	1219
Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly Pro Val Ser Ile Gln	
360 365 370	
gta aat gct ggc gat cgc att ggc atc aca gga ccc aac ggt gct ggt	1267
Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly Pro Asn Gly Ala Gly	
375 380 385	
aaa tcc aca ttg ctg cgc gga cta ttg gga aac caa gaa ccc acc agc	1315
Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn Gln Glu Pro Thr Ser	
390 395 400 405	
ggt act gcc acg atg ggc acg agc gtg gcg atc gga gaa atc gat cag	1363
Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile Gly Glu Ile Asp Gln	
410 415 420	
gca cga gcg tta ctt gat cca cag ttg cca ctg att tct gcg ttt gaa	1411
Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu Ile Ser Ala Phe Glu	
425 430 435	
aag cat gtt cca gac tta ccg atc agt gag gtg cgc aca ctg ctc gcg	1459
Lys His Val Pro Asp Leu Pro Ile Ser Glu Val Arg Thr Leu Leu Ala	
440 445 450	
aaa ttt ggg ctg aat gat aat cat gtg gaa cgg gac gtc gaa aag cta	1507
Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg Asp Val Glu Lys Leu	
455 460 465	
tct cct ggc gag cgc acg cgc gcc gga ctt gcg ctg cta cag gtg cgg	1555
Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala Leu Leu Gln Val Arg	
470 475 480 485	
ggc gtc aac gtg ctt gtt ctt gat gag ccc acc aac cac ctt gac ctg	1603
Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr Asn His Leu Asp Leu	
490 495 500	
gag gcc atc gag caa ttg gag caa gcg ttg gcc tcg tat gat ggt gtg	1651
Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala Ser Tyr Asp Gly Val	
505 510 515	
ttg ctg ctg gtc acg cac gat cgt cgc atg ttg gac gct gtg cag acc	1699
Leu Leu Leu Val Thr His Asp Arg Arg Met Leu Asp Ala Val Gln Thr	
520 525 530	

aat cgt cgt tgg cat gtc gag gct ggc gaa gtt agg gag cta 1741
 Asn Arg Arg Trp His Val Glu Ala Gly Glu Val Arg Glu Leu
 535 540 545

taaccgtttc cgtattgatg cca 1764

<210> 290
 <211> 547
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 290
 Met Thr Glu Thr Leu Val Val Asn Gly Leu Ala Gly Gly Tyr Gly His
 1 5 10 15
 Arg Thr Leu Phe Asn Asp Val Asn Leu Thr Val Ala Ala Gly Asp Val
 20 25 30
 Val Gly Val Val Gly Val Asn Gly Ala Gly Lys Ser Thr Phe Leu Lys
 35 40 45
 Ile Leu Ala Gly Val Glu Lys Pro Leu Ala Gly Thr Ile Ala Leu Ser
 50 55 60
 Pro Ala Asp Ala Phe Val Gly Tyr Leu Pro Gln Glu His Thr Arg Thr
 65 70 75 80
 Ser Gly Glu Thr Ile Ala Val Tyr Ile Ala Arg Arg Thr Gly Cys Gln
 85 90 95
 Ala Ala Thr Thr Ala Met Asp Asp Thr Ala Glu Ala Phe Gly Ala Asp
 100 105 110
 Pro Asp Asn Ala Ala Leu Ala Asp Ala Tyr Ala Glu Ala Leu Asp Arg
 115 120 125
 Trp Met Ala Ser Gly Ala Ala Asp Leu Asp Glu Arg Ile Pro Ile Val
 130 135 140
 Leu Ala Asp Leu Gly Phe Glu Leu Pro Thr Ser Thr Leu Met Glu Gly
 145 150 155 160
 Leu Ser Gly Gly Gln Ala Ala Arg Val Gly Leu Ala Ala Leu Leu Leu
 165 170 175
 Ser Arg Phe Asp Ile Val Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp
 180 185 190
 Leu Asp Gly Leu Glu Gln Leu Glu Asn Phe Val Gln Gly Leu Arg Gly
 195 200 205
 Gly Val Val Leu Val Ser His Asp Arg Glu Phe Leu Ser Arg Cys Val
 210 215 220
 Thr Thr Val Leu Glu Leu Asp Leu His Gln Asn Ser His His Val Tyr
 225 230 235 240
 Gly Gly Gly Tyr Asp Ser Tyr Leu Glu Glu Arg Ala Val Leu Arg Gln
 245 250 255

His Ala Arg Asp Gln Tyr Glu Glu Phe Ala Glu Lys Lys Lys Asp Leu
 260 265 270
 Val Ala Arg Ala Arg Thr Gln Arg Glu Trp Ser Ser His Gly Val Arg
 275 280 285
 Asn Ala Ile Lys Arg Ala Pro Asp Asn Asp Lys Leu Arg Lys Lys Ala
 290 295 300
 Ala Ala Glu Ser Ser Glu Lys Gln Ala Gln Lys Val Arg Gln Met Glu
 305 310 315 320
 Ser Arg Ile Ala Arg Leu Glu Glu Val Glu Glu Pro Arg Lys Glu Trp
 325 330 335
 Lys Leu Gln Phe Ser Val Gly Lys Ala Ser Arg Ser Ser Ser Val Val
 340 345 350
 Ser Thr Leu Asn Asp Ala Ser Phe Thr Gln Gly Asp Phe Thr Leu Gly
 355 360 365
 Pro Val Ser Ile Gln Val Asn Ala Gly Asp Arg Ile Gly Ile Thr Gly
 370 375 380
 Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Arg Gly Leu Leu Gly Asn
 385 390 395 400
 Gln Glu Pro Thr Ser Gly Thr Ala Thr Met Gly Thr Ser Val Ala Ile
 405 410 415
 Gly Glu Ile Asp Gln Ala Arg Ala Leu Leu Asp Pro Gln Leu Pro Leu
 420 425 430
 Ile Ser Ala Phe Glu Lys His Val Pro Asp Leu Pro Ile Ser Glu Val
 435 440 445
 Arg Thr Leu Leu Ala Lys Phe Gly Leu Asn Asp Asn His Val Glu Arg
 450 455 460
 Asp Val Glu Lys Leu Ser Pro Gly Glu Arg Thr Arg Ala Gly Leu Ala
 465 470 475 480
 Leu Leu Gln Val Arg Gly Val Asn Val Leu Val Leu Asp Glu Pro Thr
 485 490 495
 Asn His Leu Asp Leu Glu Ala Ile Glu Gln Leu Glu Gln Ala Leu Ala
 500 505 510
 Ser Tyr Asp Gly Val Leu Leu Leu Val Thr His Asp Arg Arg Met Leu
 515 520 525
 Asp Ala Val Gln Thr Asn Arg Arg Trp His Val Glu Ala Gly Glu Val
 530 535 540
 Arg Glu Leu
 545

<210> 291

<211> 1638

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1615)

<223> RXN01605

<400> 291

```

attgaagtca ggcgcgagga agccgcgagg gaatcagacg acggggcacct actacttcgg 60
cattgaaatt ccgaagaact tcagcgattc tattgccagc gtg acc agc gat tca 115
                               Val Thr Ser Asp Ser
                               1 5

ccc gcg cca gca acc gtc aac gcg gta ttc aac aac agc aac ggc ttc 163
Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn Asn Ser Asn Gly Phe
                               10 15 20

att gcc tcc atg ctg ggc aac cag gtg gtc aac act gtt gtg gag acc 211
Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn Thr Val Val Glu Thr
                               25 30 35

atg gac acg gaa ttc ggc gtc cgc att gtg gat aac atg ctc gtc ggt 259
Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp Asn Met Leu Val Gly
                               40 45 50

ttc tcc acc ttg ggc gac ggc atg aac caa gcc gcc gaa ggt gcc act 307
Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala Ala Glu Gly Ala Thr
                               55 60 65

acg ctc agc gat ggc gtc ggt tcc gcc aac gac ggt gca gtt cag ctt 355
Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp Gly Ala Val Gln Leu
                               70 75 80 85

gcc gac ggc gcg gtc acc ctg cgc gac ggc atc gca agt gcc aat gag 403
Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile Ala Ser Ala Asn Glu
                               90 95 100

ggt gcg caa tcg ctt gcc gac ggc gcc agc cag ctc gac acc ggc ctc 451
Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln Leu Asp Thr Gly Leu
                               105 110 115

ggc tcc gcg gct aca ggc agc caa acg ctc gcc gac ggt cta tcc agc 499
Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala Asp Gly Leu Ser Ser
                               120 125 130

ctg tct gcg ggc acc gcc caa cta ggc caa ggc gca acc cag gtt tca 547
Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly Ala Thr Gln Val Ser
                               135 140 145

gat ggc gtg ggc caa ctt gtc gac caa gta gca cca ctg acc gcc tat 595
Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala Pro Leu Thr Ala Tyr
                               150 155 160 165

gtt cca gac atc aac tct cag ttg atc acc ctg cgc gac ggc gca gcc 643
Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu Arg Asp Gly Ala Ala
                               170 175 180

acc att gcc tct gaa cta tct gat ccc tcc agc acc tac cgc tcc ggc 691
Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser Thr Tyr Arg Ser Gly
                               185 190 195

```

gtg gac tcc gct gtg agc gca tcc cag caa cta gca gcc ggc ctg caa	739
Val Asp Ser Ala Val Ser Ala Ser Gln Gln Leu Ala Ala Gly Leu Gln	
200 205 210	
acc ctg aaa gac gga tcc agc caa ctc agc atc ggt gca cgc acc ctc	787
Thr Leu Lys Asp Gly Ser Ser Gln Leu Ser Ile Gly Ala Arg Thr Leu	
215 220 225	
gct gat ggc acc agc caa ttg gcc gca ggt tcc gaa cag cta gtt gtt	835
Ala Asp Gly Thr Ser Gln Leu Ala Ala Gly Ser Glu Gln Leu Val Val	
230 235 240 245	
ggc gca caa gca ctg cgc gac ggc acc gtc cag ctt gat gaa ggc tcc	883
Gly Ala Gln Ala Leu Arg Asp Gly Thr Val Gln Leu Asp Glu Gly Ser	
250 255 260	
agc gaa ctc gcc ctc aaa ctc acc gac ggc gca agc caa gta cca acc	931
Ser Glu Leu Ala Leu Lys Leu Thr Asp Gly Ala Ser Gln Val Pro Thr	
265 270 275	
ttc gct gac ggc gca gac acc acc atc gca acc cca gtt gaa aca gaa	979
Phe Ala Asp Gly Ala Asp Thr Thr Ile Ala Thr Pro Val Glu Thr Glu	
280 285 290	
caa gca gga gac acc aca ccg ctc ttc ggt att ggt ctc gca cca ttc	1027
Gln Ala Gly Asp Thr Thr Pro Leu Phe Gly Ile Gly Leu Ala Pro Phe	
295 300 305	
ttc atg gct gtc ggc ctg ttc atg gga gca acc gtt gcc tgg atg atc	1075
Phe Met Ala Val Gly Leu Phe Met Gly Ala Thr Val Ala Trp Met Ile	
310 315 320 325	
ctg cac cca atc agt cgc cgc gca ctc gac tcc cgc atg gga ggc ttc	1123
Leu His Pro Ile Ser Arg Arg Ala Leu Asp Ser Arg Met Gly Gly Phe	
330 335 340	
cga ggc acc ctg gca agc tac ctt cca tca aca gtc tta ggc ctt ggc	1171
Arg Gly Thr Leu Ala Ser Tyr Leu Pro Ser Thr Val Leu Gly Leu Gly	
345 350 355	
caa gca acc atc atg tgg gca gta ctg tac ttc ctg ctc gac ctc aat	1219
Gln Ala Thr Ile Met Trp Ala Val Leu Tyr Phe Leu Leu Asp Leu Asn	
360 365 370	
cca gct cac cca gct gga ctg tgg atg gcg atg gtc gcc atc tca tgg	1267
Pro Ala His Pro Ala Gly Leu Trp Met Ala Met Val Ala Ile Ser Trp	
375 380 385	
gta ttc atc tcc att acc cat atg ttc aac aac gtg gca gga ccc tcc	1315
Val Phe Ile Ser Ile Thr His Met Phe Asn Asn Val Ala Gly Pro Ser	
390 395 400 405	
gca ggc cgt gtg ctg tcc atc gtg atg atg tcc ttc cag cta gtc tcc	1363
Ala Gly Arg Val Leu Ser Ile Val Met Met Ser Phe Gln Leu Val Ser	
410 415 420	
tcc ggt ggc cta tac cca cca gaa acc cag cca gca ttc ttc cac tgg	1411
Ser Gly Gly Leu Tyr Pro Pro Glu Thr Gln Pro Ala Phe Phe His Trp	
425 430 435	

ttc cac acc tac gac ccg atc acc tac gca gtc aac ctc gtg cgc caa 1459
 Phe His Thr Tyr Asp Pro Ile Thr Tyr Ala Val Asn Leu Val Arg Gln
 440 445 450

atg atc ttc aac gaa acc cca tcc aac gac cca cgc ttc ata caa gca 1507
 Met Ile Phe Asn Glu Thr Pro Ser Asn Asp Pro Arg Phe Ile Gln Ala
 455 460 465

atc tgg gta ctg ctc ttc atc tgg gca ctg atg ctc gcc atc tcc acc 1555
 Ile Trp Val Leu Leu Phe Ile Trp Ala Leu Met Leu Ala Ile Ser Thr
 470 475 480 485

ctg gcg aat aga aca aac aag gtt ctt cgc atg aag gac tac cac cca 1603
 Leu Ala Asn Arg Thr Asn Lys Val Leu Arg Met Lys Asp Tyr His Pro
 490 495 500

gaa ctg aag gtc taaaagcttt tcccgcccggtt 1638
 Glu Leu Lys Val
 505

<210> 292

<211> 505

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 292

Val Thr Ser Asp Ser Pro Ala Pro Ala Thr Val Asn Ala Val Phe Asn
 1 5 10 15

Asn Ser Asn Gly Phe Ile Ala Ser Met Leu Gly Asn Gln Val Val Asn
 20 25 30

Thr Val Val Glu Thr Met Asp Thr Glu Phe Gly Val Arg Ile Val Asp
 35 40 45

Asn Met Leu Val Gly Phe Ser Thr Leu Gly Asp Gly Met Asn Gln Ala
 50 55 60

Ala Glu Gly Ala Thr Thr Leu Ser Asp Gly Val Gly Ser Ala Asn Asp
 65 70 75 80

Gly Ala Val Gln Leu Ala Asp Gly Ala Val Thr Leu Arg Asp Gly Ile
 85 90 95

Ala Ser Ala Asn Glu Gly Ala Gln Ser Leu Ala Asp Gly Ala Ser Gln
 100 105 110

Leu Asp Thr Gly Leu Gly Ser Ala Ala Thr Gly Ser Gln Thr Leu Ala
 115 120 125

Asp Gly Leu Ser Ser Leu Ser Ala Gly Thr Ala Gln Leu Gly Gln Gly
 130 135 140

Ala Thr Gln Val Ser Asp Gly Val Gly Gln Leu Val Asp Gln Val Ala
 145 150 155 160

Pro Leu Thr Ala Tyr Val Pro Asp Ile Asn Ser Gln Leu Ile Thr Leu
 165 170 175

Arg Asp Gly Ala Ala Thr Ile Ala Ser Glu Leu Ser Asp Pro Ser Ser

		180					185					190				
Thr	Tyr	Arg 195	Ser	Gly	Val	Asp	Ser 200	Ala	Val	Ser	Ala	Ser 205	Gln	Gln	Leu	
Ala	Ala 210	Gly	Leu	Gln	Thr	Leu 215	Lys	Asp	Gly	Ser	Ser 220	Gln	Leu	Ser	Ile	
Gly 225	Ala	Arg	Thr	Leu	Ala 230	Asp	Gly	Thr	Ser	Gln 235	Leu	Ala	Ala	Gly	Ser 240	
Glu	Gln	Leu	Val	Val 245	Gly	Ala	Gln	Ala	Leu 250	Arg	Asp	Gly	Thr	Val 255	Gln	
Leu	Asp	Glu	Gly 260	Ser	Ser	Glu	Leu	Ala 265	Leu	Lys	Leu	Thr	Asp 270	Gly	Ala	
Ser	Gln 275	Val	Pro	Thr	Phe	Ala 280	Asp	Gly	Ala	Asp	Thr	Thr 285	Ile	Ala	Thr	
Pro 290	Val	Glu	Thr	Glu	Gln	Ala 295	Gly	Asp	Thr	Thr	Pro 300	Leu	Phe	Gly	Ile	
Gly 305	Leu	Ala	Pro	Phe	Phe 310	Met	Ala	Val	Gly	Leu 315	Phe	Met	Gly	Ala	Thr 320	
Val	Ala	Trp	Met	Ile 325	Leu	His	Pro	Ile	Ser 330	Arg	Arg	Ala	Leu	Asp 335	Ser	
Arg	Met	Gly	Gly 340	Phe	Arg	Gly	Thr	Leu 345	Ala	Ser	Tyr	Leu 350	Pro	Ser	Thr	
Val	Leu	Gly 355	Leu	Gly	Gln	Ala 360	Thr	Ile	Met	Trp	Ala 365	Val	Leu	Tyr	Phe	
Leu 370	Leu	Asp	Leu	Asn	Pro	Ala 375	His	Pro	Ala	Gly	Leu 380	Trp	Met	Ala	Met	
Val 385	Ala	Ile	Ser	Trp	Val 390	Phe	Ile	Ser	Ile	Thr 395	His	Met	Phe	Asn	Asn 400	
Val	Ala	Gly	Pro	Ser 405	Ala	Gly	Arg	Val	Leu 410	Ser	Ile	Val	Met	Met 415	Ser	
Phe	Gln	Leu	Val 420	Ser	Ser	Gly	Gly	Leu 425	Tyr	Pro	Pro	Glu	Thr 430	Gln	Pro	
Ala	Phe 435	Phe	His	Trp	Phe	His	Thr 440	Tyr	Asp	Pro	Ile	Thr 445	Tyr	Ala	Val	
Asn 450	Leu	Val	Arg	Gln	Met	Ile 455	Phe	Asn	Glu	Thr	Pro 460	Ser	Asn	Asp	Pro	
Arg 465	Phe	Ile	Gln	Ala	Ile 470	Trp	Val	Leu	Leu	Phe 475	Ile	Trp	Ala	Leu	Met 480	
Leu	Ala	Ile	Ser	Thr 485	Leu	Ala	Asn	Arg	Thr 490	Asn	Lys	Val	Leu	Arg 495	Met	
Lys	Asp	Tyr	His 500	Pro	Glu	Leu	Lys	Val 505								

<400> 293																
tcgtcgcgaaa aactggcgat actattgata acgggcatgg gttcaccttc gataaagcac 60																
ggctctatgct ggactatcgc cttttgacac gagtatcgca atg gtc ccg aac aca 115																
Met Val Pro Asn Thr 5																
gtc ctt atc cat gac gaa acc gcc gat ctg gcg acg cag atc cag cgg 163																
Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala Thr Gln Ile Gln Arg 20																
ctg gaa cat atc atg gcg tgc ctg cgc gat ccg gtc agc gga tgc ccg 211																
Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro Val Ser Gly Cys Pro 35																
tgg gat att gaa cag acc ttt gcc agc atc gcg ccc cac acg att gag 259																
Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala Pro His Thr Ile Glu 50																
gaa ggc tac gag gtt gcc gac gcc atc gcg cag gaa gac tgg ccc gag 307																
Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln Glu Asp Trp Pro Glu 65																
cta cgc ggc gag ttg ggc gat ttg ctg ttt cag acc gtg ttt cac gcc 355																
Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln Thr Val Phe His Ala 85																
caa atg gcg cgc gag gca ggc cat ttc gct ttg gtt gac gtg gtg aag 403																
Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu Val Asp Val Val Lys 100																
gca att tcg gac aag atg gtt ttg cgc cat ccg cac gtg ttc ggc gcg 451																
Ala Ile Ser Asp Lys Met Val Leu Arg His Pro His Val Phe Gly Ala 115																
cag tcg aac gcg aaa tcc gcc gac cag cag gtg gaa gat tgg gaa gtc 499																
Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val Glu Asp Trp Glu Val 130																
atc aag gcg ccc gag cgc gcg ggc aaa gcg caa aag ggc gtt ttg gat 547																
Ile Lys Ala Pro Glu Arg Ala Gly Lys Ala Gln Lys Gly Val Leu Asp 145																
ggc gtc gcg ctg gga ctg cct gcc ctg atg cgc gcg acg aag ctg caa 595																
Gly Val Ala Leu Gly Leu Pro Ala Leu Met Arg Ala Thr Lys Leu Gln 165																
aac aac gcc gcg cgc gtt ggg ttt gat tgg ccc gac att ggg cag gta 643																
Asn Asn Ala Ala Arg Val Gly Phe Asp Trp Pro Asp Ile Gly Gln Val																

170 175 180 664

ctt gga aag gtg acc gag gaa
 Leu Gly Lys Val Thr Glu Glu
 185

<210> 294
 <211> 188
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 294
 Met Val Pro Asn Thr Val Leu Ile His Asp Glu Thr Ala Asp Leu Ala
 1 5 10 15
 Thr Gln Ile Gln Arg Leu Glu His Ile Met Ala Cys Leu Arg Asp Pro
 20 25 30
 Val Ser Gly Cys Pro Trp Asp Ile Glu Gln Thr Phe Ala Ser Ile Ala
 35 40 45
 Pro His Thr Ile Glu Glu Gly Tyr Glu Val Ala Asp Ala Ile Ala Gln
 50 55 60
 Glu Asp Trp Pro Glu Leu Arg Gly Glu Leu Gly Asp Leu Leu Phe Gln
 65 70 75 80
 Thr Val Phe His Ala Gln Met Ala Arg Glu Ala Gly His Phe Ala Leu
 85 90 95
 Val Asp Val Val Lys Ala Ile Ser Asp Lys Met Val Leu Arg His Pro
 100 105 110
 His Val Phe Gly Ala Gln Ser Asn Ala Lys Ser Ala Asp Gln Gln Val
 115 120 125
 Glu Asp Trp Glu Val Ile Lys Ala Pro Glu Arg Ala Gly Lys Ala Gln
 130 135 140
 Lys Gly Val Leu Asp Gly Val Ala Leu Gly Leu Pro Ala Leu Met Arg
 145 150 155 160
 Ala Thr Lys Leu Gln Asn Asn Ala Ala Arg Val Gly Phe Asp Trp Pro
 165 170 175
 Asp Ile Gly Gln Val Leu Gly Lys Val Thr Glu Glu
 180 185

<210> 295
 <211> 357
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(334)
 <223> RXS02979

<400> 295

ctagggtcaag gaacttcact cggctagtcc ttagactcaa atgtgttcag acaaactg 60
gcaccgtaag gcacgaaagt taccgaaagg actgggtccc atg acc gcc cca aac 115
Met Thr Ala Pro Asn
1 5
act ctc aag caa aca act ctt cgc tct gat gag ttc tct tgc cca tcc 163
Thr Leu Lys Gln Thr Thr Leu Arg Ser Asp Glu Phe Ser Cys Pro Ser
10 15 20
tgt gtc tcc aag att gaa aac aaa ttg aat gga ttg gat ggc gtc gac 211
Cys Val Ser Lys Ile Glu Asn Lys Leu Asn Gly Leu Asp Gly Val Asp
25 30 35
aat gca gag gtg aag ttc tcc tcc gga aga atc ctt gtt gat cac gac 259
Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile Leu Val Asp His Asp
40 45 50
ccc agc aag gtc tct atc aag gat cta gtc gct gca gtc gca gag gtt 307
Pro Ser Lys Val Ser Ile Lys Asp Leu Val Ala Ala Val Ala Glu Val
55 60 65
ggc tac acc gca aag cca tca gca atc taaaactctc agttagacca 354
Gly Tyr Thr Ala Lys Pro Ser Ala Ile
70 75
tta 357

<210> 296

<211> 78

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

Met Thr Ala Pro Asn Thr Leu Lys Gln Thr Thr Leu Arg Ser Asp Glu
1 5 10 15
Phe Ser Cys Pro Ser Cys Val Ser Lys Ile Glu Asn Lys Leu Asn Gly
20 25 30
Leu Asp Gly Val Asp Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile
35 40 45
Leu Val Asp His Asp Pro Ser Lys Val Ser Ile Lys Asp Leu Val Ala
50 55 60
Ala Val Ala Glu Val Gly Tyr Thr Ala Lys Pro Ser Ala Ile
65 70 75

<210> 297

<211> 357

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(334)

<223> RXS02987

<400> 297

```

gttggttgat ccagggtcaag gaattaaccc ggaaaggacc gtatctttaa aggtgcaagc 60
acaggaacat gacgataaaa gatgaaagga cctgggttacg atg acc gcc ccc gcc 115
                                     Met Thr Ala Pro Ala
                                     1                               5

acg ctg aag aac acc acc ttg cgc tct gat gag ttc acc tgt ccg agc 163
Thr Leu Lys Asn Thr Thr Leu Arg Ser Asp Glu Phe Thr Cys Pro Ser
                10                15                20

tgt gtc gcc aag atc gaa aac aag ctg aat ggt ttg gac ggc gtg gag 211
Cys Val Ala Lys Ile Glu Asn Lys Leu Asn Gly Leu Asp Gly Val Glu
                25                30                35

aat gcg gag gtg aag ttc tcc tcc gga cgc atc ctg atc acc cac gac 259
Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile Leu Ile Thr His Asp
                40                45                50

cca cag aag gtc tcc gta cgt gac ctg gtc acc gcg gta gcc gag gtc 307
Pro Gln Lys Val Ser Val Arg Asp Leu Val Thr Ala Val Ala Glu Val
                55                60                65

ggg tac acc gcc aag ccg tcg gcg atc tgacgcactc ccgacccac 354
Gly Tyr Thr Ala Lys Pro Ser Ala Ile
                70                75

aag 357

```

<210> 298

<211> 78

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

```

Met Thr Ala Pro Ala Thr Leu Lys Asn Thr Thr Leu Arg Ser Asp Glu
  1                5                10                15

Phe Thr Cys Pro Ser Cys Val Ala Lys Ile Glu Asn Lys Leu Asn Gly
      20                25                30

Leu Asp Gly Val Glu Asn Ala Glu Val Lys Phe Ser Ser Gly Arg Ile
      35                40                45

Leu Ile Thr His Asp Pro Gln Lys Val Ser Val Arg Asp Leu Val Thr
      50                55                60

Ala Val Ala Glu Val Gly Tyr Thr Ala Lys Pro Ser Ala Ile
      65                70                75

```

<210> 299

<211> 492

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(469)

<223> RXS03095

<400> 299

aacgcctcaa ttagtgccag accttgccga cgcgagacca aacttcacca tttcaaacca 60

tccctagcca caacaacggc agttgtgcaa tgatctgcgt atg aat gca gat aag 115
 Met Asn Ala Asp Lys
 1 5

aaa atg tgc gga atg aac ccg gat agc caa tac gtc gaa ctt gcc gtc 163
 Lys Met Cys Gly Met Asn Pro Asp Ser Gln Tyr Val Glu Leu Ala Val
 10 15 20

gaa gtt ttc gga ctc ctc gcg gac gcc act cga gtt cgc atc atc ttg 211
 Glu Val Phe Gly Leu Leu Ala Asp Ala Thr Arg Val Arg Ile Ile Leu
 25 30 35

gca ctt cga aac agt ggt gaa ctt tcc gta aac cac ctc gcg gac atc 259
 Ala Leu Arg Asn Ser Gly Glu Leu Ser Val Asn His Leu Ala Asp Ile
 40 45 50

gtc gat aaa tcc ccc gca gca gtt tcc caa cac ctc gcc cgg ctg cgc 307
 Val Asp Lys Ser Pro Ala Ala Val Ser Gln His Leu Ala Arg Leu Arg
 55 60 65

atg gcc cga atc gtg tcc acc cgt caa gaa ggt caa cga gtt ttc tac 355
 Met Ala Arg Ile Val Ser Thr Arg Gln Glu Gly Gln Arg Val Phe Tyr
 70 75 80 85

aaa ctc acc aat gaa cac gca tca cag cta gtc tcc gac gct att ttt 403
 Lys Leu Thr Asn Glu His Ala Ser Gln Leu Val Ser Asp Ala Ile Phe
 90 95 100

cag gcg gaa cac acc att gcg gac ggc cag act ccc cca cac cac cac 451
 Gln Ala Glu His Thr Ile Ala Asp Gly Gln Thr Pro Pro His His His
 105 110 115

cga gaa cga gaa caa tca tgaccacca cagtcaccaa gaa 492
 Arg Glu Arg Glu Gln Ser
 120

<210> 300

<211> 123

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

Met Asn Ala Asp Lys Lys Met Cys Gly Met Asn Pro Asp Ser Gln Tyr
 1 5 10 15

Val Glu Leu Ala Val Glu Val Phe Gly Leu Leu Ala Asp Ala Thr Arg
 20 25 30

Val Arg Ile Ile Leu Ala Leu Arg Asn Ser Gly Glu Leu Ser Val Asn
 35 40 45

His Leu Ala Asp Ile Val Asp Lys Ser Pro Ala Ala Val Ser Gln His
 50 55 60

Leu Ala Arg Leu Arg Met Ala Arg Ile Val Ser Thr Arg Gln Glu Gly
 65 70 75 80

Gln Arg Val Phe Tyr Lys Leu Thr Asn Glu His Ala Ser Gln Leu Val
 85 90 95

Ser Asp Ala Ile Phe Gln Ala Glu His Thr Ile Ala Asp Gly Gln Thr
 100 105 110

Pro Pro His His His Arg Glu Arg Glu Gln Ser
 115 120

<210> 301

<211> 10

<212> PRT

<213> Corynebacterium glutamicum

<400> 301

Ala Pro Ala Leu Gly Pro Thr Leu Ser Gly
 1 5 10

<210> 302

<211> 10

<212> PRT

<213> Corynebacterium glutamicum

<220>

<223> All occurrences of Xaa indicate any amino acid

<400> 302

Gly Xaa Xaa Xaa Gly Pro Xaa Xaa Gly Gly
 1 5 10

<210> 303

<211> 20

<212> DNA

<213> Corynebacterium glutamicum

<400> 303

ctccaggatt gctccgaagg

20

<210> 304

<211> 20

<212> DNA

<213> Corynebacterium glutamicum

<400> 304

cacagtgggt gaccactggc

20

<210> 305

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 305

ggaaacagta tgaccatg

18

<210> 306

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 306

gtaaaacgac ggccagt

18